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(54) Title: CELL DEATH RELATED DRUG TARGETS IN YEAST AND FUNGI

(57) Abstract: The invention describes the use of nucleic acids and polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi for the preparation of a medicament for treating diseases associated with yeast or fungi or for the treatment of proliferative disorders or for preventing apoptosis in certain diseases. Methods are provided to identify compounds which selectively modulate the expression or functionality of said polypeptides in the same or a parallel pathway. Also provided are compounds as well as pharmaceutical compositions, medicaments and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.

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CELL DEATH RELATED DRUG TARGETS IN YEAST AND FUNGI

The present invention relates to the identification of genes and proteins encoded thereof from yeast and fungi whose expression is modulated upon programmed cell death and which genes, proteins or functional fragments and equivalents thereof may be used as selective targets for drugs to treat infections caused by or associated with yeast and fungi or for the treatment of proliferative disorders or for the prevention of apoptosis in certain diseases.

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Invasive fungal infections (e.g. Candida spp, Aspergillus spp., Fusarium spp., Zygomycetes spp.) (Walsh, 1992) have emerged during the past two decades as important pathogens causing formidable morbidity and mortality in an increasingly diverse and progressively expanding population of immunocompromised patients. Those with the acquired immune deficiency syndrome (AIDS) constitute the most rapidly growing group of patients at risk for life-threatening mycosis. But fungal infections have also increased in frequency in several populations of other susceptible hosts, including very-low-birth-weight infants, cancer patients receiving chemotherapy, organ transplant recipients, burn patients and surgical patients with complications.

These fungal infections are not limited to humans and other mammals, but are also important in plants where they can cause diseases or cause the production of unwanted compounds (e.g. Fusarium spp., Aspergillus spp., Botritis spp., Cladosporium spp.).

Although recent advances in antifungal chemotherapy have had an impact on these mycoses, expanding populations of immunocompromised patients will require newer approaches to antifungal therapy. The discovery of novel antifungal agents is thus an essential element of any new antifungal therapy.

Classical approaches for identifying anti-fungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic, or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic model organism. These tests are cumbersome and provide no information about a compound's mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular target.

Cells from multicellular organisms can commit suicid in response to specific signals or injury by an intrinsic program of cell d ath. Apoptosis is a form of programmed c II death which leads to elimination of unnecessary or damaged cells. To

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survive, all cells from multicellular organisms depend on the constant repression of this suicide program by signals from other cells (Raff, 1992). It has been assumed that such an altruistic form of cell survival arose with multicellularity and would have been counterselected in unicellular organisms. Recent findings indicate, however, that a similar process of cell survival also operates in single-celled eukaryotes.

It has been found that expression of the mammalian Bax gene triggers cell death in Saccharomyces cerevisiae and the fission yeast Schizosaccharomyces pombe with morphological changes similar to apoptosis (Jürgensmeier et al., 1997). However, the mechanism of Bax lethality in S. cerevisiae remains unclear.

Since it has been discovered that the mammalian *Bax* gene triggers apoptotic changes in yeast (Ligr *et al.*, 1998), this can be an indication that the molecular pathways eventually leading to programmed cell death may also be partially present in yeast cells and other unicellular eukaryotes.

It is an aim of the present invention to provide nucleic acid as well as polypeptide sequences which represent potential molecular targets for the identification of new compounds which can be used in alleviating diseases or conditions associated with yeast or fungi infections.

It is a further aim of the present invention to provide uses of these nucleic acid and amino acid molecules for the preparation of a medicament for treating diseases associated with yeast or fungi.

It is also an aim of the invention to provide pharmaceutical compositions and vaccines comprising these nucleic acids or polypeptides.

It is also an aim of the present invention to provide vectors comprising these nucleic acids, as well as host cells transfected or transformed with said vectors.

It is also an aim of the invention to provide antibodies against these polypeptides, which can be used as such, or in a composition as a medicine for treating diseases associated with yeast and fungi.

It is another aim of the invention to provide methods to selectively identify compounds capable of inhibiting or activating expression of such polypeptides in yeast or fungi infections. The nucleic acid and polypeptide molecules alternatively can be incorporated into an assay or kit to identify these compounds.

It is also an aim of the invention to provide a method of preventing infection with yeast or fungi.

It is also an aim of the invention to provide probes and primers derived from the nucleic acid sequences of the invention.

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All the aims of the present invention have been met by the embodiments as set out below.

The present inventors identified a range of specific nucleotide sequences which are involved in the molecular pathways eventually leading to programmed cell death. The present inventors were able to identify via macro array screening a range of genes involved in a pathway eventually leading to programmed cell death in the yeast *Saccharomyces cerevisiae*. As explained in Example 2, genes showing a difference of a factor 5 or more in expression as a result of *Bax*-induced cell death, were identified as differentially expressed candidate genes. Some of these genes are clearly down-regulated in a *Bax*-expressing strain, while other genes show an upregulated expression (Table 1). Example 3 describes a further experiment wherein the results of differential expression were analysed using the PathwaysTM software and differentially expressed nucleic acid sequence were identified.

According to a first embodiment, the invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 20 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214. 25 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 30 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470. 472, 474, 476, 478, 480, 482, or 484, or encoding a functional guivalent. derivative or bioprecursor of said protein:
- 35 (b) a nucleic acid molecul encoding a protein having an amino acid sequence which is mor than 70% similar, preferably more than 75% or 80% similar, more

preferably more than 85%, 90% or 95% similar and most pref rably more than 97% similar to any of the amino acid sequenc s shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100. 5 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 10 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 15 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 20 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8. 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 25 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 30 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 35 484:

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- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 20 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 25 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275. 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 30 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;
 - (f) a nucleic acid sequenc encoding a functional fragment of any of the nucleic acid sequences as specified in a) to); and
- 35 (g) the complement of any of the nucleic acid sequences as sp cified in a) to f),

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for the preparation of a medicament for treating diseases associated with yeast or fungi.

Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using BLOSUM62 as a scoring matrix.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means the degree of sequence relatedness between two polypeptide or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton, 1988). Methods commonly employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux et al., 1984), BLASTP, BLASTN and FASTA (Altschul et al, 1990).

The nucleic acid sequences to be used according to this aspect of the invention from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 457, 459, 461, 463, 465, 467, 469, 471 and 473.

The invention also relates to nucleic acid sequences from *Candida albicans*, as repr sented by the SEQ ID NOs 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371,

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373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481, and 483.

The expression "a pathway eventually leading to programmed cell death" refers to a sequence of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, hydrogen peroxide, diamide and farnesol.

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The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy individuals as well as in immunocompromised patients.

The expression "treating diseases associated with yeast and fungi" not only refers to diseases or infections caused by said organisms but also refers to allergic reactions caused by said organisms, such as the so-called "professional diseases" in, for instance, bakery and brewery and that are caused by yeast or fungi which are commonly known as "non-pathogenic".

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 20 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 25 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483 but isolated from other yeast and fungi 30 strains which are also involved in a pathway eventually leading to programmed cell death.

According to the invention, these sequences and their homologues in other yeast and fungi as well as the polypeptides which they encode represent novel molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides.

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Furthermore, the invention also relates to the potential use of said sequences in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by Candida spp., Aspergillus spp., Microsporum spp., Trichophyton spp., Fusarium spp., Zygomycetes spp., Botritis spp., Cladosporium spp., Malassezia spp., Epidermophyton floccosum, Blastomyces dermatitidis, Coccidioides immitis, Histoplasma capsulatum, Paracoccidioides brasiliensis, Cryptococcus neoformans, and Sporothrix schenckii.

According to another embodiment, the invention also relates to a nucleic acid sequence encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;

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(d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481 or 483;

- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481 or 483; and.
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and
- (g) the complement of any of the nucleic acid sequences as specified in a) to f).

According to a more specific embodiment, these nucleic acid sequences are derived from Saccharomyces cerevisiae, Candida albicans or Aspergillus fumigatus.

A nucleic acid sequence according to the invention may comprise an mRNA sequence or alternatively a DNA sequence and preferably a cDNA sequence. A nucleic acid sequence according to the invention may also comprise any modified nucleotide known in the art.

The present invention further relates to a nucleic acid molecule capable of selectively hybridising to at least one of the nucleic acid molecules according to the invention, or the complement thereof.

The term "selectively hybridising" or "specifically hybridising means hybridising under conditions wherein sequences can be detected which are homologues of the sequences of the invention, but which are for instance derived from heterologous cells or organisms, and wherein said sequences do not hybridize with known sequences. In a preferred embodiment, mammalian homologues can be detected. It is well known to the person skilled in the art which methods for hybridisation can be used and which conditions ar necessary for selectively or specifically hybridising. Preferably, hybridization under high stringency conditions can be applied (Sambrook et al., 1989).

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As such, the present invention also relates to the use of the nucleic acid sequences of the invention for detecting homologues in heterologous organisms including but not limited to mammalian organisms.

The term "nucleic acid sequence" also includes the complementary sequence to any single stranded sequence given, or the antisense version thereof.

The invention also relates to mRNA, DNA or cDNA versions of the nucleic acid molecules of the invention.

The present invention more particularly relates to an antisense molecule comprising a nucleic acid sequence capable of hybridizing to any of the above defined nucleic acid sequences.

Polynucleotides according to the invention may be inserted into vectors in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense nucleic acids may also be produced by synthetic means.

The present invention also advantageously provides nucleic acid sequences of at least approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically with any of the nucleic acid molecules of the invention. The primers will specifically amplify any of the nucleic acid molecules of the invention.

The probes or primers according to the invention may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the sample.

According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different probes in discrete locations. Such arrays can be used to screen for compounds interacting with said probes.

Advantageously, the nucleic acid sequenc s, according to the invention may be produced using recombinant or synthetic means, such as for xample using PCR cloning m chanisms which generally involve making a pair of primers, which may be from approximat by 10 to 50 nucleotides to a region of the gene which is desired to be

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cloned, bringing the primers into contact with mRNA, cDNA, or genomic DNA from the yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined herein are well known in the art, such as described in Sambrook et al. (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ³²P, ³³P or ³⁵S, enzyme labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using techniques known in the art.

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According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to a control sequence, such as a suitable inducible promotor, or the like, to ensure expression of the proteins according to the invention in a suitable host cell. The expression vector may also comprise a reporter molecule. The expression vector may advantageously be a plasmid, cosmid, virus or other suitable vector which is known to those skilled in the art. The expression vector and the host cell defined herein also form part of the present invention. Preferably the host cell is a lower eukaryotic cell such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of the invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

The invention further relates to any nucleic acid as defined above for use as a medicament.

Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi-associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expr ssion of the corresponding polypeptides, leading to impaired growth or death of yeast and fungi with reductions of associated illnesses or diseases.

According to another embodiment, the invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 5 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 10 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 15 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of 20 said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 25 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 30 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 35 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,

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434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; and,
 - (d) a functional fragment of any of said proteins as defined in a) to c), for the preparation of a medicament for treating diseases associated with yeast or fungi.

The term "functional fragment" of a protein means a truncated version of the original protein or polypeptide referred to. The truncated protein sequence can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence. A functional fragment can also relate to a subunit with similar function as said protein. Typically, the truncated amino acid sequence will range from about 5 to about 60 amino acids in length. More typically, however, the sequence will be a maximum of about 50 amino acids in length, pref rably a maximum of about 60 amino acids. It is usually desirable to select sequences of at least about 10, 12 or 15 amino acids.

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Functional fragments include those comprising an epitope which is specific or unique for the proteins according to the invention. Epitopes may be determined using, for example, peptide scanning techniques as described in Geysen *et al.* (1996). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 50, 75, 100, 125, 150, 175 or 200 amino acids.

The polypeptides to be used according to this aspect of the invention from Saccharomyces cerevisiae, are represented by SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62. 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106. 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 458, 460, 462, 464, 466, 468, 470, 472 and 474. Also according to the invention is the use of the polypeptides from Candida albicans as represented by the SEQ ID NOs 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 476, 478, 480, 482 and 484.

The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative amino acid changes.

The nucleic acid molecules or the polypeptides of the invention may be provided in a pharmaceutically acceptable carrier, diluent or excipient therefor.

The present invention also relates to a vaccine for immunizing a mammal against infections caused by yeast and fungi comprising at least one (recombinant) nucleic acid molecule or at least one (recombinant) polypeptide of the invention in a pharmaceutically acceptable carrier.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carri rs ar typically large, slowly metabolizing macromolecules such as proteins, polysaccharldes, polylactic acids, polyglycolic acids, polymeric amino acids,

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amino acid copolymers; and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A "vaccine" is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete. A vaccine may also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions.

The term "therapeutic" refers to a composition capable of treating infections caused by yeast or fungi.

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Some of the pathways leading to apoptosis are conserved between mammalian cells and yeast or fungi. Therefore, targets which are part of such a conserved pathway may be used to stimulate or inhibit the apoptosis in mammalian cells. E.g. stimulation of apoptosis is desirable in the treatment of tumor cells/tissues.

According to another embodiment, the present invention provides a method of identifying compounds which selectively inhibit, induce or interfere with the expression/production of the polypeptides encoded by the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved. Compounds may carry agonistic or antagonistic properties. The compounds to be screened may be of extracellular, intracellular, biologic or chemical origin.

Such a screening method may comprise the following steps (a) contacting a compound to be tested with cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound, (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast of fungi cells is indicative of selective action of said compound on a polypeptide in the sam or a parall I pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

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The term "cells" as used above relat s to any type of cells such as, but not limited to bacterial, yeast, fungal, plant or human cells.

Compounds found using this approach may additionally be tested on their efficiency in killing or inhibiting the growth of wild type cells in order to confirm their utility as medicament for treating wild type pathogenic strains/tumor cells.

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According to the invention, the term "mutation" includes point mutations, deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or polypeptide. In case point mutations occur, the number of nucleotides will be identical compared to the original sequence; only a change in nucleotide sequence can be observed. This stands in contrast with the other listed mutations where the number of the nucleotides will be different from the number observed in the wild type sequence and consequently will also reflect in a change of the nucleotide sequence.

Changes in morphologic and/or functional properties of cell components which can be monitored include for example morphological and molecular changes such as abnormal cell morphology, nuclear fragmentation, DNA breakage or changes in the expression of certain enzymes such as caspases, as well as monitoring changes in membrane potential or activity of mitochondria and release of cytochrome c from mitochondria. All these changes can be monitored on the whole cell which is contacted to the compound to be tested.

The invention also relates to a method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound, (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected cells compound on a polypeptide in the same or a parallel pathway, (c) alt matively monitoring th growth, death rate or activity of said transformed, transf cted or infected cells compar d to transformed, transfected or infected cells which w r not contacted with the compound to be t sted, wherein

differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.

Alternative methods for identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said compounds are involved, may comprise the use of any other method known in the art resulting in gene activation, gene inactivation, gene modulation or gene silencing.

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The invention also relates to a method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene and (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested. This enables to analyse the influence of the compound onto all/most aspects of transcriptional activation. Alternatively additional tests can routinely be performed to test the influence of the compound onto mRNA stability, translation and protein stability. All these aspects influence the concentration of corresponding proteins and consequently influence the effect of these on the metabolism of the cell.

The invention further relates to a method of identifying compounds which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2, (b) detecting the complex formed between the compound to be tested and said polypeptide, (c) alternatively, examining the diminution/increase of complex formation between said polypeptide and a receptor/binding partner, caused by the addition of the compound being tested, (c) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.

Detection of the complex formation can be performed using several approaches. First, binding of a compound onto a polypeptide can be studied using classical binding tests: one of the binding partners, compound or polypeptide is labeled and interaction of both is m asured. Most of these tests comprise following st ps:

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incubating both binding partners in conditions where binding is allowed, separation of free label from bound label present in the complex formed between both partners, and measuring the number of labeled complexes formed. Separation of free and bound label can be performed via filtration, centrifugation or other means as known by the person skilled in the art. Other techniques allow visualisation of complex formation without the need of such a separating step. For example, test systems using SPA (scincillation proximity assay) beads are based on the principle that radioactive ³H can only be measured when present in scincillation fluid. SPA beads contain scincillation fluid and can be coated with one of the binding partners. When this bead is approached and binds the other binding partner which is radioactively labeled, a signal will be detected allowing the complex to be visualised. Binding of the radioactive compound onto the scincillation bead is needed in order to result in a detectable signal; non-bound radioactive partners that stay free into the solution will not result in a detectable signal.

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The protein or peptide fragments according to the invention employed in such a method may be for example in solution or coated on suspended beads as described above. Alternatively, these can be affixed to a solid support, borne on a cell or phage surface or located intracellularly.

When protein or peptide fragments are coated on solid supports, they can be tested for their binding affinity for large numbers of compounds. These can be used in different kinds of high throughput screenings in order to identify compounds having suitable binding affinity to the polypeptides according to the invention. Platform technologies or technologies based on SPR (see below) can be applied.

One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine the diminution or increase of complex formation between the protein according to the invention and a receptor/binding partner caused by the compound being tested.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

This technique is based on functional reconstitution in vivo of a transcription factor which activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, xpressing in the host cell a first hybrid DNA s qu nce needing a first fusion of a fragment or all of a nucleic acid sequence

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according to the invention and either said DNA binding domain or said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

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An example of such a technique utilizes the GAL4 protein in yeast. GAL4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a protein-binding domain. Nucleotide vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of GAL4. These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of GAL4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a GAL-4 transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as B-galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes. Altematively, other reporter proteins can be used such as EGFP (enhanced green fluorescent protein), or hEGFP. This latter has a decreased lifetime enabling the system to screen for compounds improving the interaction of studied binding partners.

The two-hybrid approach was first developed for yeast, and is an ideal screening system when looking for compounds active in killing yeast or fungi. Indeed, proteins expressed in this system will most probably carry the correct modifications as found in the pathogenic yeast strains. In addition, compounds active in this test system allow to screen and select compounds which are able to enter the cell, this selection is not possible when using *in vitro* test systems. When compounds are needed to target mammalian cells, modification of the studied proteins can be different, changing the structure of corr sponding proteins. Moreover working with y ast might block certain compounds to enter the cell, which are normally able to traverse the mammalian cell membran. Consequently, working with mammalian two-hybrid system for this purpose

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will give already an immediate selection of the compounds that may enter mammalian cells.

Alternative in vitro methods can be used to investigate protein - protein interactions. Protein interaction analysis in vitro can shed light on their role in the intact cell by providing valuable information on specificity, affinity, and structure-function relation ship. Significant process in this respect has become with the advent, in the last few years, of commercially available biosensor technology. This allows to study macromolecular interactions in real-time, providing a wealth of high-quality data that can be used for kinetic analysis, affinity measurements, competition studies, etc. A major advantage of biosensor analysis is that there is no requirement for labeling one of the interacting components and then separating bound from free molecules- a fact that simplifies experimental procedures and provides more accurate measurements. The principle of surface plasmon resonance (SPR) is based on the detection of a change of the refractive index of the medium when a compound or protein binds to an immobilised partner molecule. For the SPR technology, one needs to load one of the interacting partners to the chip surface, followed by the superfusion of the second binding partner or more molecules. The second partner can be available as purified product, but alternatively a complex suspension containing this partner can also be used. Interaction of two or more compounds can be analysed, alternatively, compounds can be identified interfering or increasing this binding affinity towards each other.

SPR is not restricted to protein-protein interactions; any macromolecule with a suitable size will change the refractive index of the medium in contact with the biosensor surface and therefore give a signal. Studies have been done with protein-DNA interactions, as well as protein-lipid interactions. Moreover intact viruses, abd even cells, can also be injected over the biosensor surface, in order to analyse their binding to receptors, lectins, and so on.

Alternatively, NMR is also an excellent tool for a detailed study of protein-protein or DNA-protein interactions. Isotope edited or isotope filtered experiments whereby one compound is isotopically labeled with 15N or 13C are an ideal way to study these complexes. This method does not allow high throughput analysis of compounds interfering or enhancing molecular interactions. Nevertheless, medium or low throughput systems can be used to confirm results obtained by the high throughout assays or in cases wher none of the binding partn rs are labeled. Oth r techniqu s which can be used to study interactions ar : overlay, ligand blotting, band-shift, co-

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immuno-precipitation, size exclusion chromatography and microcalorimetry (In. "Protein trageting Protocols" Ed. Clegg R.A. Humana Press, Totowa, New Yersey).

Compounds modulating pathways leading to apoptosis may change the activity of the polypeptide of the invention. Therefore screening tests may be setup looking for altered protein activity of the polypeptide of the invention. Based on the amino acid sequence a possible function of the polypeptide might be envisaged; activities can be confirmed and corresponding activity test can be started.

Alternatively additional tests can be performed to test the influence of the compound onto protein stability, post-translational modification, precursor processing and protein translocation. All these aspects influence the concentration and/or activity of corresponding proteins and consequently influence the effect of these onto the metabolism of the cell. Also here, medium or low throughput systems can be used to confirm results obtained by the high throughout assays.

In cases compounds need to be found to target tumor cells, screening assays will have to be used focused on the stimulation of the apoptotic pathway. This invention therefore also relates to in vitro and in vivo model systems comprising tumor tissue or cells expressing the polypeptides according to the invention which can be used to screen for therapeutic agents. In vivo modelsystems allow to test for compound efficacity but also the toxicity of these compounds can be tested. The compounds identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from Saccharomyces cerevisiae, Schizosaccharomyces pombe, Candida albicans, or Aspergillus fumigatus.

The invention also relates to a compound identified using any of the methods of the invention.

Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament. The invention also relates to a method for treating diseases associated with yeast or fungi comprising admixing a compound obtainable by a m thod of the invention with a suitable pharmac utically acceptable carrier.

Th compounds of the invention can be used for th preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections,

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for instance Candida spp., Aspergillus spp., Microsporum spp., Trichophyton spp., Fusarium spp., Zygomycetes spp., Botritis, spp., Cladosporium spp., Malassezia spp., Epidermophyton floccosum, Blastomyces dermatitidis, Coccidioides immitis, Histoplasma capsulatum, Paracoccidioides brasiliensis, Cryptococcus neoformans, and Sporothrix schenckii infections.

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These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

A medicament according to the invention not only relates to fungistatic compounds for treating humans or mammals but also relates to fungicides for treating plants.

The invention also relates to genetically modified yeast or fungi in which modification results in the overexpression or underexpression of at least one of the nucleic acids or polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified yeast or fungi. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament for prophylactic or therapeutic use.

Also according to the invention is the use of a compound obtainable by a method of the invention for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

According to another embodiment, the invention also relates to an isolated protein which is involved in a pathway for programmed cell death of yeast or fungi selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482, or 484 or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably mor than 75% or 80% similar, more pr ferably mor than 85%, 90 or 95% similar and most pr ferably more than 90% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304,

306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482, or 484;

- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482, or 484; and,
- 15 (d) a functional fragment of any of said proteins as defined in a) to c).

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According to the invention, the polypeptides as defined above may be used as a medicament.

Also encompassed within the present invention are antibodies, monoclonal or polyclonal, capable of specifically binding to one or more epitopes of the proteins of the invention. The term "specific binding" implies that there is substantially no cross-reaction of the antibody with other proteins.

The antibodies according to the invention may be produced according to techniques which are known to those skilled in the art. Monoclonal antibodies may be prepared using conventional hybridoma technology as described by Kohler and Milstein (1979). Polyclonal antibodies may also be prepared using conventional technology well known to those skilled in the art, and which comprises inoculating a host animal, such as a mouse, with a protein or epitope according to the invention and recovering the immune serum. The present invention also includes fragments of whole antibodies which maintain their binding activity, such as for example, Fv, F(ab') and F(ab')₂ fragments as well as single chain antibodies.

Antibodies according to the invention may also be used in a method of detecting the presence of a polypeptide according to the invention, which method comprises reacting the antibody with a sample and identifying any protein bound to said antibody. A kit may also be provided for performing said method which comprises an antibody according to the inv ntion and means for reacting the antibody with said sample.

The antibodies according to the invention may be used as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may be used in the preparation of a medicament for treating diseases associated with yeast and fungi such as, but not restricted to, Candida albicans, Aspergillus spp., Fusarium spp., Botritis, spp., Cladosporium spp.

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The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response.

According to another embodiment, the invention relates to a genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of the invention or a human homologue thereof or at least one of the polypeptides of the invention or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

Human homologues according to the invention can be obtained by selective hybridisation of the yeast and candida nucleic acid molecules of the invention against human genome or cDNA libraries according to methods well known in the art (Sambrook et al., 1989). Human polypeptide homologues are obtained from the corresponding human nucleic acid homologous nucleotide sequences.

The invention also relates to a method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of the invention or a human homologue thereof and/or at least one of the polypeptides of the invention or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism as described in the invention.

The invention further relates to the compounds identifiable according to the above-described method and its use as a medicament.

The invention further relates to a method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 40 or 41 with a suitable pharmaceutically acceptable carrier.

The xpression "proliferative disorders" or "proliferative diseases" r fers to an abnormality within a patient or animal such as cancer. Normal c IIs start to proliferate du to a change in the coding or non-coding sequenc of the DNA resulting in a swollen or distend d tissue. Mutation may arise without obvious cause. An abnormal

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benign or malignant mass of tissue is formed that is not inflammatory. Cells of preexistent tissue start to divide unexpectedly and resulting cell mass possesses no physiologic function.

The expression "apoptosis" or "apoptosis-related diseases" includes diseases such as autoimmunity diseases, ischemia, diseases related with viral infections or neurodegenerations.

The invention also relates to the use of compounds obtainable by the above described methods for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.

According to another embodiment, the invention relates to the use of a nucleic acid molecule or a polypeptide described in the invention or human homologues thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

The invention also relates to a pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule of the invention or a human homologue thereof or a polypeptide of the invention or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.

The invention also relates to a vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule of the invention or a human homologue thereof or at least one polypeptide of the invention or a human analogue thereof in a pharmaceutically acceptable carrier.

The invention also relates to the use of an antibody of the invention capable of binding to at least one of the polypeptides of the invention or a human homologue thereof for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

According to yet another embodiment, the invention relates to an expression vector comprising a human homologue of a nucleic acid sequence of the invention. Said expression vector may comprise an inducible promoter and may further comprise a sequence encoding a reporter molecule.

The invention also relates to a host cell transformed, transfected or infected with any of the above described vectors.

According to another mbodiment the invention r lates to a nucleic acid molecule comprising a human homologue of at least on of th nucl ic acid sequences described in the invention.

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The invention also relates to an antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to a nucleic acid molecule which is a human analogue of the invention.

The invention also relates to a polypeptide encoded by the nucleic acid molecule comprising said human homologues of the nucleic acids described in the invention.

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The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are hereby incorporated by reference.

FIGURE AND TABLE LEGENDS

- Figur 1. Saccharomyces cerevisiae sequences based on information obtained from the Saccharomyces Genome Database (SGD) (SEQ ID Nos 1 to 284)
- Figure 2. Candida albicans sequences (SEQ ID Nos 285 to 456).
- 5 Figure 3. Yeast genome macroarray containing a total of 6144 gene ORFs spotted on 2 nylon membrane filters. The filters are cut in the upper right corner for orientation and the DNA is on the labelled side of the filter. Each filter contains 2 fields and each field is divided into 8 grids, organised in 24 rows and 8 columns.
- The spots represent the genome wide expression profile without (A) and with (B) Bax modulated expression (Example 2).
 - Figure 4. Results from a second experiment analogous and analysed as described in the examples section (Example 3).
- 15 Table 1. Genes modulated by Bax expression in S. cerevisiae. This list includes all the genes for which mRNA levels changed more than fivefold in a first experiment (see Example 2). The factor by which the transcript level was affected, is expressed as the Qt value. A Qt value higher than 1 indicates upregulation while a Qt value lower than 1 indicates a downregulation. For instance, a Qt of 0.5 indicates a two-fold lower transcript level of a particular mRNA due to Bax expression in S. cerevisiae. Upregulation or downregulation of a specific mRNA is stated when Qt had a value of at least five or at most 0,21, respectively.
- 25 <u>Table 2.</u> Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed significantly in a second experiment (see Example 3). In this experiment, the Qt values were calculated using the Pathways Software (Research Genetics).

EXAMPLES

Exampl 1. Differential g n xpr ssion analysis upon Bax-induced cell death Materials and media

Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980) was used for the construction and the amplification of plasmids. Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cereviseae* strain INVSc1 (Invitrogen®) was transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with YIpUTyL or_YIpUTYLMuBax, after linearisation in the Ty δ element (Zhu, 1986).

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Cloning of mouse BAX cDNA

Mouse *Bax* cDNA, encoding the mouse Bax-α protein, was cloned by Pfu DNA polymerase (Stratagene®) chain reaction amplification (PCR) from an EL4/13.18 thymoma cDNA library (BCCMTM/LMBP-LIB15) by making use of the primers:

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5'-ATGGACGGGTCCGGGAGCAG-3' and

5'-TCAGCCCATCTTCTTCCAGATGGTGAG-3'.

The resulting PCR product was cloned in a *Hin*cll-openend pUC19 according to standard procedures (Sambrook J. *et al.*, 1989).

20 Plasmid constructions

The 2μ ori and the *URA3* marker gene were removed from pUT332 (Gatignol *et al.*, 1990) by successive digestions with *Cla*l and *Bgl*II. A *Bam*HI-*Hin*dIII GAL1 promoter fragment was ligated into the *Bgl*II-*Hin*dIII-opened plasmid. A *Xba*I-*Fsp*I FLP terminator fragment was inserted into this *Xba*I-*Hin*dIII(blunted)-opened plasmid so that the plasmid YIpUT was obtained. Insertion of a blunted *Eco*RI-*Bsa*AI Ty δ element in the *Kpn*I-*Aat*II-opened and blunted YIpUT resulted in the plasmid YIpUTy. Subsequent insertion of the *LEU2* marker gene, as a blunted *Bsa*AI-*Bsr*GI fragment, in the *Bam*HI-opened and blunted YIpUTy resulted in the plasmid YIpUTyL.

Mouse Bax cDNA was excised from pUC19 by digestion with Xbal and Hindll and subcloned into the Xbal-HindllI-opened plasmid YlpUTyL, obtaining the final expression plasmid YlpUTyLMuBax.

The plasmid YlpUTyLMuBax has been deposited in the BCCM[™]/LMBP culture collection as p5CTyGALmBax with accession number 3871 under restricted us .

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GeneFilters

The Yeast GeneFilters[™] were purchased from Research Genetics Inc. (Huntsville, AL, USA).

The Yeast GeneFilters[™] are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon membrane filters (Filter I and II). The filters are cut in the upper right corner and the DNA is on the labeled side of the filter.

Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8 columns.

Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3 and 4 are organized in the same way as fields 1 and 2.

The Yeast ORF target

The yeast filters consist of over 6000 PCR products corresponding to 6144 yeast ORFs derived from the SGD. The PCR reactions used ORF specific primer pairs designed to amplify the entire open reading frame. The primers were generated from unique sequences containing the start codon ATG and termination codon (kindly provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains the complete open reading frame including the start and stop codons. These products were purified and resuspended at 50 nanograms per microliter in a colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

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Results

Induction of Bax-expression in yeast cells

S. cerevsiae cells (strain INVSc1) were transformed with the expression plasmid YIpUTyLMuBax or the parental plasmid YIpUTyL as a negative control. Alternative yeast strains (such as W303-1A (Thomas and Rothstein, 1989)) with equivalent properties are known in the art and can also be used.

Th Ty δ lement of both plasmids allowed a stable multi-copy integration in the g nome of the yeast cell. Southern analysis of the cells containing YlpUTyLMuBax revealed the integration of 5 GAL1-controlled Bax-cassettes near Ty lem nts.

The yeast cells containing YIpUTyLMuBax and the yeast cells containing YIpUTyL were grown overnight in in 10 ml minimal glucose-containing medium. The precultures were then further diluted to an OD₆₀₀ of 0,2 in 100 ml minimal glucose-containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells containing YIpUTyL were washed and a dilution thereof was transferred into 100 ml galactose-containing medium and incubated for 15 hours. After this additional period the cultures reached an OD₆₀₀ of 1. The yeast cells containing YipUTyLMuBax were also washed and transferred into 100 ml galactose-containing medium and incubated for 15 hours.

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· RNA isolation

Total RNA was isolated using RNApureTM Reagent (Genhunter Corporation Nashville, TN, USA) according to the GenHunter protocol. 1.5 10⁹ cells were concentrated in a microcentrifuge tube and 1ml RNApureTM Reagent was added together with 1 g of glass pearls. The yeast cells were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNA digestion. Chloroform (150 μl) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA pellet was resuspended in 50 μl RNAse free dH₂O.

First strand cDNA synthesis in the presence of α -33P dCTP

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Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1 YIpUTyLMuBax or INVSc1 YIpUTyL yeast cells and incorporation of α -33P dCTP as follows: 2 μ I (1 μ g/ml) of Oligo dT was added to 20 μ g of total RNA in a maximal volume of 8 μ I RNase-free dH₂O and incubated at 70°C for 10 min. After cooling down on ice for 1 min, the following components were added:

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- 6 µl 5x concentrated First Strand Buffer (GIBCO-BRL)
- 1 µl 0,1 M DTT
- 1 μl RNase Block (40 units/μl) (Stratagene)
- 1,5 µl 20 mM dXTP-solution (X = A, G and T) (Pharmacia)
- 1,5 μl SuperScriptTM Revers Transcriptase (200 units/μl) (GIBCO-BRL)
- 35 10 μ l α -33P dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham)

and incubated f r 2 h at 37°C during which first strand cDNA synthesis took place.

Unincorporated label was separated from the probe on a Sephadex G-50 column (Pharmacia). The radioactivity incorporated in the probe was measured by liquid scintillation. The specific activity of the probes was 3 or 5 108 cpm/µg for both the INVSc1YIpUTyL and the INVSc1YIpUTyLMuBax probe.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

Hybridisation with the S. cerevisiae Yeast GeneFilters™ and signal detection

The Yeast GeneFiltersTM were successively hybridised with the α-³³P dCTP labelled cDNA probes using the MicroHybTM solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during hybridisation. The MicroHyb solution contains formamide to allow hybridisation to occur at lower temperatures.

The hybridisation experiment was performed essentially as follows: during prehybridisation, the Yeast GeneFiltersTM were placed in a hybridisation flask (35x250 mm) filled with 5 or 10 ml MicroHybTM solution (42°C) containing 5 µl polydA (0,5 or 1 µg/ml) and incubated for 24 hours at 42°C whilst rotating (10 rpm). After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating. Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third wash step was performed in a second wash buffer (0,5x SSC, 1% SDS) for an additional 15 min at room temperature. The Yeast GeneFiltersTM were placed in a PhosphorImagerTM cassette with storage phosphorscreen. After 4 days of development the screen was developed and scanned using the PhosphorImagerTM 455 SI from Molecular Dynamics. The results of these can be seen in Figure 3.

In-between the hybridisation experiments, the filters were stripped off by incubation in 500 ml of a 0,5% SDS solution (prewarmed to near boiling temperature) during at least 1 hour at room temperature.

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Quantification of the hybridisation signals was done using the ImageQuantTM 4.1 software tool from Molecular Dynamics (Sunnyvale, CA). The quantification was performed per grid of the Yeast GeneFiltersTM, and by drawing a roster of 24 columns and 8 rows onto each grid of each filter. As such, each rectangle of the roster corresponds to a spot on the Yeast GeneFiltersTM. Subsequently, from each grid a volume-report (quantification) was drawn up and the data were transferred to a MicrosoftTM Excel sheet. Also for each grid a correction factor was calculated. Signals neighboring big and dark spots were separately quantified. For each grid, a background level was calculated.

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Statistical processing of quantification results

The statistical processing of the results was accomplished in MicrosoftTM Excel. For each grid, the following statistical functions were separately defined:

- 1. The frequency of occurrence of the values in a precisely defined intensity range(data range), established between 1000 and 61000, split up in intervals of 5000.
 - 2. The frequency in terms of percentage.
 - 3. The cumulated frequency in terms of percentage.

These numeric values were used for the graphical display of the cumulated frequency in terms of percentage.

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Subsequently, the results of the two experiments (hybridization with cDNA from YIpUTyL containing INVSc1 cells and hybridization with cDNA from YIpUTyLMuBax containing INVSc1 cells) were integrated by determination of a second range of statistical functions:

- 1. The average of the values of the two experiments for each spot on the filter.
- 2. The standard deviation on this average. This is a measure for the distribution of the values around this average.
- 3. The standard deviation in terms of percentage.

The quotient of the values of the second experiment (Bax expression) against the values from the first experiment (control) was determined. This immediately ave the factor by which the expression of a specific gene is changed upon Bax induction.

In order to process all these data and to be able to discriminate between differences in gene expression, a gene showing a standard deviation in terms of percentage of at least 90% and a difference of a factor 5 in expression as a result of Bax induction, was identified as a differentially expressed candidat gene. (Table 1). Requantification of these candidates confirmed their selection.

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When the expression patt rn of all 6144 gen s is compared in the two experiments, it could be concluded that the expression profile f 142 genes (this is 2,3%) has been changed with at least of factor 5. An overview of these genes as well as the factors with which they are up- or down-regulated is shown in Table 1. The sequences of these genes and the amino acid sequences which they encode are shown in Figure 1.

<u>Example 3</u>. Quantification of Hybridisation Signals using the PathwaysTM software

Quantification of the hybridisation signals was done using the Pathways TM Software (Research Genetics) and these signals were normalised against all data points. Comparison of these normalised data revealed differentially expressed candidate genes. Visual inspection of the hybridisation spots confirmed their selection. An overview of these genes as well as the factors with which they are up- or down-regulated is shown in Table 2.

Surprisingly, using this Software package for analysing the results in this example and when compared to the results of example 2, some additional genes were found which expression are up-or down-regulated upon Bax expression in S. cerevisiae.

The sequences of up- and down regulated genes and the corresponding amino acid sequences from Examples 2 and 3 are shown in Figure 1.

Example 4 Search for homologues in Candida albicans

Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minesota). The commercial sequence database used was the PathoSeqTM microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA).

Sequence similarity search s were performed using the BLAST software package version 2. The identity b tween 2 sequences was calculated as p rcentage identical residues, the similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix.

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$\underline{\text{Example 5}}$. Screening f r c mpounds modulating expression of polypeptides involved in induction of cell death of *C. albicans*

The method proposed is based on observations (Sandbaken *et al.*, 1990; Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to the wild type (WT) cell.

Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally sensitive to compounds with other mechanisms of action.

This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test compound.

The assay to be set up involves measurement of growth or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to a wild type (WT) Candida albicans strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of antisense or strains which carry disruptions in an essential gene. An in silico approach to find novel genes in Candida albicans will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

30 Example 6. Assay for High Throughput screening for drugs

 $35~\mu l$ minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems). A 96-channel pipettor (Hydra, Robbins Scientific) transfers 2.5 μl of R-compound at $10^{-3}~M$ in DMSO from a stock plat into the assay plate.

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The selected *Candida albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at -70°C. The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C. For the parent strain, CAI-4, the medium is always supplemented with 20 μg/ml uridine. A single colony is scooped up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250.000 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20.000 to 50.000 cells/ml. Cultures are grown at 30°C while shaking at 250 rpm until a final OD₆₀₀ of 0.24 (+/-0.04) is reached.

200 μ l of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 μ l total volume. MW96 plates are incubated (static) at 30°C for 48 hours.

15 Optical densities are measured after 48 hours.

Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

Tabl 1.

		
ORF	Qt	Sequence ID Number
YAR061W	7.80	SEQ ID NO 1
YAR073W	11.19	SEQ ID NO 3
YBL048W	5.07	SEQ ID NO 5
YBL051C	5.22	SEQ ID NO 7
YBL066C	6.04	SEQ ID NO 9
YBL078C	6.94	SEQ ID NO 11
YBR072W	26.56	SEQ ID NO 13
YBR073W	5.46	SEQ ID NO 15
YBR086C	7.14	SEQ ID NO 17
YBR093C	11.05	SEQ ID NO 19
YBR181C	0.15	SEQ ID NO 21
YCL007C	20.99	SEQ ID NO 23
YCL016C	23767.57	SEQ ID NO 25
YCR052W	10.51	SEQ ID NO 27
YCR064C YCR073WA	14.91	SEQ ID NO 29
	5.92	SEQ ID NO 31
YDL010W YDL036C	5.31	SEQ ID NO 33
YDL088C	5.34	SEQ ID NO 35
YDL125C	0.16 6.80	SEQ ID NO 37
YDL133CA	0.80	SEQ ID NO 39
YDL136W	0.21	SEQ ID NO 41 SEQ ID NO 43
YDL167C	6.37	
YDL184C	0.37	SEQ ID NO 45 SEQ ID NO 47
YDL191W	0.21	SEQ ID NO 49
YDR103W	6.26	SEQ ID NO 51
YDR238C	5.75	SEQ ID NO 53
YDR259C	9.68	SEQ ID NO 55
YDR294C	8.38	SEQ ID NO 57
YDR430C	5.66	SEQ ID NO 59
YDR438W	6.47	SEQ ID NO 61
YDR450W	0.16	SEQ ID NO 63
YDR471W	0.11	SEQ ID NO 65
YDR486C	5.27	SEQ ID NO 67
YDR499W	6.14	SEQ ID NO 69
YDR507C	6.34	SEQ ID NO 71
YDR515W	5.42	SEQ ID NO 73
YDR518W	6.15	SEQ ID NO 75
YDR519W	5.57	SEQ ID NO 77
YER102W	0.19	SEQ ID NO 79
YER153C	5.63	SEQ ID NO 83
YFL014W	41.08	SEQ ID NO 85
YFL015C	5.62	SEQ ID NO 87
YFR022W	9.44	SEQ ID NO 89
YGL011C	6.14	SEQ ID NO 91
YGL031C	0.11	SEQ ID NO 93
YGL032C	0.14	SEQ ID NO 95
YGL043W	10.74	SEQ ID NO 97
YGL102C	0.15	SEQ ID NO 99
YGL103W	0.17	SEQ ID NO 101
YGL130W J	8.35	SEQ.ID NO.103

YGL147C	1 0.00	1 050 10 110 105
	0.08	SEQ ID NO 105
YGL213C	6.02	SEQ ID NO 107
YGL235W	6.23	SEQ ID NO 109
YGL260W	6.61	SEQ ID NO 111
YGR085C	0.16	SEQ ID NO 113
YGR118W	0.17	SEQ ID NO 115
YGR142W	8.91	SEQ ID NO 117
YGR236C	12.72	SEQ ID NO 119
YGR277C	6.27	
YGR284C		SEQ ID NO 121
	5.95	SEQ ID NO 123
YGR285C	5.84	SEQ ID NO 125
YHR010W	0.20	SEQ ID NO 127
YHR021C	0.16	SEQ ID NO 129
YHR141C	0.10	SEQ ID NO 131
YHR217C	7.6	SEQ ID NO 133
YIL112W	11.15	SEQ ID NO 135
YIL115C	7.67	SEQ ID NO 137
YIL148W	0.13	SEQ ID NO 139
YIL150C	6.83	SEQ ID NO 141
YIL167W	6.66	SEQ ID NO 143
YJL034W	11.61	SEQ ID NO 145
YJL035C		
YJL070C	14.48	SEQ ID NO 147
D	5.29	SEQ ID NO 149
YJL078C	5.16	SEQ ID NO 151
YJL179W	0.19	SEQ ID NO 153
YJL180C	0.14	SEQ ID NO 155
YJL181W	0.21	SEQ ID NO 157
YJL187C	0.17	SEQ ID NO 159
YJL188C	0.1	SEQ ID NO 161
YJL189W	0.08	SEQ ID NO 163
YJL190C	0.09	SEQ ID NO 165
YJL197W	0.13	SEQ ID NO 167
YJL198W	0.2	SEQ ID NO 169
YJR049C	0.17	SEQ ID NO 171
YKR094C	0.14	SEQ ID NO 173
YLR040C	10.13	SEQ ID NO 175
YLR048W	8.55	SEQ ID NO 177
YLR088W	6.09	SEQ ID NO 179
YLR159W	0.18	SEQ ID NO 181
YLR167W	0.06	SEQ ID NO 183
YLR232W	7.4	SEQ ID NO 185
YLR233C	7.63	SEQ ID NO 187
YLR234W	5.68	SEQ ID NO 189
YLR238W	6.74	SEQ ID NO 189 SEQ ID NO 191
YLR241W	6.48	
YLR321C	12.17	SEQ ID NO 193
YLR322W		SEQ ID NO 195
YLR325C	5.54	SEQ ID NO 197
	0.06	SEQ ID NO 199
YLR344W	0.12	SEQ ID NO 201
YLR367W	0.19	SEQ ID NO 203
YLR393W	7.05	SEQ ID NO 205
YLR423C	8.61	SEQ ID NO 207
YML026C	0.11	SEQ ID NO 209
YML063W	0.16	SEQ ID NO 211
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YML128C	5.1	SEQ ID NO 213
YML130C	5.41	SEQ ID NO 215
YMR022W	6.45	SEQ ID NO 217
YMR118C	5.13	SEQ ID NO 219
YMR143W	0.08	SEQ ID NO 221
YMR174C	6.75	SEQ ID NO 223
YMR191W	9.56	SEQ ID NO 225
YMR230W	0.13	SEQ ID NO 227
YNL054W	5.19	SEQ ID NO 229
YNL067W	0.12	SEQ ID NO 231
YNL075W	0.16	SEQ ID NO 233
YNL096C	0.14	SEQ ID NO 235
YNL162W	0.07	SEQ ID NO 237
YNL178W	0.11	SEQ ID NO 239
YNL182C	0.18	SEQ ID NO 241
YNL190W	0.07	SEQ ID NO 243
YNL208W	5.87	SEQ ID NO 245
YNL210W	0.02	SEQ ID NO 247
YOL031C	5.32	SEQ ID NO 249
YOL048C	14.34	SEQ ID NO 251
YOR010C	7.27	SEQ ID NO 253
YOR019W	5.19	SEQ ID NO 255
YOR027W	6.03	SEQ ID NO 257
YOR031W	5.35	SEQ ID NO 259
YOR096W	0.12	SEQ ID NO 261
YOR248W	0.18	SEQ ID NO 263
YOR293W	0.11	SEQ ID NO 265
YOR312C	0.12	SEQ ID NO 267
YOR369C	0.21	SEQ ID NO 269
YPL047W	5.09	SEQ ID NO 271
YPL090C	0.1	SEQ ID NO 273
YPL137C	10.41	SEQ ID NO 275
YPL159C	5.61	SEQ ID NO 277
YPL175W	5.95	SEQ ID NO 279
YPL180W	7.68	SEQ ID NO 281
YPL218W	6.26	SEQ ID NO 283
YPR102C	0.17	SEQ ID NO 285

Tabl 2.

ORF	Qt	Sequence ID Number
YGR236C	7.25	SEQ ID NO 119
YDR442W	0.049	SEQ ID NO 459
YGR182C	0.602	SEQ ID NO 467
YGR106C	0.478	SEQ ID NO 465
YKR040C	2.23	SEQ ID NO 471
YJL188C	0.075	SEQ ID NO 161
YOR096W	0.067	SEQ ID NO 261
YOR293W	0.107	SEQ ID NO 265
YDR450W	0.056	SEQ ID NO 63
YML026C	0.051	SEQ ID NO 209
YHR021C	0.114	SEQ ID NO 129
YLR167W	0.033	SEQ ID NO 183
YGL147C	0.061	SEQ ID NO 105
YGR085C	0.107	SEQ ID NO 463
YOR312C	0.083	SEQ ID NO 267
YOL127W	0.101	SEQ ID NO 473
YHR010W	0.077	SEQ ID NO 127
YDR471W	0.046	SEQ ID NO 65
YDL191W	0.128	SEQ ID NO 49
YDL136W	0.125	SEQ ID NO 43
YLR325C	0.061	SEQ ID NO 199
YJL189W	0.07	SEQ ID NO 163
YIL148W	0.145	SEQ ID NO 139
YHR141C	0.069	SEQ ID NO 131
YBL003C	0.119	SEQ ID NO 457
YDR529C	0.352	SEQ ID NO 461
YGR183C	0.781	SEQ ID NO 469

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CLAIMS

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- 1. Use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:
 - (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300,

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- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6. 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46. 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478. 480, 482, or 484;
- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261,

263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483;

- (e) a nucleic acid sequence which is more than 70% identical, preferably more 10 than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 15 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 20 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 25 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483; and
 - (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e).
- (g) the complement of any of the nucleic acid sequences as specified in a) to f), for the preparation of a medicament for treating diseases associated with yeast or fungi.
- Use of a polypeptide which is involved in a pathway ventually leading
 to programmed cell death of yeast or fungi, said polypeptide being selected from:

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(a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40. 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234. 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,

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- 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (c) a protein having an amino acid sequence which is more than 70% identical. preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340. 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400. 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; and,
 - (d) a functional fragment of any of said proteins as defined in a) to c), for the preparation of a medicament for treating diseases associated with yeast or fungi.
- 3. A pharmaceutical or fungicidal composition comprising a nucleic acid molecule as defined in claim 1 or a polypeptide as defined in claim 2 together with a pharmaceutically acceptable carrier diluent or excipient therefor.
- 30 4. A vaccine for immunizing a mammal against yeast or fungal infections comprising at least one nucleic acid molecule as defined in claim 1 or at least one polypeptide as defined in claim 2 in a pharmaceutically acceptable carrier.
- 5. A genetically modifi d yeast or fungus in which modification results in the over xpression or under xpression of at least one of the nucleic acids as defined in claim 1 or the polypeptides as defined in claim 2, which overexpression or

underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified yeast or fungus.

6. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

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- (a) contacting a compound to be tested with yeast or fungal cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound,
- (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway.
- (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast of fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.
- 7. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:
 - (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1, which expression results in underexpression of said polypeptide, in addition to contacting on or more wild typ c lls with said compound,
 - (b) monitoring th growth, death rat or activity of said transformed, transfected or infected c lls compared to said wild type cells; wh r in differential growth or activity of said transformed, transfected or infected yeast or fungal cells is

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- indicative f selective action of said compound on a polypeptide in the same or a parallel pathway,
- (c) alternatively monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast of fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.
- 8. A method of identifying compounds which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises:
 - (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2,
 - (b) detecting the complex formed between the compound to be tested and said polypeptide,
 - (c) alternatively, examining the diminution of complex formation between said polypeptide and a binding partner, caused by the addition of the compound being tested.
 - (d) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.
- 9. A method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises:
 - (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene,
 - (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being t sted.

- 10. A method according to any of claims 6 to 9 wher in said yeast or fungus is chosen from Saccharomyces cerevisiae, Schizosaccharomyces pombe, Candida albicans, or Aspergillus furnigatus.
- 5 11. A compound identifiable according to the method of any of claims 6 to 9.
 - 12. A compound according to claim 11 for use as a medicament.
- 13. A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound according to claim 12 with a suitable pharmaceutically acceptable carrier.
 - 14. Use of a compound according to claim 11 or 12 for the preparation of a medicament for treating diseases associated with yeast and fungi.
 - 15. Use of a compound according to claim 11 or 12 or a genetically modified organism as defined in claim 5 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.
- 20 16. Use of a compound according to claim 12 where the yeast or fungus is chosen from Candida spp., Aspergillus spp., Microsporum spp., Trichophyton spp., Fusarium spp., Zygomycetes spp., Botritis, spp., Cladosporium spp., Malassezia spp., Epidermophyton floccosum, Blastomyces dermatitidis, Coccidioides immitis, Histoplasma capsulatum, Paracoccidioides brasiliensis, Cryptococcus neoformans, and Sporothrix schenckii.
 - 17. A nucleic acid sequence encoding a polypeptide which is involved in a pathway for programmed cell death of yeast or fungi selected from:
- 30 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452,

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- 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483; and,

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- (f) a nucleic acid sequence encoding a functional fragment of any f the nucleic acid sequences as specified in a) to e),
- (g) the complement of any of the nucleic acid sequences as specified in a) to e).
- 5 18. A nucleic acid according to claim 16 characterized in that it is derived from *Candida albicans*.
 - 19. A nucleic acid molecule capable of selectively hybridizing to a nucleic acid sequence as defined in claim 1 or the complement thereof.
 - 20. A nucleic acid sequence according to any of claim 17 to 19 which is mRNA
- 21. A nucleic acid sequence according to any of claims 17 to 19 which is 15 DNA.

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- 22. A nucleic acid sequence according to any of claims 17 to 19 which is cDNA.
- 23. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridizing to the nucleic acid sequences according to any of claims 17 to 22.
- 24. An isolated protein which is involved in a pathway for programmed cell death of yeast or fungi selected from:
 - (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
 - (b) a protein having an amino acid sequence which is mor than 70% similar, pr f rably more than 80% similar, more preferably mor than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308,

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- 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 922, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484; and,
- 15 (d) a functional fragment of any of said proteins as defined in a) to c)
 - 25. An expression vector comprising a nucleic acid sequence according to any of claims 17 to 23.
- 26. An expression vector according to claim 25 which comprises an inducible promoter.
 - 27. An expression vector according to claim 25 or 26 which comprises a sequence encoding a reporter molecule.
 - 28. A host cell transformed, transfected or infected with the vector of any of claims 25 to 27.
- 29. A nucleic acid molecule according to any of claims 17 to 23 for use as a 30 medicament.
 - 30. A polypeptide according to claim 24 for use as a medicament.
- 31. An antibody capable of specifically binding to a polypeptide according to 35 claim 24.

- 32. An antibody according to claim 31 for use as a medicament.
- 33. A pharmaceutical composition comprising an antibody according to claim 31 or 32.

34. Use of an antibody according to claim 31 or 32, or an antibody capable of binding to at least one of the polypeptides as defined in claim 2, for the preparation of a medicament for treating diseases associated with yeast and fungi.

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- 35. Use of an antibody according to claim 34 where the fungus is *Candida* albicans.
- 36. A nucleic acid probe which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 and which
 selectively hybridises with any of said nucleic acid molecules.
 - 37. A nucleic acid primer which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 and which selectively amplifies any of said nucleic acid molecules.

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38. A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or a human homologue thereof or at least one of the polypeptides as defined in claim 2 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

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- 39. A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences as defined in claim 1 or a human homologue thereof and/or at least one of the polypeptides as defined in claim 2 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 38.
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- 40. A compound identifiable according to the method of claim 39.

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- 41. A compound according to claim 40 for us as a medicament.
- 42. A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 40 or 41 with a suitable pharmaceutically acceptable carrier.
- 43. Use of a compound according to claim 40 or 41 for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.
 - 44. Use of a nucleic acid molecule selected from any of the nucleic acid molecules as defined in claim 1 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

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- 45. Use of a polypeptide selected from any of the polypeptides as defined in claim 2 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
- 20 46. A pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule as defined in claim 1 or a human homologue thereof or a polypeptide as defined in claim 2 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.

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47. A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule as defined in claim 1 or a human homologue thereof or at least one polypeptide as defined in claim 2 or a human analogue thereof in a pharmaceutically acceptable carrier.

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48. Use of an antibody according to claim 31 or 32 or an antibody capable of binding to at least one of the polypeptides as defined in claim 2 or a human homologue ther of for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

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- 49. An expression vector comprising a human homologue of a nucleic acid sequence as defined in claim 1.
- 50. An expression vector according to claim 49 which comprises an inducible promoter.

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- 51. An expression vector according to claim 49 or 50 which comprises a sequence encoding a reporter molecule.
- 52. A host cell transformed, transfected or infected with the vector of any of 10 claims 49 to 51.
 - 53. A nucleic acid molecule comprising a human homologue of at least one of the nucleic acid sequences as defined in claim 1.
- 15 54. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to the nucleic acid molecule of claim 53.
 - 55. A polypeptide encoded by a nucleic acid molecule according to claim 53.

FIG. 1:

YAR061W, 67 aa (SEQ ID NO 2) MPYHYLFLALFTYLATSNVVSGSTQACLPVGPRKNGMNVNFYKYSLLDSTTYSYPQYMTS GYASNWN

YAR073W, 1712 bp, CDS: 501-1712 (SEQ ID NO 3) AGTGGCTCATGATCTGTAAATGATCGGTTGACCGCAGTATTATATAATAACATCCGTATA AGTACATATACTACCATGTCTGTTCTCTACATTGCTTTTTATTCAAGATTATTGGTTTTC CTAACCGCCGCGCGCAGGTACCCCGCGCATCTCTTCTTCTCGAAGAAAGCGGAAAAA ACAAAAAAAAGTATAAATAGTGGAGTCTTTTCCCATTTAACATTTAGAAAAAATTCG AATGGAAATTTCTTGCCGAACATTTAACCGGAGACCCTTGGCGGCTTTTTCTCAGTTTCG TGGGCTAGTACATTTTACCTAGTATGCTGGGAACTTTTTTTCCGTATTCTATTCTATTCC TTGCCTTACTTTTCTTATCATTTTTTATATAACCAATTTCAAAAATACTTTTTAACTGTC ATAGACGCATTTTGTTTATTACAAATTAAAAGAATCAAATATAATATGTGCAATTAATAA CTCCACAAGTAGCGAAAGCAATGGCCGCCATTAGAGACTACAAGACCGCACTAGATCTTA CCAAGAGCCTACCAAGACCGGATGGTTTGTCAGTGCAGGAACTGATGGACTCCAAGATCA GAGGTGGGTTGGCTTATAACGATTTTTTAATCTTACCAGGTTTAGTCGATTTTGCGTCCT CTGAAGTTAGCCTACAGACCAAGCTAACCAGGAATATTACTTTAAACATTCCATTAGTAT CCTCTCCAATGGACACTGTGACGGAATCTGAAATGGCCACTTTTATGGCTCTGTTGGATG GTATCGGTTTCATTCACCATAACTGTACTCCAGAGGACCAAGCTGACATGGTCAGAAGAG TCAAGAACTATGAAAATGGGTTTATTAACAACCCTATAGTGATTTCTCCAACTACGACCG TTGGTGAAGCTAAGAGCATGAAGGAAAAGTATGGATTTGCAGGCTTCCCTGTCACGGCAG ATGGAAAGAGAAATGCAAAGTTGGTGGGTGCCATCACCTCTCGTGATATACAATTCGTTG AGGACAACTCTTTACTCGTTCAGGATGTCATGACCAAAAACCCTGTTACCGGCGCACAAG GTATCACATTATCAGAAGGTAACGAAATTCTAAAGAAAATCAAAAAGGGTAGGCTACTGG TTGTTGATGAAAAGGGTAACTTAGTTTCTATGCTTTCCCGAACTGATTTAATGAAAAATC AGAAGTACCCATTAGCGTCCAAATCTGCCAACACCAAGCAACTGTTATGGGGTGCTTCTA TTGGGACTATGGACGCTGATAAAGAAAGACTAAGATTATTGGTAAAAGCTGGCTTGGATG TCGTCATATTGGATTCCTCTCAAGGTAACTCTATTTTCCAATTGAACATGATCAAATGGA TTAAAGAAACTTTCCCAGATTTGGAAATCATTGCTGGTAACGTTGTCACCAAGGAACAAG CTGCCAATTTGATTGCTGCCGGTGCGGACGGTTTGAGAATTGGTATGGGAACTGGCTCTA TTTGTATTACCCAAAAAGTTATGGCTTGTGGTAGGCCACAAGGTACAGCCGTCTACAACG TGTGTGAATTTGCTAACCAATTCGGTGTTCCATGTATGGCTGATGGTGGTGTTCAAAAAC ATTGGTCATATTATTACCAAAGCTTTGGCTCTTGGTTCTTCTACTGTTATGATGGGTGGT ATGTTGGCCGGTACTACCGAATCACCAGGTGA

YAR073W, 403 aa (SEQ ID NO 4)
MAAIRDYKTALDLTKSLPRPDGLSVQELMDSKIRGGLAYNDFLILPGLVDFASSEVSLQT
KLTRNITLNIPLVSSPMDTVTESEMATFMALLDGIGFIHHNCTPEDQADMVRRVKNYENG
FINNPIVISPTTTVGEAKSMKEKYGFAGFPVTADGKRNAKLVGAITSRDIQFVEDNSLLV
QDVMTKNPVTGAQGITLSEGNEILKKIKKGRLLVVDEKGNLVSMLSRTDLMKNQKYPLAS
KSANTKQLLWGASIGTMDADKERLRLLVKAGLDVVILDSSQGNSIFQLNMIKWIKETFPD
LEIIAGNVVTKEQAANLIAAGADGLRIGMGTGSICITQKVMACGRPQGTAVYNVCEFANQ
FGVPCMADGGVQKHWSYYYQSFGSWFFYCYDGWYVGRYYRITR

YBL048W, 103 aa (SEQ ID NO 6)
MILFKNLVFLPSILIGYISIRVSLLVWVNWVLVWSSCFQVAFIFSLWYFILSIYTFFYSK
KIKQIISYEPSYFVFSYRAIDLCPERVLLYFFCIFNNVVFPML

YBL051C, 2507 bp, CDS: 501-2507 (SEQ ID NO 7) GGGAAATATCAATTCCCGTATTTCAATGTTAGTAATTTGCCTTCGTAAATTACGGAATCA CATAGCTTTCATTTGTTCCTTTGATATATTTCCCTACTACATACTCTTTTCAATAACTC TACAGGGTCTGACATTITTAACTTTCAGGTTAATGATGGTGTTCTTACTATATTCTCGAG TCGTACAGAAGTTAGTTCAGATAAACTGCTTCGGTGCTGCCCACTTCTTATCATTACTTC **AACTTTACCTTCCCTATACCTGTGTGTCCTTATTAATTCAAGTTAATCCGAGGTAATAGA** TTAGGGTAACCTTCAATGATGTCACGAAACACGGATGCTGCAACTTTGCGATTTTTTCCT GGAAAAGAATAACAATTAAAGGCAGCCTTTCAGCTGAGATTACCAGCAGGTCTTTGGAGA GTGTTCAACAACAATAAGAAATGGAGACCAGTTCTTTTGAGAATGCTCCTCCTGCAGCCA TCAATGATGCTCAGGATAATAATATAAATACGGAGACTAATGACCAGGAAACAAATCAGC AATCTATCGAAACTAGAGATGCAATTGACAAAGAAAACGGTGTGCAAACGGAAACTGGTG AGAACTCTGCAAAAAATGCCGAACAAAACGTTTCTTCTACAAATTTGAATAATGCCCCCA CCAATGGTGCTTTGGACGATGATGTTATCCCAAATGCTATTGTTATTAAAAACATTCCGT ATGCCTTCAATTACCACTTTGATAACGGTATTTTCAGAGGACTAGCCTTTGCGAATTTCA CCACTCCTGAAGAAACTACTCAAGTGATAACTTCTTTGAATGGAAAGGAAATCAGCGGGA GGGAGAAGAGAGAAAAGAGGACAATTAGAAGAACAACACAGATCGTCATCTAATCTTT TATTCTCGACTCTAATGAACGGCATTAATGCTAATAGCATGATGAACAGTCCAATGAATA ATACCATTAACAATAACAGTTCTAATAACAACAATAGTGGTAACATCATTCTGAACCAAC CCCAGATGTCCACTGAGAGATTTTATGCGCCTTTACCATCAACTTCCACTTTGCCTCTCC CACCCCAACAACTGGACTTCAATGACCCTGACACTTTGGAAATTTATTCCCAATTATTGT TATTTAAGGATAGAGAAAAGTATTATTACGAGTTGGCTTATCCCATGGGTATATCCGCTT CCCACAAGAGAATTATCAATGTTTTGTGCTCGTACTTAGGGCTAGTAGAAGTATATGATC CAAGATTTATTATTATCAGAAGAAAGATTCTGGATCATGCTAATTTACAATCTCATTTGC AACAACAAGGTCAAATGACATCTGCTCATCCTTTGCAGCCAAACTCCACTGGCGGCTCCA TGAATAGGTCACAATCTTATACAAGTTTGTTACAGGCCCATGCAGCAGCTGCAGCGAATA GTATTAGCAATCAGGCCGTTAACAATTCTTCCAACAGCAATACTATTAACAGTAATAACG GTAACGGTAACAATGTCATCATTAATAACAATAGCGCCAGCTCAACACCCAAAAATTTCTT CACAGGGACAATTCTCCATGCAACCAACACTAACCTCACCTAAAATGAACATACACCATA GTTCTCAATACAATTCCGCAGACCAACCGCAACAACCTCAACCACAAACACAGCAAAATG TTCAGTCAGCTGCGCAACAACAACAATCTTTTTTAAGACAACAAGCTACTTTAACACCAT CCTCAAGAATTCCATCCGGTTATTCTGCCAACCATTATCAAATCAATTCCGTTAATCCCT TACTGAGAAATTCTCAAATTTCACCTCCAAATTCACAAATCCCAATCAACAGCCAAACCC

TATCCCAAGCGCAACCACCAGCACAGTCCCAAACTCAACAACGGGTACCAGTGGCATACCAAAATGCTTCATTGTCTTCCCAGCAGTTGTACAACCTTAACGGCCCATCTTCAGCAAACTCACAGTCCCAACTGCTTCCACAGCACAAATGGCTCAGTACATTCTAATTTCTCATATCAGTTTTATCACGATGAGTCCATGTTGTCCGCACACAATTTGAATAGTGCCGACTTGATCTATAAATCTTTGAGTCACTCTGGACTAGATGATGGCTTGAACAGGGCTTGAATCGTTCTTAAGCGGACTGGATTACAAAACCAAAACAAGAAGAATCTATGGTAA

YBL051C, 668 aa (SEQ ID NO 8)
METSSFENAPPAAINDAQDNNINTETNDQETNQQSIETRDAIDKENGVQTETGENSAKNA
EQNVSSTNLNNAPTNGALDDDVIPNAIVIKNIPFAIKKEQLLDIIEEMDLPLPYAFNYHF
DNGIFRGLAFANFTTPEETTQVITSLNGKEISGRKLKVEYKKMLPQAERERIEREKREKR
GQLEEQHRSSSNLSLDSLSKMSGSGNNNTSNNQLFSTLMNGINANSMMNSPMNNTINNNS
SNNNNSGNIILNQPSLSAQHTSSSLYQTNVNNQAQMSTERFYAPLPSTSTLPLPPPQQLDF
NDPDTLEIYSQLLLFKDREKYYYELAYPMGISASHKRIINVLCSYLGLVEVYDPRFIIIR
RKILDHANLQSHLQQQGQMTSAHPLQPNSTGGSMNRSQSYTSLLQAHAAAAANSISNQAV
NNSSNSNTINSNNGNGNNVIINNNSASSTPKISSQGQFSMQPTLTSPKMNIHHSSQYNSA
DQPQQPQPQTQQNVQSAAQQQQSFLRQQATLTPSSRIPSGYSANHYQINSVNPLLRNSQI
SPPNSQIPINSQTLSQAQPPAQSQTQQRVPVAYQNASLSSQQLYNLNGPSSANSQSQLLP
QHTNGSVHSNFSYQSYHDESMLSAHNLNSADLIYKSLSHSGLDDGLEQGLNRSLSGLDLQ
NQNKKNLW

YBL066C, 3674 bp, CDS: 501-3674 (SEQ ID NO 9) ATCCCAAGAAGAATTAGACTGATTTTTACCTACCCTTCCACCGTCGGAAGAAACACTT CGAAGGCTAAATTTGGTCAATTTAATGAAATTAAACCCTATTTAAGATTCACCAAGTCGA ACTTTTATCTATCTTTCATTCTTATTATATCTCATCTCGTACGAAGGGCCGCTCATTGGA TAATAAACTCTCTGCAGAAACCTTAATGTCAAAGGTCCCGTATACAGATTATATTGGCTC TGCGTATACGCATTCTCGTCATGGTGAAGGATAATCGAGATTCTGACCAAGACCAAGATT TTAGTTCTGCTCACATGAAAAGACAACCGGAGCAGCAACAGTTGCAACAGCACCAGTTCC CAAGTAAGAAACAACGAATATCTCACCATGATGACAGTCATCAAATCAACCATAGACCAG TTACCTCATGTACACATTGTAGACAGCACAAAATCAAATGCGATGCTAGTCAAAATTTCC GGCCTAAGAAGGGCTCACAGTTGCAACTACTGAGACAAGATGTGGATGAAATCAAATCTA **AACTCGATACTCTTCTGGCCAATGACAGCGTTTTTCGTTCATCTTTTACAACAGATTCCCA** TGGGCAATAGCCTTTTGAATAAGCTCAATCTGCATCCAACTCCAACTCCGGGTACTATTA TCCCTAACCCAGATTCTTCTCCTTCCTCAGGTTCTCCAACTTCTTCCGCGGCTCAACGAG ATTCTAAGGTTTCAGTTCAAACTTATTTGTCCAGGGAACCCCAACTCTTACAAGCAAATC AGGGCAGCAATACGAATAAATTTAAAGCAAATAATGAAGCATCTTCTCACATGACGTTGC GCGCATCTTCTTTAGCGCAAGATTCGAAAGGCTTGGTTGCAACAGAGCCAAATAAGCTGC CCCCGCTGCTAAATGACTCAGCATTGCCTAATAATTCAAAAGAATCTTTACCTCCTGCTT TGCAAATGGCTTTTTATAAGAACAACTCTGCAGGTAACACTCCGAACGGCCCCTTCTCTC CAATTCAAAAAACATATTCCCCTCATACTACGTCGACCACCGTTACAACGACAACAAATC AACCACCATTTGCAGCAACAAGCCACGTAGCAACAATAACAATGCAGATAGGACGAAGA CGCCGGTAGTAGCCACCACCACGACTATGCCATTATTGCCTTCGCCGCATGCAAATGTAG ATGAGTTTGTACTGGGCGATATTAGTATTTCCATTGAAAAAGCGAATAGATTACACCATA TTTTCGTGACTAGGTATCTGCCGTATTTTCCTATTATGTATTCCAATAACGCCACCGAAT CTGAACCGACGATGTATTGCAAGCTAAGCTCTTTGATCAAGCAACTTGCCATAGAGACCT GCTGGATAAGAACACCTAGATCCACACATATTTCGCAAGCTTTGTTAATATTGTGCATTT GGCCTTTGCCTAACCAAAAAGTCCTAGATGATTGTTCTTACCGTTTTGTAGGATTAGCAA AGTCACTGTCTTATCAATTAGGTTTGCACAGAGGTGAATTCATTTCTGAATTCACAAGAA CTCAAACATCAATGCCAAATGCAGAAAAGTGGAGAACTAGGACTTGGCTGGGAATATTTT TATTAGAAAAAGCCTTATCCTGTGGTGACGAAGAATCAGAAGAAGATAACAATGACAGTA TTGACAATAACAACAATGATAAAAGGAACAAGAAGACGAGCCGCACGTTGAAAGTAAAT ACAAACTACCGGGCAGTTTTAGAAGATTGCTCAGCCTGGCGAATTTCCAAGCAAAATTGT CTCATATCATTGGTTCTTCCACTTCCAGTCCTGATGGTTTATTGGAACCAAAGTATCGTG

CTGAGACACTGTCCATCTTGGGAAAAGAGTTAGATTTATTAGCAAAAACTTTAAATTTCC CATTCCTACCGAAACACCTCCTACCGATCAAATTCCATATGTCACAGAGGCCTATCTAA TGCCTATTTATATTAGACAAGCTGCTACATTTTCTGCACTGATTCTCTTTAAATTGCAGT TGACTCCTTTACTTCCTGACAAATATTTTGATTCAGCAAGGCAATCCGTGGTCACTATCC ATAGACTTTATAGAAATCAGTTAACTGCGTGGGCCACTAGTGTTGAGAATGATATTTCGA GAACTGCAAGTATGTTAGAAAAACTGAACTTCGTACTGATCATGCATCCAGAAGTTTTTTG TGGAAGAAGACGGTATTATTTCTAGGATGAGATCACATTTAACAGGGTCTCTATTCTATG ATTTGGTTTGGTGTTCACGAGGCGAGAAGAGGGAAATGGATCCCGAATATAACAAGC AAGCCTTAGAGAAAGCCGCTAAGAAAAGAAAATTTTCCTCAAATGGTATCTACAATGGCA CTTCGTCTACGGGTGGCATAACGGACAGAAAACTATATCCATTGCCACTATATAACCATA TCTCCAGAGATGACTTTGAAACTGTAACAAAAACAACACCAAGTGGAACCACTGTTACCA CTTTAGTTCCTACTAAGAATGCCTTAAAGCAGGCAGAAAAGCTAGCCAAGACAAATAACG GAGATTCTGACGGTTCTATAATGGAGATTAACGGGATACCTCTTTCCATGCTCGGGGAAA CAGGCAGCGTAAAATTTCAAAGTTTATTCGCTAATACCTCGAATAGTAACGATTATAATA ATAATAGGACGTTATTGGATGCGTCTAATGACATATCAATTCCCTCTAATTCAATTTATC CAGTGGCTTCTGTCCCCGCTTCGAATAACAATCCACAAAGTACTAAGGTAGACTATTATA GTAACGGACCTAGTGTAATTCCTGATCTCTCCATGAAAAGATCAGTAAGCACTCCCGTTA ATCATTTCCTGCGTCCGTTCCAGGGTTAAGGAACCACCCCGTTGGCAACTTATCTAATA ATGTTACATTGGGAATAGACCACCCTATTCCAAGGGAGCACAGTAATTTACAAAATGTCA CCATGAATTATAATAATCAATTCAGCAACGCCAACGCGATTGGAAGATCACAAAGTAGTA TGTCCCATTCACGTACACCTTTGTTTCGGTCAATATATGACAGTTGGATTCCGCGTCCGA CCCCGGTCCTCTAA

YBL066C, 1057 aa (SEQ ID NO 10) MVKDNRDSDQDQDFSSAHMKRQPEQQQLQQHQFPSKKQRISHHDDSHQINHRPVTSCTHC ROHKIKCDASONFPHPCSRCEKIGLHCEINPOFRPKKGSQLQLLRQDVDEIKSKLDTLLA NDSVFVHLLQQIPMGNSLLNKLNLHPTPTPGTIIPNPDSSPSSGSPTSSAAQRDSKVSVQ TYLSREPQLLQANQGSNTNKFKANNEASSHMTLRASSLAQDSKGLVATEPNKLPPLLNDS ALPNNSKESLPPALQMAFYKNNSAGNTPNGPFSPIQKTYSPHTTSTTVTTTTNQPPFAAT SHVATNNNADRTKTPVVATTTTMPLLPSPHANVDEFVLGDISISIEKANRLHHIFVTRYL PYFPIMYSNNATELYSQSQLLFWTVMLTACLSDPEPTMYCKLSSLIKQLAIETCWIRTPR STHISQALLILCIWPLPNQKVLDDCSYRFVGLAKSLSYQLGLHRGEFISEFTRTQTSMPN AEKWRTRTWLGIFFAELCWASILGLPPTSQTDYLLEKALSCGDEESEEDNNDSIDNNNND KRNKKDEPHVESKYKLPGSFRRLLSLANFQAKLSHIIGSSTSSPDGLLEPKYRAETLSIL GKELDLLAKTLNFQSDDTVNIYFLYVKLTVCCFAFLPETPPTDQIPYVTEAYLTATKIVT LLNNLLETHQLIELPIYIRQAATFSALILFKLQLTPLLPDKYFDSARQSVVTIHRLYRNQ LTAWATSVENDISRTASMLEKLNFVLIMHPEVFVEEDGIISRMRSHLTGSLFYDLVWCVH EARRREMDPEYNKQALEKAAKKRKFSSNGIYNGTSSTGGITDRKLYPLPLYNHISRDDFE TVTKTTPSGTTVTTLVPTKNALKQAEKLAKTNNGDSDGSIMEINGIPLSMLGETGSVKFQ SLFANTSNSNDYNNNRTLLDASNDISIPSNSIYPVASVPASNNNPQSTKVDYYSNGPSVI PDLSMKRSVSTPVNHFPASVPGLRNHPVGNLSNNVTLGIDHPIPREHSNLQNVTMNYNNQ FSNANAIGRSQSSMSHSRTPLFRSIYDSWIPRPTPVL

YBL078C, 854 bp, CDS: 501-854 (SEQ ID NO 11)
TAGTGGAGTACGAATTAGTTAAAGATACTATCGACTTTGAAGCCATTGTCAAAGAACATT
TTGATATGTTAAGCAAGACCTGTAGATCCGACATTGCCAAATATGACGGCTCAAAGACAG
ACCCAATTGGTGATGAAGAACAATCTATTAATGACACCCATTTTCAAATTAAAAGTGTTCA
AATTATGAAAACAACTCATATAAATACGTACAAATTTTTCTCTACTCGAAGTGATATAGA
TGTATATGTGTAAGTTTACGTTTAAGTTAGGACCATGTAATGCTAACTGTCTCCACCGAT
AATGTTGTATAATACCCGTGAAATCATAGCACATGATATATCATCACCCGGAGGCCGGTT
ATTTTCGGCGGCGGCAAAAATATTTGGTATAATTATGGAAATACAAAAAAGGGGAACCATT
AAAGGTTGAGGAGGGGATTGATAAGAGAATCTAATAATTGTAAAGTTGAGAAAAATCATAA
TAAAAATAATTACTAGAGACATGAAGTCTACATTTAAGTCTGAATATCCATTTGAAAAAA
GGAAGGCGGAGTCGGAGAGGATTGCTGACAGGTTCAAGAATATCCTGTGATTTGCG
AAAAAGCTGAAAAGTCAGATATTCCAGAGATTGATAAGCGTAAATATCTAGTTCCTGCTG
ACCTTACCGTAGGGCAATTTGTTTATGTTATAAGAAAAGAGAATTATGCTACCCCCTGAGA
AGGCCATCTTCATTTTTTGTCAATGATACTTTGCCACCTTACTCAGGAGAAAATA

CATTTGGCAGGTAG

YBL078C, 117 aa (SEQ ID NO 12) MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRKYLVPADLTVGQF VYVIRKRIMLPPEKAIFIFVNDTLPPTAALMSAIYQEHKDKDGFLYVTYSGENTFGR

YBR072W, 1145 bp, CDS: 501-1145 (SEQ ID NO 13) GCAGCAGCAACTCCGTGTGTACCCCTAACTCCGTGTGTACCCCTAAAGAACCTTGCCTGT ATGCGTCCÁAAAATATAGGGTGCTCGTAACAGTAAGGTATTCGCACTTAGCGTGCTCGCA ACACAAAATTAAGTAATATGCGAGTTTTTAGATGTCCTTGCGGATCTATGCACGTTCTTGA GTGGTATTTCATAACAACGGTTCTTTTTCACCCTTATTCCTAAACATATAAATAGGACCT CCATTAGTTAGAGATCTGTTTTTAATCCATTCACCTTTCATTCTACTCTCTTTATACTAAT AAAACCACCGATAAAGATATATCAGATCTCTATTAAAACAGGTATCCAAAAAAGCAAACA AACAAACTAAACAAATTAACATGTCATTTAACAGTCCATTTTTTGATTTCTTTGACAACA TCAACAACGAAGTTGATGCCTTTAACAGATTGCTGGGTGAAGGCGGCTTAAGAGGCTACG CACCAAGACGTCAGTTAGCAAACACACCCGCAAAGGATTCTACTGGCAAGGAAGTTGCTA GACCAAATAACTATGCTGGCGCTCTTTATGATCCCAGAGATGAAACCTTAGATGATTGGT TCGACAATGACTTGTCCCTGTTCCCATCTGGTTTCGGTTTCCCTAGAAGTGTCGCAGTTC CAGTTGATATTTTGGACCATGACAACTACGAGTTGAAAGTCGTGGTTCCTGGTGTCA AAAGCAAGAAGGACATTGATATTGAGTACCATCAAAACAAGAACCAAATTTTGGTTTCTG GTGAAATTCCATCTACCTTGAATGAAGAGAGTAAAGACAAGGTCAAGGTCAAGGAGAGCA GCTCTGGTAAGTTCAAGAGAGTCATCACTTTGCCAGACTACCCAGGTGTGGATGCAGACA ACATTAAAGCAGACTACGCAAATGGTGTTTTGACATTAACAGTTCCAAAATTGAAGCCTC AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA ACTAA

YBR072W, 214 aa (SEQ ID NO 14)
MSFNSPFFDFFDNINNEVDAFNRLLGEGGLRGYAPRRQLANTPAKDSTGKEVARPNNYAG
ALYDPRDETLDDWFDNDLSLFPSGFGFPRSVAVPVDILDHDNNYELKVVVPGVKSKKDID
IEYHQNKNQILVSGEIPSTLNEESKDKVKVKESSSGKFKRVITLPDYPGVDADNIKADYA
NGVLTLTVPKLKPQKDGKNHVKKIEVSSQESWGN

YBR073W, 3377 bp, CDS: 501-3377 (SEQ ID NO 15) AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA TGGCTTGAAACATATGTCATCACATCTGAGCGATTTTACCTCTTAGAATTAGTTTAGATA TATATGAGTTGATGAATAAATAGTTATAAAAACTTGCTTTGGCTTCGATATATGACCGTT ATTTTTGACTAAGTTTTAACGAAGGAATCTAACCTCGTTCTTGTAATTACCAAAATCTTC AACAACGCGCTGTTGGAGGTATCTCTATGGATGTGGCTTGAAATATGGATGTCTTGCCTA CTTCTACTTCTGGGAAAGGCATTTTTACTCGATCGCGTTAATATATGCATCAAGAAAATA AATCGAGTTTTTGTATTGAAATGGCGGTAATAAGCGTTAAACCTCGACGAAGAGAGAAGA TCCTACAGGAGGTAAAAAACAGCTCGGTATATCAAACGGTATTTGATTCCGGTACTACTC AAATGCAGATACCGAAATATGAGAACAAGCCATTCAAGCCTCCAAGAAGGGTTGGATCAA ATAAGTACACAACTCAAACCAACCGCCACTGCAGTCACAACAGCCCCTATATCTAAAG CCAAAGTTACTGTCAACTTGAAAAGAAGCATTTCGGCGGGACCTACTTTAAATCTTGCCA AGAAGCCGAATAATCTGTCCTCAAATGAAAACACTAGATATTTTACTATCATGTACAGGA AGCCTACTACCAAAAAGCACAAGACTTGGAGTGGTGATGGCTACGCTACCTTAAAAGCCA GTAGCGATAAGTTATGCTTTTATAACGAAGCAGGGAAATTTCTTGGGTCAAGTATGCTAC CAAGTGATTCAGATTCTCTCTCGAAACTCTTTTCAAAGCAGGCTCCAATGAAGTACAAT TGGATTACGAATTGAAGGAAAATGCAGAAATACGTAGCGCCAAAGAAGCCTTATCACAAA ACATGGGAAATCCCAGCCCACCGACCACAAGCACAGAAACAGTGCCTTCTACGAAGA ATGACGGTGGCAAATACCAAATGCCTCTGTCTCAGCTGTTTTCACTAAACACTGTGAAAA GATTCAAATCAGTAACAAAGCAAACAAATGAACACATGACCACAGTACCTAAAACCAGTC AAAATTCCAAAGCCAAAAAATATTATCCAGTATTTGATGTCAACAAAATCGATAATCCTA TAGTAATGAACAAAAATGCAGCCGCTGAAGTTGACGTAATTGTTGATCCATTACTGGGCA AATTCTTGCGCCCTCATCAGAGGGAAGGGGTGAAGTTCATGTATGATTGCTTAATGGGCT TGGCAAGACCAACTATTGAAAATCCGGATATCGATTGTACTACTAAAAGTTTAGTGTTAG

AAAATGACTCAGATATTAGTGGATGCCTTTTTGGCTGATGATATGGGTTTAGGTAAAACAC TAATGAGTATAACTTTGATTTGGACATTAATTAGGCAAACTCCTTTTGCATCAAAAGTTT CATGTTCGCAATCAGGCATACCATTAACTGGACTTTGTAAGAAGATTTTAGTCGTTTGTC CCGTTACTTTAATAGGAAATTGGAAAAGAGAATTTGGAAAAATGGTTAAATTTGTCAAGAA TAGGTGTTTTGACATTAAGCTCAAGGAATTCTCCTGATATGGATAAAATGGCTGTCAGAA ATTTTTTAAAAGTGCAACGAACTTATCAAGTCTTGATTATTGGCTACGAAAAACTCTTGA GCCATCGACTAAAAAACGGGGCTTCTAAAATTTTAAATACGCTGAAGAGTTTAGACATAA GAAGGAAGCTTTTGCTTACGGGAACTCCTATACAAAATGATCTTAATGAGTTTTTCACTA TTATAGATTTCATAAACCCAGGAATCCTTGGAAGCTTCGCTTCTTTCAAAAGAAGATTCA TTATCCCTATAACTAGAGCCAGAGACACTGCAAACAGATACAACGAAGAATTGTTGGAAA CAAATGCGATTTTAGAAAAGTACCTTCCTCCAAAGACGGATATAATTTTATTCTGTAAAC CATACAGCCAACAGATATTGGCATTCAAAGATATTTTGCAGGGCGCACGTTTAGATTTTG GACAATTGACGTTCAGTTCTTCGCTAGGACTAATAACATTACTGAAAAAGGTTTGTAACT CTCCTGGATTGGTTGGCTCAGATCCCTATTACAAATCACATATAAAGGATACCCAATCTC AGGACAGCTATAGTCGTTCTTTGAACTCTGGTAAGTTAAAGGTATTAATGACATTACTAG AAGGTATTAGGAAGGGTACCAAGGAGAAGGTCGTCGTAGTGTCTAACTACACTCAAACAT TGGATATAATTGAAAATTTGATGAATATGGCTGGGATGTCACATTGCAGACTCGACGGTT CCATACCTGCTAAACAAAGGGACTCTATCGTCACATCTTTCAATCGGAATCCAGCCATAT GACTTATTTATTTGATAATGATTGGAATCCTTCAGTAGATTTGCAAGCGATGTCACGAA TTCATAGAGATGGTCAAAAAAAGCCGTGCTTCATATATAGACTTGTCACAACTGGGTGTA TCGATGAGAAAATATTGCAAAGGCAATTAATGAAGAACAGTTTGAGCCAAAAATTTCTAG GTGACTCGGAGATGAGAAATAAAGAATCTTCTAATGATGATCTTTTCAATAAAGAGGACT TGAAGGACCTGTTTTCTGTCCATACAGATACCAAGAGTAACACACATGACTTAATTTGTT CTTGCGATGGTTTAGGTGAGGAAATTGAATATCCTGAAACAAATCAACAGCAGAACACCG TAGAGCTGAGAAAGCGTAGCACTACGACATGGACAAGTGCGCTGGATTTACAAAAGAAAA TGAATGAAGCAGCCACCAACGATGATGCCAAAAAGTCACAATACATTAGGCAATGTCTCG TTCATTATAAGCATATCGATCCAGCAAGACAAGATGAATTATTTGATGAGGTTATCACAG ATTCGTTCACCGAATTGAAAGATAGTATTACCTTTGCGTTTGTAAAGCCCGGCGAGATAT GTCTCAGAGAACAATGA

YBR073W, 958 aa (SEQ ID NO 16) MAVISVKPRRREKILQEVKNSSVYQTVFDSGTTQMQIPKYENKPFKPPRRVGSNKYTQLK PTATAVTTAPISKAKVTVNLKRSISAGPTLNLAKKPNNLSSNENTRYFTIMYRKPTTKKH KTWSGDGYATLKASSDKLCFYNEAGKFLGSSMLPSDSDSLFETLFKAGSNEVOLDYELKE NAEIRSAKEALSQNMGNPSPPTTSTTETVPSTKNDGGKYQMPLSQLFSLNTVKRFKSVTK QTNEHMTTVPKTSQNSKAKKYYPVFDVNKIDNPIVMNKNAAAEVDVIVDPLLGKFLRPHO REGVKFMYDCLMGLARPTIENPDIDCTTKSLVLENDSDISGCLLADDMGLGKTLMSITLI WTLIRQTPFASKVSCSQSGIPLTGLCKKILVVCPVTLIGNWKREFGKWLNLSRIGVLTLS SRNSPDMDKMAVRNFLKVQRTYQVLIIGYEKLLSVSEELEKNKHLIDMLVCDEGHRLKNG ASKILNTLKSLDIRRKLLLTGTPIQNDLNEFFTIIDFINPGILGSFASFKRRFIIPITRA RDTANRYNEELLEKGEERSKEMIEITKRFILRRTNAILEKYLPPKTDIILFCKPYSQQIL AFKDILQGARLDFGQLTFSSSLGLITLLKKVCNSPGLVGSDPYYKSHIKDTQSQDSYSRS LNSGKLKVLMTLLEGIRKGTKEKVVVVSNYTQTLDIIENLMNMAGMSHCRLDGSIPAKQR DSIVTSFNRNPAIFGFLLSAKSGGVGLNLVGRSRLILFDNDWNPSVDLOAMSRIHRDGOK KPCFIYRLVTTGCIDEKILQRQLMKNSLSQKFLGDSEMRNKESSNDDLFNKEDLKDLFSV HTDTKSNTHDLICSCDGLGEEIEYPETNQQQNTVELRKRSTTTWTSALDLQKKMNEAATN DDAKKSQYIRQCLVHYKHIDPARQDELFDEVITDSFTELKDSITFAFVKPGEICLREO

CACAAGCGGTTGAGCATACTATGTCGCAGACAATTACATCTCTAGATCCGAATTGTGTTA TTGTATTCAATAAACTTCGAGTGCAAACGAGAAGAGTTTGAATGTCGAATTCAAACGTT TGAATATACATTCTATTATCGAACCTGGCCATGATCTGCAAACAAGCTATGCGTTTATTA GAATCCATCAGGATAATGCGAAACCGCTTTTTTCATTTTGCAGAATCTGGACTTCATTG **AATCCATCATACCATATCATGATACTGAATTGTCCGATGATTTGCATAAACTGATTTCTA** TCAGCAAATCAAAAATACTGGAGGCTCCAAAACAGTATGAGTTGTACAACCTATCGAATT TGACCAATAATCCCAAACAATCCTTATATTTTGCATTCTTACAGAACTATAAAAATGGT TGATTCCCTTCTCCTTTTTTGGATTATCAATTAGATTTTTATCTAATTTTACGTATGAAT TCAATTCCACATACTCGCTGTTCGCCATCCTATGGACATTGTCATTTACAGCCTTTTGGC TTTATAAATATGAACCATTTTGGTCTGATAGACTGAGTAAATACTCATCATTTTCTACCA TTGAGTTTCTTCAAGATAAACAGAAAGCCCAAAAAAAAGCTAGTTCGGTTATCATGTTGA AGAAATGTTGTTTATTCCTGTGGCTTTGTTGTTTGGCGCAATATTACTATCATTCCAGC TATATTGTTTTGCGTTGGAAATTTTCTACAAGCAAATTTATAACGGCCCAATGATTTCCA TCTTGTCTTTTTTGCCTACTATACTTATTTGCACGTTTACTCCGGTTTTAACTGTGATTT ACAACAAATATTTCGTAGAACCAATGACAAAGTGGGAAAATCATAGCAGTGTTGTGAATG CAAAGAAATCTAAAGAAGCTAAGAACTTTGTTATTATTTTTTCTATCCAGTTACGTTCCCC TATTAATTACACTATTTCTTTATCTGCCAATGGGGCATTTGTTGACCGCAGAAATAAGAA TTCAATTTAGCATGGAAAACTTTGTTCCAAGCCTTGTTAGCATTGCTCAGCAGAAAATTA ATGGACCAAATCCTAACTTTGTCAAAGCTGAGAGTGAAATCGGTAAAGCTCAACTCAGCT CATCAGATATGAAAATTTGGTCAAAGGTTAAGTCGTACCAAACAGACCCCTGGGGAGCAA CATTTGATTTGGACGCCAACTTCAAAAAGCTTCTTCTACAATTCGGGTATCTTGTTATGT TTTCTACAATTTGGCCACTAGCTCCATTTATCTGTTTGATAGTCAATTTGATTGTTTACC AAGTCGATTTGAGGAAAGCTGTGCTTTATAGTAAACCTGAGTATTTTCCATTTCCAATCT ACGATAAGCCATCCTCTGTGTCTAATACCCAAAAACTGACGGTTGGTCTATGGAACTCTG TCTTAGTTATGTTCTCCATCTTAGGTTGTGTTATCACTGCTACTTTGACCTATATGTACC ACCTAGCAAATCCAATAAACCACTCGTGGATAAATATTGTACTATATGCTGTTTTTATTG AGCATGTTAGTGTTGCTATTTTCTTCCTTTTCTCTAGTATTTTGAAATCTTCCCATGATG ACGTTGCAAATGGCATTGTGCCAAAGCATGTAGTTAACGTGCAAAACCCACCAAAACAAG AAGTCTTTGAAAAAATTCCCTCCCCTGAATTTAATTCGAATAACGAAAAAGAACTAGTTC CTTCTGCCAATGGATATGAGGCACATGCTGCCACTCATGCCAACAATGATCCGTCTTCTT TATCCTCAGCCTCCTCGCCTTCATTATCTTCTTCTTCTTCTAGCAGCAAAACCGGTGTAG TCAAAGCTGTTGATAACGATACAGCCGGATCTGCTGGTAAAAAGCCATTGGCCACAGAAA GTACTGAAAAAAGAAATTCTTTGGTGAAGGTGCCTACCGTTGGCTCATATGGTGTTGCGG GCGCCACTTTACCAGAAACAATTCCAACATCTAAAAATTACTACTTAAGGTTTGATGAGG ACGGTAAATCCATTAGGGATGCGAAATCCAGTGCAGAATCTTCCAACGCCACCAATAACA ACACCTTAGGCACGGAAAGTAAGCTTTTGCCAGATGGTGACGCCGTTGATGCACTAAGTA GAAAAATTGATCAAATACCCAAAATTGCTGTTACTGGTGGCGAAAATAACGAAAATACCC AGGCCAAAGACGATGCTGCCACTAAGACTCCACTCATTAAAGATGCAAATATTAAGCCTG AAAAGACTGAAGTAAGCACGAAAAATGGCCCATCAAGATCTATTTCCACGAAGGAAACTA AGGATTCTGCGAGACCATCTAATAACAATACTACTACTACTACTACTACAGATGCTACTC AGCCCCACCATCATCACCACCACCACCGCCATCGTGATGCTGGAGTGAAGAATGTCACGA ACAATTCTAAGACAACCGAATCCTCTTCCTCTTCATCGGCGGCAAAGGAAAAACCAAAAC ATAAAAAGGGGCTATTGCATAAGCTGAAAAAGAAGCTTTAA

YBR086C, 946 aa (SEQ ID NO 18)
MSQTITSLDPNCVIVFNKTSSANEKSLNVEFKRLNIHSIIEPGHDLQTSYAFIRIHQDNA
KPLFSFLQNLDFIESIIPYHDTELSDDLHKLISISKSKILEAPKQYELYNLSNLTNNPKQ
SLYFAFLQNYIKWLIPFSFFGLSIRFLSNFTYEFNSTYSLFAILWTLSFTAFWLYKYEPF
WSDRLSKYSSFSTIEFLQDKQKAQKKASSVIMLKKCCFIPVALLFGAILLSFQLYCFALE
IFYKQIYNGPMISILSFLPTILICTFTPVLTVIYNKYFVEPMTKWENHSSVVNAKKSKEA
KNFVIIFLSSYVPLLITLFLYLPMGHLLTAEIRTKVFNAFSILARLPTHDSDFIIDTKRY
EDQFFYFIVINQLIQFSMENFVPSLVSIAQQKINGPNPNFVKAESEIGKAQLSSSDMKIW
SKVKSYQTDPWGATFDLDANFKKLLLQFGYLVMFSTIWPLAPFICLIVNLIVYQVDLRKA
VLYSKPEYFPFPIYDKPSSVSNTQKLTVGLWNSVLVMFSILGCVITATLTYMYQSCNIPG
VGAHTSIHTNKAWYLANPINHSWINIVLYAVFIEHVSVAIFFLFSSILKSSHDDVANGIV

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PKHVVNVQNPPKQEVFEKIPSPEFNSNNEKELVQRKGSANEKLHQELGEKQPASSANGYE AHAATHANNDPSSLSSASSPSLSSSSSSSKTGVVKAVDNDTAGSAGKKPLATESTEKRNS LVKVPTVGSYGVAGATLPETIPTSKNYYLRFDEDGKSIRDAKSSAESSNATNNNTLGTES KLLPDGDAVDALSRKIDQIPKIAVTGGENNENTQAKDDAATKTPLIKDANIKPVVNAAVN DNQSKVSVATEQTKKTEVSTKNGPSRSISTKETKDSARPSNNNTTTTTTTDATQPHHHHH HHRHRDAGVKNVTNNSKTTESSSSSSAAKEKPKHKKGLLHKLKKKL

YBR093C, 1904 bp, CDS: 501-1904 (SEQ ID NO 19) ACGTATTTGGAAGTCATCTTATGTGCGCTGCTTTAATGTTTTCTCATGTAAGCGGACGTC GTCTATAAACTTCAAACGAAGGTAAAAGGTTCATAGCGCTTTTTCTTTGTCTGCACAAAG AAATATATATAAATTAGCACGTTTTCGCATAGAACGCAACTGCACAATGCCAAAAAAAG TAAAAGTGATTAAAAGAGTTAATTGAATAGGCAATCTCTAAATGAATCGATACAACCTTG GCACTCACACGTGGGACTAGCACAGACTAAATTTATGATTCTGGTCCCTGTTTTCGAAGA GATCGCACATGCCAAATTATCAAATTGGTCACCTTACTTGGCAAGGCATATACCCATTTG GGATAAGGGTAAACATCTTTGAATTGTCGAAATGAAACGTATATAAGCGCTGATGTTTTG CTAAGTCGAGGTTAGTATGGCTTCATCTCTCATGAGAATAAGAACAACAACAAATAGAGC AAGCAAATTCGAGATTACCAATGTTTAAATCTGTTGTTTATTCAATTTTAGCCGCTTCTT TGGCCAATGCAGGTACCATTCCCTTAGGCAAACTAGCCGATGTCGACAAGATTGGTACCC AAAAAGATATCTTCCCATTTTTGGGTGGTGCCGGACCATACTACTCTTTCCCTGGCGACT GACATGGTGAAAGATACCCTACTGTCAGTCTGGCTAAGACTATCAAGAGTACATGGTATA AGTTGAGCAATTACACTCGTCAATTCAACGGCTCATTGTCATTCTTGAACGATGATTACG AGTTTTTCATCCGTGATGACGATGATTTGGAAATGGAAACCACTTTTGCCAACTCGGACG ATGTTTTGAACCCATACACTGGTGAAATGAACGCCAAGAGACATGCTCGTGACTTCTTGG CTCAATACGGTTACATGGTCGAAAACCAAACCAGTTTCGCCGTTTTTTACCTCTAATTCTA AGAGATGTCATGACACTGCTCAATATTTCATTGATGGTTTAGGTGACCAATTCAACATCA CCTTGCAGACTGTCAGTGAAGCTGAATCCGCTGGTGCCAACACTTTGAGTGCTTGTAACT CATGTCCTGCTTGGGACTACGATGCCAATGATGACATTGTAAATGAATACGACACCT ACTTGGATGACATTGCCAAGAGATTGAACAAGGAAAACAAGGGTTTGAACTTGACCTCAA CTGACGCTAGTACTTTATTCTCGTGGTGTGCATTTGAAGTGAACGCTAAAGGTTACAGTG ATGTCTGTGATATTTTCACCAAGGATGAATTAGTCCATTACTCCTACTACCAAGACTTGC ACACTTATTACCATGAGGGTCCAGGTTACGACATTATCAAGTCTGTCGGTTCCAACTTGT TCAATGCCTCAGTCAAATTATTAAAGCAAAGTGAGATTCAAGACCAAAAGGTTTGGTTGA GTTTTACCCACGATACCGATATCCTAAACTTTTTGACCACCGCTGGTATAATTGACGACA AAAACAACTTAACTGCCGAATACGTTCCATTCATGGGCAACACTTTCCACAGATCCTGGT ACGTTCCTCAAGGTGCTCGTGTCTACACCGAAAAATTCCAATGTTCTAACGACACCTACG TCAGATACGTCATTAACGATGCTGTTGTTCCAATTGAAACCTGTTCCACTGGTCCAGGGT TCTCTTGTGAAATCAATGACTTCTACGACTATGCTGAAAAGAGAGTAGCCGGTACTGACT TCCTAAAGGTCTGTAACGTCAGCAGCGTCAGTAACTCTACTGAATTGACCTTCTACTGGG ACTGGAACACTACTCATTACAACGCCAGTCTATTGAGACAATAG

YBR093C, 467 aa (SEQ ID NO 20)
MFKSVVYSILAASLANAGTIPLGKLADVDKIGTQKDIFPFLGGAGPYYSFPGDYGISRDL
PEGCEMKQLQMVGRHGERYPTVSLAKTIKSTWYKLSNYTRQFNGSLSFLNDDYEFFIRDD
DDLEMETTFANSDDVLNPYTGEMNAKRHARDFLAQYGYMVENQTSFAVFTSNSKRCHDTA
QYFIDGLGDQFNITLQTVSEAESAGANTLSACNSCPAWDYDANDDIVNEYDTTYLDDIAK
RLNKENKGLNLTSTDASTLFSWCAFEVNAKGYSDVCDIFTKDELVHYSYYQDLHTYYHEG
PGYDIIKSVGSNLFNASVKLLKQSEIQDQKVWLSFTHDTDILNFLTTAGIIDDKNNLTAE
YVPFMGNTFHRSWYVPQGARVYTEKFQCSNDTYVRYVINDAVVPIETCSTGPGFSCEIND
FYDYAEKRVAGTDFLKVCNVSSVSNSTELTFYWDWNTTHYNASLLRQ

TAATTTGAATAGTGTGCCCTTCAAAACATTTGGAAGTCATTAATTGAAACTATCCAGTGT GAATAGACGACTGAGCCATCATGAAGGTATGTAATATCACCCAAATCCTTAGAATTCTAA TGAATCAGCACGCCTAACCGGCTGTTTCTGACTGTTTGATAAACGTATACCCACAAATT AGTGCACTATAATAAAAATTCTCAAGAACAACGTTGTTTAAACGAGATAATTCCCTCTAA TATACACGTACCGACACTTAGGAAAATATCTCGCTAAGTTCAAATTAAGGAATGAAAAAG GAATTTACGAAAAGGGTTTAGAAATATCAATGAAAATAAGAAAAACCTGTAACGGAAGAA AGGACAGCAGGGATTCGTTGGAATTTGTCGATATTGGCTTCGGACAACTTTACTAACAAA TGGTATTATTATAACAGTTGAACATTTCTTACCCAGTCAACGGGTCTCAAAAGACCTTC GAAATTGATGAACACCGTATTCGTGTTTTCTTCGACAAGAGAATCGGTCAAGAAGTC GATGGTGAAGCCGTTGGTGATGAATTCAAGGGCTACGTCTTCAAGATCTCTGGTGGTAAC GÁCAAACAAGGTTTCCCAATGAAGCAAGGTGTTTTGTTGCCAACTAGAATCAAGTTGTTG GTCAGAGGTGCCATTGTTGGTCCAGATTTGGCTGTCTTGGCTTTGGTCATTGTCAAGAAG GGTGAACAAGAATTGGAAGGTCTAACTGACACTACTGTTCCAAAGAGATTGGGTCCAAAG AGAGCTAACAACATCAGAAAGTTCTTCGGTTTGTCCAAGGAAGATGACGTTCGTGATTTC GTCATCAGAAGAGAAGTCACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAA AGATTGGTTACTCCTCAAAGATTGCAAAGAAAGAGACACCAAAGAGCTTTGAAGGTCAGA AACGCTCAAGCTCAAAGAGAAGCTGCTGCCGAATACGCTCAATTGTTGGCTAAGAGATTG TCTGAAAGAAAGGCTGAAAAGGCCGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCT

YBR181C, 236 aa (SEQ ID NO 22)
MKLNISYPVNGSQKTFEIDDEHRIRVFFDKRIGQEVDGEAVGDEFKGYVFKISGGNDKQG
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAIVGPDLAVLALVIVKKGEQE
LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVTKGEKTYTKAPKIQRLVT
PQRLQRKRHQRALKVRNAQAQREAAAEYAQLLAKRLSERKAEKAEIRKRRASSLKA

YCL007C, 893 bp, CDS: 501-893 (SEQ ID NO 23) ATTACTTTAAATTGTTTGTCTATTCCAACATAATCATTAGCAGCACATGTCGAGCAACAG ATAAACACAGCAGCGCACGGTGAACCACATAAGTGTATGTGCACACGCGTGTTTTGTGC AGTGTATTACCAACTTGCGCATGCAAGGATATCACACTCCTGTTTCTGCCTCATGTCTTT TAAAACGCTTCCACGGGACATGGGTTCTAATTATGGAGAAGATCAAGCTTTGAAATGGCC CGTTTACACATTTTGATACAACCGTAGACGGCGTCTCGTTTCAAAGACCGTGTGGTTGTC TATCAGTATATACTCATTGTGTTTTTCAAAAAATCTCTGGGTTGTTTAGATGCCACTATA TTTCTATTCGTATTTATTTTTATGTATACTTATTTTGCTTATTTTTCTTATACTCAGGAA ACGTCACTTGGCTTGATATACTCGACGCTTTATTCTGCAAATTCAGGTCTCAAATCTGAA CGGCGTGGAGCCACCAAGGGATGGAGCTGGCAAAGGAACGTAATGGCCCACATCAAAAAC ACAAACTCTTGTTAGTAAAAAAGAAAGGGAAACTAGTAATATGGAGACACATCGTAAAAA AAATGTTGCACATACGCTTGGTTGTTCTTTGGAGCCATTATCCAGAACAGCACGGACATG GCACTAACCACTATGAATACACCAACAACAGTATAGCTAAATTGGACGCGCAGAGAGTTA GTAGAAGAAGAAGAAAAAGGGAAGCGGAGAGAAGAGATTATGACACATACAAACTAC TCATTACTCTTTGTTCTTTATTATTCGTTGGACCTTTGTTTCTTAAAGTATAG

YCL007C, 130 aa (SEQ ID NO 24)
MELAKERNGPHQKHHGQCQNHCTSPNTVRQNKTNKLLLVKKKGKLVIWRHIVKKMLHIRL
VVLWSHYPEQHGHGTNHYEYTNNSIAKLDAQRVSRRRKKREAERRDYDTYKLLITLCSL
LFVGPLFLKV

AATCAGAATTTGAGACCAGAGAGACACATGGCGAATTGAACTTGAATTCAGTACCAATAT
ACAACGGAGAACTGGATTTCTCCGACAAAATCATGAAGAGGTCATCTACAAAGGTTATCG
GGACCCTGGAAGAACTACTTGAGAACTCACCATGTTCTGCGCTAGAAGGTATATCAAAAT
GGCATAAGATTGGTGGATCTGTGAAAGACGGTGTGTTGTGTATTCTTTCACAAGACTTCC
TTTTCAAAGCACTGCATGTACTACTGATGAGCGCAATGGCAGAATCACTCGATCTACAGC
ATCTGAATGTTGAGGATACACATCACGCTGTGGGGAAGGACATTGAGGACGAGTTCAATC
CATACACAAGAGAAATCATTGAAACAGTGCTGAATAAATTTGCTGTTCAAGAGCAAGAGG
CTGAAAACAATACGTGGCGCTTGAGAATAACCGTTTTATAGCTCAGTGGTACCGGGATTCAAG
CGCTAAGGAAATATGTTTCTGGAATAAGCATGCCAATTGACATTGACATGCTGCGAGGCTATC
ATTTCAAGCCTACCACTTTCTTCCCATGTGACATTGACATTGACATGCTGCGAGGCTATC
ATTTCAAGCCTACCGATAAGACTGTCCAGTATATAGCGAAAAGCACACTACCAATGGACC
CCAAAGAACGGTTTAAAGTCCTGTTTAGGCTACAGTCGAGTTTCATCATGAAGT
AGCCTCTAATTGAAGAACTAAATTCAAGAGGTATGAAAATAGACAGTTTCATCATGAAGT
ATGCCCGCCGTAAAAAGACTGGGCAAAAAGACCGTTGGAGCAGGTAG

YCL016C, 309 aa (SEQ ID NO 26)
MREFVPEQPITFDETLLFGLSKPYMDVVGFAKTESEFETRETHGELNLNSVPIYNGELDF
SDKIMKRSSTKVIGTLEELLENSPCSALEGISKWHKIGGSVKDGVLCILSQDFLFKALHV
LLMSAMAESLDLQHLNVEDTHHAVGKDIEDEFNPYTREIIETVLNKFAVQEQEAENNTWR
LRIPFIAQWYGIQALRKYVSGISMPIDEFLIKWKSLFPPFFPCDIDIDMLRGYHFKPTDK
TVQYIAKSTLPMDPKERFKVLFRLQSQWDLEDIKPLIEELNSRGMKIDSFIMKYARRKRL
GKKTVVTSR

YCR052W, 1952 bp, CDS: 501-1952 (SEQ ID NO 27) GTCATCGACAGCAAATTGCTGGAAGAGTTCAAGGACAACGTGAGATACACCTTGGAAAAT GACCCTGAGGAAGGAGCCGATGAGGCCACTCTGCAACGCAGGAGGCAGTTGGAACAGATC ATTACGGGAGACAACGCTGAGGAGGAGTTGGAAAGGTACATCCGTGCTATGGTCAGAGAG CAGATGCTGGGCCAGGGCTCCATGGCGGGTTCCGGGGACGAACCAGATTCCAAGAGAAGA AAATAACGACCCAGCACAAAGGCTCTTACAGCTTGCTAAAAGAAATTGAACGCGACGCTA CATGAACTACTTCTCTTACATAGTCTTTTCCCTTATGTATCTTTTCTGTACATTAA TAGACGTTCTTACAAGGTAAAATTTCACCGCGTTTTTAAATAGAATGAAAAAAACGTTGT AGAGTGAAAGAAAAGCAACAAATATACAGTTCACAAGGCAGCTTCGTATAGTAATACAGC ACGAAAAACAGCTCATAGAAATGGTAACAGACCAATCCGGTCCCTGTTACATATCCAA CGGATGCTTATATCCCCACGTATCTGCCCGATGATAAGGTCTCCAATCTGGCAGATTTGA AAAAATTGATAGAAATGGATTCCAGACTAGATTTGTATCTGACAAGAAGGAGGCTGGATA CGTCCATCAATTTACCTACAAACACCAAGACCAAGGACCATCCCCCCAATAAAGAGATGC TGAGGATTTACGTCTACAACACTACGGAAAGCAGCCCTCGCAGCGATTCTGGCACCCCAG CGGACTCAGGCAAGACTACATGGACACTGAGAATAGAAGGTAAGCTTCTGCACGAGTCCG CAAACGGAAAGCACCCATTTAGTGAGTTTTTTGGAAGGTGTCGCGGTCGACTTTAAAAGAC ATCTGCAACAACCCGAATACAATGATCAAGATAGCACCATGGGCGATAACGACAACGGCG AGGATGAGGACAGTGCAGAGGCAGAATCCAGGGAGGAAATTGTAGACGCACTGGAATGGA **ACTACGATGAAAACAACGTTGTGGAGTTTGATGGTATCGACATCAAGAGGCAAGGCAAGG** ATAATTTGCGATGCAGTATAACCATCCAGTTGAGGGGTGTCGACGGTGGAAAAGTACAGT ACTCGCCCAACTTAGCTACCTTGATAGGTATGCAAACGGGCTCCGTTAATGACGCGGTTT AAGATGGTTCCAACGATGCCGAAGACAGCAGTAACGAGAATAACAATAAAAACGGTGCTG GTGACGATGATGGCGTCGAGGGAAGTACTCCAAAGGATAAGCCCGAATTGGGTGAAGTGA AGCTAGATTCACTCTTACAAAAGGTATTGGATACAAACGCCGCGCACCTCCCCTTGATGA ATGTTGTGCAAACCGTGAACAAACTGGTATCACCCCTACCGCCCATCATCCTAGATTATA CAATTGATCTTTCCAAAGATACCACCTATGGTGCTACCACCTTGGATGTAGATGTCGC ACATTCTCCACCAGCCTCAACCCCAGCCAAATTTACAAAAAGAGGAAGAAACAGATGCTG AAGACACAGCAAAACTACGTGAAATCACAAAGCTTGCCTTGCAGTTGAACTCTAGTGCTC AAAAATACCAGTTTTTCCACGAACTGTCTTTGCATCCAAGAGAAACGCTGACTCACTACT TATGGTCTTCCAAGCAAAACGAGCTTGTGCTGCAGGGCGACCAATACTTCAATGAAGATG CTGCAAGAACGAGTGACATATACAGTAACAACAATGACAGGTCACTAATGGGCAATA TCTCACTACTGTACTCCCAAGGAAGACTATAA

YCR052W, 483 aa (SEQ ID NO 28) MVTQTNPVPVTYPTDAYIPTYLPDDKVSNLADLKKLIEMDSRLDLYLTRRRLDTSINLPT NTKTKDHPPNKEMLRIYVYNTTESSPRSDSGTPADSGKTTWTLRIEGKLLHESANGKHPF SEFLEGVAVDFKRLKPLGMGKKRKRDSSLSLPLNLQQPEYNDQDSTMGDNDNGEDEDSAE AESREEIVDALEWNYDENNVVEFDGIDIKRQGKDNLRCSITIQLRGVDGGKVQYSPNLAT LIGMQTGSVNDAVYSIYKYILINNLFVTEQTEAQDGSNDAEDSSNENNNKNGAGDDDGVE GSTPKDKPELGEVKLDSLLQKVLDTNAAHLPLMNVVQTVNKLVSPLPPIILDYTIDLSKD TTYGATTLDVDVSHILHQPQPQPNLQKEEETDAEDTAKLREITKLALQLNSSAQKYQFFH ELSLHPRETLTHYLWSSKQNELVLQGDQYFNEDAARTSDIYSNNNNDRSLMGNISLLYSQ GRL

YCR064C, 911 bp, CDS: 501-911 (SEQ ID NO 29) GCGTCGCGTTCTCGCGTCTGTTTTGTTTTTTCGCGTTCCAATGACCAAAATGGGAAAGTG TGGCCAGAACAATACTGCAACGTGCATATAGTCGTTAGTCTGTGCTTGCACATCCACGGC AGCCGCAGTGGACGCACTGATGGAAGGACACCTGTGTGCCCTTTTTGCGTGCTTCTTCCT CTAACTGTGCACGAGGCACCCTGCAGATGCAAGTGCTACCGTTGTTAGTTTCGTTCTTTT GAATGCAGCGCAGACAGCACAGTTTTCATACCCGGTTTTGCGCCATTTGGCAATTAGCA ATTTATCAGCATACTTTTCCTTTATCAACCAATCGTAAAGGTCTTTGGAGATGGCCTTTC TCTTGTAGTACAGAGTATATATGTATCTAGAGCGCTGGTGGTGGAGTTGCATTATCTCCC AGAGCTGCTCATTGGACTTTGCTGCGAGCTTAGACGACTTGTCCTTTTGGGCATCTCTGA GTTGGATTTCGAAATCTGTGAGGGTTGGCTTGATTTTTTCGAACCCGTCAGGTGCAGGCT TGGATCTTCTGGTCTTTATGCGCGGCATGTCGTTTTGTGAGGTGAGCTTTGCTAGTCTTG AGTATTTCACTTTCCGTTGTGAACGACAAATGTACTATGCGTTCAAGAGCCAACGCAGTA TCATCGTCAAAGTTCCTACCACAACGCGTGTGATTGATCTTGTACTGGTTGTAAATGTGC TAAGTCTGTGA

YCR064C, 136 aa (SEQ ID NO 30) MYLERWWWSCIISQSCSLDFAASLDDLSFWASLSWISKSVRVGLIFSNPSGAGLDLLVFM RGMSFCEVSFASLDGCRGVYIDDESLRKFFFFFQYFTFRCERQMYYAFKSQRSIIVKVPT TTRVIDLVLVVNVLSL

YCR073W-A, 1448 bp, CDS: 501-1448 (SEQ ID NO 31) GTTTATGGCTGGAATGACTTGATAATCTCTTCACGAGCTTACTTGAGATGGTATGAGGAG CCAGAACTCTCCCGCCTTCAGCCGCTTTTTGTTGCTGTTTTTCAGTATATCCATCATCA TTTTCACCTACAAGGAACTACCTTTTATAGCCACCCTAAGTAAAACAACATTAGCTTAGC ATCCTCAATTCTTATCGTATGTTGCTGCTATTTTTATCCTATTGTTCCTGGCATCGC TTTTTTACATAAGGTACCAAGGCAAGAGAAAAGACCCGCGAAATTTTCAATTCGAGACAT AGGGTTAATACGAAATATGTTAAGGTCTAGTTTCCAAAAAATGAAGAAAATGTGATTAGA CATCCTGGGGAAATTAGGTTTAAATAGGGCGGGCGCTACAGGGGTTTTCCTAACAAATTT CAATGATAATAGTGGCATCATCATCGTCATATCCAGTGTAGGTATGGACTAGAACAGAAA GCAATTTGCAGCAAGACAATATGACTACGACGTACCCAAGATATTCGCGTTTCACGAGT TTTCAGACGTGGCAGAGGCCGTAGCTGACCATGTAGTCCACGCGCAAGACGGTGCATTGG CTCCAAAGAACGAGGGAAACACTCTGTTCCCAACATCAGCATGAATGCACTGGATATGA CGAGAGAGGCCTCTTGCAAAAGCACAGCATCTGCCGCGGAAGGGAAAAGTGGTAGCAGTG GTAGTGGCAGTGGTAGCAGTAAGCCCAAAAAGGAGAAACGGTTCAAGATTGCTCTCCCG GTGGGTCATTGATCGAAGTGCTACACGAAGGTCTGCTAAAACGAGACGATGTACGGTGGG GAGACTGGGACATTTACTTTGCAGACGAGAGACTTGTACCCTTCAGCTCGAATGAAAGCA ATTATGGATGCGCCAAAAGGAAGATTTTGGACCTGATAGACACGGCGAAGTATGGAACTC CGAAGGTGTACCACATTGACGAGTCATTGATTGACGACCCGCAAGAATGCGTTGATAACT ATGAAAAGGTGCTAATCCGCGGGTTTGCCGGTAGAGATTCCGTCAAACTTCCGATGTTCG ACTTGTTCCTGCTTGGTTGTGCCCCCGATGGTCATATCGCATCACTCTTCCCTAACTTCC AGGACAATCTACGTGAGAAACTTGCATGGGTGGTGCCCGTGGAGAACGCTCCTAGTGGGC CCTCGACCAGAATTTCGCTGACTATACCTGTAATCTGCCATTCTCACAGGGTTACTTTCG TTGTCGAAGGTGCAACCAAGGCGCCCATCATCAAGACCATTATGGAAAGGCCTGAAAAGG GCCTACCTAGCAGTATTGTCAACGAAGGTGCTGCTGGTCGTGTATCATGGTTTGTTGACG ACGATGCTCTTACGGACGTCCTCGTCACCAAAAAAAAGTATAAATTCCACCAAGGTTTGT CTATTTAA

YCR073W-A, 315 aa (SEQ ID NO 32)

MTTTVPKIFAFHEFSDVAEAVADHVVHAQDGALAPKNERKHSVPNISMNALDMTREASCK STASAAEGKSGSSGSGSSKPKKEKRFKIALSGGSLIEVLHEGLLKRDDVRWGDWDIYF ADERLVPFSSNESNYGCAKRKILDLIDTAKYGTPKVYHIDESLIDDPQECVDNYEKVLIR GFAGRDSVKLPMFDLFLLGCAPDGHIASLFPNFQDNLREKLAWVVPVENAPSGPSTRISL TIPVICHSHRVTFVVEGATKAPIIKTIMERPEKGLPSSIVNEGAAGRVSWFVDDDALTDV LVTKKKYKFHQGLSI

YDL010W, 1196 bp, CDS: 501-1196 (SEQ ID NO 33) TAGTAATTAGTTTCTTATGATGGATTTAATGGCGTAGTTCATCCGCGTTTAATTTAACTA GAGGATAATCTACTTGCAGCATGAATGAAAATAGTAAGCCAGTAAGGATGCACTGACAGA CTCAGCTACCGATTAGTGTTGTTGACTTTTCCGCAAGATCCTTTTCTCCCTCTTTGGACC TAGTCATCCCTCCACAAGATTCGCTCTTAAGTAGTGGCGCAGGCTGTTCGCTTTTAAG CATAGTGCTTAATGTCGAAGGCTTTATAGATCCCAAATACTACGCCTTGAGAAATTGAAT GCACTAGCAGTTAGTTAACTTTCTGGAACGCGCATGACGCGTCCCGGGGCGCCTTGAGGCG GAACTTTTAAGCAAATTATCGTAAGATAGAAAAGACGAAACCTTAGCAACCTAGCGGTTT **AATATAGAAACAATTTTATTATGATACCTTCCAATAAGAGAAATGCTAGAATTTTAAGCA** TTACAACGCTATTATTGTTGTTAGTGTTTTTCGTAGCGCAAAATGCGAACTTCTTGACGG TAGAGATAAAAGAGGAAACTTCTAAAGCATTTAGTACTAATATGGACAATATGGCTGGAG GATCTTCCAGGGAATATGCTGCTATGCCGACTTCTACCACGAATAAGGGGAGCTCTGAAG TAGACGAAGAAATTAATGAAATAAAACAGAAGGTGGGACTCCAACAGCCCCATAGCATCGG TTGATGATAGTTTGTCGGCCATTAAAAACGATAAAGGGTCGCGAATAACCAAAGCTTTTA ATGTTCAAAAAGAATACTCCCTCATACTAGACTTGTCTCCGATTATAATATTTAGTAAAA GCACCTGTTCATATAGCAAGGGCATGAAGGAACTGCTTGAAAATGAGTATCAGTTTATCC CAAACTACTATATTATAGAACTTGACAAACATGGACATGGGGAAGAGCTGCAAGAATATA TCAAGTTGGTGACCGGTAGAGGAACTGTTCCAAACCTTTTGGTTAATGGAGTATCAAGAG GAGGTAATGAAGAAATCAAGAAACTGCACACTCAAGGGAAACTTTTAGAATCATTACAAG TCTGGAGTGATGGTAAATTCTCGGTTGAGCAACGTGAAAAACCTTCCAATAATTGA

YDL010W, 231 aa (SEQ ID NO 34) MIPSNKRNARILSITTLLLLLVFFVAQNANFLTVEIKEETSKAFSTNMDNMAGGSSREYA AMPTSTTNKGSSEVDEEINEIKQKVGLQQPIASVDDSLSAIKNDKGSRITKAFNVQKEYS LILDLSPIIIFSKSTCSYSKGMKELLENEYQFIPNYYIIELDKHGHGEELQEYIKLVTGR GTVPNLLVNGVSRGGNEEIKKLHTQGKLLESLQVWSDGKFSVEQREKPSNN

YDL036C, 1889 bp, CDS: 501-1889 (SEQ ID NO 35) TCAAATCCAGCTTCTTTTCAAGCAATATTGTCACAAACGATGATGAGAATAGCATTGAAG AGGATAAGAATTTACGCTATTCAGATGCTAGTGCATCTGAAAATTATCTGGTCAAGCCCA CAATACCAGGTACGACTCCTGATCCAATAATTGAGGCGCAGAACGATAATGATAGTAGTG ATAGTAGCGGCATAGATTTGATAGCCTTCTTAAGAAATGGACCATTATAAAGTTTTTGTA TCGCGATGTTTGAAAATGGAAAGTAAGGAACGTAATACAAATTGACAAGTAGCCGACATG AATGACGCTCACTTCTCTTATATATGTTAGGTAGTATATGCATTATAGAATTTATTCATT AACAAAAGACCGAGTTAAGAAAAAGTTCATAAAAAACTTTTGAAAAATGGATGAGTGCTCG TATAATGGAATAGGAAACTTATGCAAAGAAATAATAGGTTAAGAAATTTGTTTACAGTGC CAGTAATAATGGCTCGACAACTCAAAAGGAATGCATTATCTGCAGGTCTTGCTTTTGCAG AAATTCAAAAGAAAAAAAAAAAAAGCGAACTCAATCAAAAAAATCGCCAGATTTGATTA ATAAATCTACTTTTCAATCACGAACGATAGGCAGCAAAAAAGAGAAACATAGACAACTAG ATCCAGAGTATGAAATTGTCATCGATGGCCCTCTAAGGAAAATCAAGCCCTACCATTTTA CGTACAGGACCTTTTGCAAAGAGCGTTGGAGAGATAAAAATTGGTTGATGTCTTTATAT CTGAATTTCGAGATCGTGAATCTGAATATTATAAAAGAACAATCGAAAACGGGGACGTTC ATATAAACGATGAAACTGCGGACTTATCTACTGTAATTCGCAATGGTGACCTGATTACGC ATCAGGTACATAGACATGAACCTCCAGTCACTTCCAGGCCTATCAAAGTTATTTTTGAAG ATGATAACATAATGGTTATTGATAAACCGAGCGGTATACCTGTTCACCCAACTGGCCGAT ATCGGTTCAATACAATTACGAAAATGCTTCAAAATAATCTCGGATTTGTTGTGAACCCAT GTAATAGGTTAGATAGGCTTACAAGTGGATTAATGTTTTTGGCAAAAACTCCGAAGGGAG CCGATAATATCGGCGATCAACTAAAAGCTCGAGAAGTCACTAAGGAATACGTGGCCAAGG TAGTTGGAGAATTTCCAGAAACGGAAGTAATTGTTGAAAAACCTCTAAAACTGATCGAGC CAAGGCTTGCTCTTAATGCAGTTTGTCAAATGGACGAGAAAGGAGCCAAACATGCAAAAA

CTGTTTTTAACAGAATCAGCTACGACGGTAAAACGAGTATTGTAAAGTGCAAACCGCTTA
CCGGGCGATCACATCAAATTAGAGTACATTTACAGTACTTAGGCCACCCAATTGCTAACG
ATCCTATTTATTCCAATGATGAAGTATGGGGTAACAATCTCGGAAAAGGCGGCCAGGCTG
ACTTCGATATAGTTATTACTAAGCTAGACGAAATAGGGAAAAAGAAAACCTGCTAAAAGTT
GGTTCCATAGTAATGGCGGGTACGGTGAGGTATTAAGGCAAGAAAAATGTTCTATTTTGTG
AATCTGATTTGTATACTGATCCTGGCCCCAATGATCTTGATCTGTGGTTACATGCCTATC
TATACGAATCAACTGAGACTGAAGAAGGAACCGAAAAAGAAAAAGTGGTGCTACAAAACAG
AGTATCCAGAATGGGCTCTGAGAAGAAGATAG

YDL036C, 462 aa (SEQ ID NO 36)
MQRNNRLRNLFTVPVIMARQLKRNALSAGLAFAGNATSNEFDEHLQNEVEREREIQKKKK
IKRTQSKKSPDLINKSTFQSRTIGSKKEKHRQLDPEYEIVIDGPLRKIKPYHFTYRTFCK
ERWRDKKLVDVFISEFRDRESEYYKRTIENGDVHINDETADLSTVIRNGDLITHQVHRHE
PPVTSRPIKVIFEDDNIMVIDKPSGIPVHPTGRYRFNTITKMLQNNLGFVVNPCNRLDRL
TSGLMFLAKTPKGADNIGDQLKAREVTKEYVAKVVGEFPETEVIVEKPLKLIEPRLALNA
VCQMDEKGAKHAKTVFNRISYDGKTSIVKCKPLTGRSHQIRVHLQYLGHPIANDPIYSND
EVWGNNLGKGGQADFDIVITKLDEIGKRKPAKSWFHSNGGYGEVLRQEKCSICESDLYTD
PGPNDLDLWLHAYLYESTETEEGTEKKKWCYKTEYPEWALRR

YDL083C, 1364 bp, exon1: 501-909, intron1: 910-1341, exon2: 1342-1364 (SEQ ID NO 37) TATTCCGACTAGAAAAAATTAAATTTTCTAACTACAAAAAATTGCCTGCATATATGTAA GGATGTAACAGGAAATGTATGGGTCACATATTAATAGCTTGTTTTACTCCATAAAAGAGT CTGATATTCAGAAAAAACACCCATACATGTTGAAAAATAATGCATTGTGAAAAAAAGTGG TTGAAAAATGTATGCGATCTAGGAAAAACTGAATTTTCCTTAGGTTGTCGCTCCTCCTCT AGAAGGATGCTGTGGCCTTTGACCTGGGCGGAAATTCTCTCTGTTTCCCTCTAGCTGAGG GAAACAGAACTGGTAGCAGTTCGTTCCGGCCAGGCCGCGTGAGCCTATACCACCGAATAT TATCCTAGCGCAGAGAGTAACACTGGCAAAGTCAAAAGTAAATGCCATGTAAAATGTATA GCAAGAATAAGCAACAAGATGTCTGCCGTCCCAAGTGTCCAAGTATGTTAAATAATTT **AAACGATGTCACGAATTTGTGAGGGATATTGAAACCATGCAGTGAGATAATTTCAATTTA** AGAACCATATCACCTGAATAAGACGGGTGGGGCAAGCACTAGATGCGAATCATAGTTTTA GAACAACGGATCACCATTTCACACGTTAAAGACCGAGTAGAAATAACCAATAAATTGTGT GGGAAAATATTATACTTAATTTCTCTGTGGAGTAAAGTAATGAGCGTCTTTTGCGGTCTT ATTTATTCATTCGCTCCCCTTGCAATGAATTTTGAACAGAATGCTCCAAAGAGGAAGTGC CAGGGTACCTCACTTGTTTCACCCTTTTACACAGTTCATAATATTTTTGAGGATTTTGAA TTTCTGTTTTACTAACATGTGACACGAAATGTTTTTCATTTTTGGTTTTATAACAGACTT TTGGTAAGAAGAAATCAGCTACCGCTGTTGCCCACGTCAAGGCCGGTAAGGGTTTGATTA AGGTCAACGGTTCTCCAATCACTTTGGTTGAACCAGAAATCCTAAGATTCAAGGTCTACG AACCATTATTGTTGGTTTGGTTTGGACAAGTTCTCCAACATCGATATCAGAGTTAGAGTCA CTGGTGGTGGTCATGTTTCTCAAGTCTACGCCATCAGACAAGCTATTGCTAAGGGTTTAG TCGCTTACCACCAAAAGTACGTTGACGAACAATCCAAGAACGAATTGAAGAAGGCCTTCA CCTCTTACGACAGAACTTTGTTGATCGCTGATTCTAGAAGACCAGAACCAAAGAAATTCG GTGGTAAGGGTGCTCGTTCTAGATTCCAAAAATCTTACCGTTAA

YDL083C, 143 aa (SEQ ID NO 38) MSAVPSVQTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF SNIDIRVRVTGGGHVSQVYAIRQAIAKGLVAYHQKYVDEQSKNELKKAFTSYDRTLLIAD SRRPEPKKFGGKGARSRFQKSYR

YDL125C, 1088 bp, exon1: 501-597, intron1: 598-708, exon2: 709-1088 (SEQ ID NO 39)
TTCAAAATACGAGTAAAGGAGATCCTAGGTGTGGATTAGTAAGGGGAGTGTGGCAACTTC
CTTTTTCCGGTTAATTCTCCGCGCTTTCGTTAGACTATTTTGCAAGGACCCAAATAGGAG
ACGCATGGAGGCTTCTACAAAACAGCGTGCCGTTTTGATGGCATGAGCAGGGGGGCGCAAA
GGAAACACCGGTAAATCGCGCAAGACCTTGTTGGCCACGTAGCCTCAAAGGTTGAATTGA
CACTTGTCTACAGAACTTGAAAAGTACAAAAGGAGGTCACATAAAACAGTAAGCTTGAGA
AGCTTTAAGATATGGTGCGAATCGTTACAGAATATTCCTTGCAGAAATAATGGCGGGTCC
GTTCTCTTCTGAAGAAGTTACCGCCCTACTGAAGCATTGCTGTACGATCGTTAATGTGA
TGTGTGTTCGACTGGAAAGCGGAGAACATTATGAAGTAAAAGGACAATCAGCACGCCTTC

YDL125C, 158 aa (SEQ ID NO 40) MEPLISAPYLTTKMSAPATLDAACIFCKIIKSEIPSFKLIETKYSYAFLDIQPTAEGHA LIIPKYHGAKLHDIPDEFLTDAMPIAKRLAKAMKLDTYNVLQNNGKIAHQEVDHVHFHLI PKRDEKSGLIVGWPAQETDFDKLGKLHKELLAKLEGSD

YDL133C-A, 25 aa (SEQ ID NO 42) MRAKWRKKRTRRLKRKRRKVRARSK

YDL136W, 1268 bp, exon1: 501-503, intron1: 504-908, 909-1268 (SEQ ID NO 43) CATGCGGACCTTGTGTTTTGTTTCTAGATTGTTTTATTTTTATGATTGTTGAAGATAT AAACCACTGTATAGTTGTATAAGATAGGATAATGATGGTGCACTGAAAATAAACTTACTA GCTCTTTAATATTGCAACGGCTTGTAACGGGCGCCATGATGACATTCAGAATTATACCAC TACTATATGAAAAATGAAAAGAGGCCCTGCTTTGAACCCGTACATTTTATTCTATAATA TTGCATCTGTGGTTTGCCTGACGGCAGCGAGTCCAACACAAAGTCTGGCATATGCTACGA TTTTACTGAAGATGAGGGTAAATAGAGGCCTGCAATCGTCATCATATGAGAAATGGATAT ATTGAAAATCTACTCACATCTCTTTTTTGGGGGTTTGGTAGTACAGTGAGAACACGATAA AGAACCAAATAGGACTAAAAATGGTATGTAGAGATGAATATACATGAAACGGACGTGATA CTGAAGAAATTTACAGCTACAGTATTACTGCAAACCTTGCAGGCAAATATCAGAGAGAT CTCACCAGCTACAACTTGGTAACAGAAATTTATAAGTTTATGGCACTTGTTAAAATTGTT TGGAAGTTTTCGAAATTATAATATTGGTCTTCAGAAACCTGGAACCACATGTGAACTATT TTTTTTGGATAATGCATTGCACAGAGCGTATTAGTGTATACGAGAATCTAAAAATTTGAA ATCAATAGGCCGGCGTTAAAGCTTACGAACTAAGAACCAAATCCAAGGAACAATTAGCTT CTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGAATTGAAGGTCCAAAAGTTGTCCAGAC CATCTTTGCCAAAGATCAAGACCGTCAGAAAGAGTATCGCCTGTGTCTTGACCGTCATCA ACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAGAGCTTTGACCAAATTCGAAGCTTCCC **AGGCTTAA**

YDL136W, 120 aa (SEQ ID NO 44) MAGVKAYELRTKSKEQLASQLVDLKKELAELKVQKLSRPSLPKIKTVRKSIACVLTVINE QQREAVRQLYKGKKYQPKDLRAKKTRALRRALTKFEASQVTEKQRKKQIAFPQRKYAIKA

YDL167C, 2660 bp, CDS: 501-2660 (SEQ ID NO 45) TGGGTGTCGTCAAACAGGATGCCGTGGAATCATACGAACCGCACATTGTGGTAGAGCTAC AAAGCGATACGAAAGAAGATATGGTATCTAACGTATCCCGTATTGTTGCTTGGGAAAAGA TGTGGTTAGAACAACATCCAGATGGAGTCACAAATGAATATCAAGGGCCTCGTAGCGATG ACGAAGACGATGAAGACAGTGAGTAGGCGTTCCATAACTTTGTGTATCTACATATATACA TATATAATTGTAAATTAGTAACAGTAGTAATAGTGGCCTATTATAAAGGGTTTTCTTT AAGTAATGTCATGTACTTGTTTAATGTGACTTTGGTAATATATTTTCATTCTCCGATGCC GATGCCCAGTGGAAAAGTTTAAAGTGAAAAATTTTTCAACACATACAAGTTTAATAAGTT GGTTTTGATGCAAATAGCATTACTAAAGAAGAGCGCTAGGATAATTGTGCATTGCTATTG TGATTTTTGATACAGAAATTATGCACTATGTGGTACTAGAGCTGCAAGTTGCGCATTTGC CAGATACCCCCAAGGATCAATGTCGCATTGCGAATATAGCATTTCAAATTGTGAATGCTG AAACATTAGTATGCCATTATGGGACCAATTCTTTACCGAGCATTGAAGTAAACGGGACGA CAAAGAGTTTGGAGAGTGCAATGGTGCAATTGGACAAGGATATTCATGACGTTATTGGTA ACGACGACTTTGTTCTTGTTTCCCTGTATTCAACATGGCATATCCGTGTTACCTTACCAC GTCAAGCGAGAGATGATGGGTTTATTCTTACTTCTTATTTACAACATCCGAAAGTATTTG ACTTATGGAAGGAATTCGATAGATGGTGTCAACCATCCGGAGATTTTGGGACAAAAGA AAGCAATCTCCAACAACAATTGTAATACTAAAAGTATTAGTATTAATGCAGCCAAAAATA CGAAGGATTTGGACGAAATAGTTAGAATATTTGGAAGTTTCAATCCCAACTGAAGAGGCAG GCTCTGTTCCAGAGATATACTCTCTTTTAAAAAGGACAACGGATATATTAATACAATTGC ACAAAAAGTGTACTTCCCCTGAAGATATGGAATCTGTCTTAACAAAACCATATGACTCAC ACACCGATATTAGAGCGTTTTTGCAAGAGAAATCTAAGATTTTGTACATGAACAATTTAC CGCCCGACACACTCAAAGTGAGTTGGAATCATGGTTTACCCAATATGGTGTTAGACCAG TTGGGTTTTGGACTGTCAAAAACATCGTAGAAGATACGTCTAACGTTAATAATAACTGGA GTCTAAATAACAGTCCCTATGTGGAAGATCAAGATAGTATCTCAGGATTTGTTGTCTTCC AAACACATGAAGAAGCAACTGAAGTACTAGCGTTGAATGGGAGATCAATCCTATCTAATC TGGCAAACACTAAGCAACCAAGGGTGGTGGAACATGTCCTTGAGCTTCAACCTTCTTCCA CAAGACCAGGTGACTGGAATTGCCCATCTTGTGGTTTTTCAAACTTTCAAAGACGTACTG ACAATAATGTTAACAGTAGTAGAAATAATTTAAACAATCGCGTGAACTCGGGATCTTCAA GCAATATTAGTAACACTGCAGCGAATCACCCCTATGGTGCCCCTGAGTTCAACATGATTG CTAACAACACGCCAGCAGCTTTAACATACAATAGAGCTCATTTTCCTGCAATTACGCCAT TGTCGCGACAAAATTCATTGAACATGGCACCATCGAACAGTGGGTCGCCGATAATTATAG CGGATCATTTTTCGGGAAATAATAATATAGCCCCAAATTATCGTTATAATAATAATATTA ACAATAACAACAATAATATTAACAATATGACCAATAATAGATATAACATTAATAACAACA TCAACGGTAATGGGAATGGTAATGGGAACAACAGTAATAACAATAACAATCATAATAACA ATCATAATAACAATCATCATAATGGTAGTATCAATAGTAATAGTAATACCAATAATAATA ATAATAATAACAATGGTAACAATAGTAATAGTAATTCCAATATCGGTATGGGAGGAT GTGGCTCCAACATGCCATTTAGAGCAGGAGATTGGAAGTGTTCCACGTGCACGTATCATA ACTTTGCTAAAAACGTAGTGTGCTTACGCTGTGGTGGTCCAAAATCAATAAGCGGCGATG CAAGTGAAACCAATCATTACATAGATTCATCAACATTTGGACCAGCGTCGCGTACTCCCA GTAATAACAATATTTCTGTTAATACTAATGGTGGTAGCAATGCTGGTCGCACCGATGGGA ACGATAACAAAGGTCGTGATATTAGTTTGATGGAATTTATGTCACCACCGTTATCGATGG CAACAAAGTCAATGAAGGAGGGAGATGGGAATGGTAGCTCGTTTAACGAGTTCAAAAGTG ACAAAGCTAACGTTAATTTTTCCAATGTTGGTGATAATAGCGCTTTCGGTAATGGTTTTA **ATAGTTCAATACGTTGGTAG**

ISLMEFMSPPLSMATKSMKEGDGNGSSFNEFKSDKANVNFSNVGDNSAFGNGFNSSIRW

YDL184C, 25 aa (SEQ ID NO 48) MRAKWRKKRTRRLKRKRRKVRARSK

YDL191W, 1354 bp, exon1: 501-503, intron1: 504-994, exon2: 995-1354 (SEO ID NO 49) TATTGACGTTTCGCTCTCAGGTCCACCGTGTTCTCAAAAGATACTTTTAAAACCTAAAAC ACACGAAATCATATTATGATAATTCAGAATGATAGTGTGGTACTGTGTCAATTGACTGTT CAAGACTGAAGAGGATCTTTGATTTGTTACTCAACAAATAATCTTCACGAAAACTTT CTCAATCTGGGGACTGTATTAATCTCAGACCCATACATATCTACACCCCATAACTTTTTAC GCGCAGCCTCTCCGGGTGAACCCCACGACAACTTACCTGGCACTCCATGCACTAACGGGC GGGTTTGGGCAGGATTCCAGCATCAATTTTGCAAAATTCACACCTGAGTAATTCATATAT GTAATATATGTTAAGCATACGCTGTCGATTAGCACTATTATTGACCGTAGAATAGGTAC AGTGAGACAGTATATTCGAAATGGTATGTTTGAGATGAACAAAATAATAAAGACTGACAA TTTGGAACGTAATTCATCCGTTGGCTATGTCTATTCAATACAGTTAGAATACGAAAGCTG ATACATCTTTAAATTCAGAGGTTTTGCTGAATTTTAATAGGGAAGTTTACGTTATGATTG GATGCCTGTGCTTAGTTCATTATAAGTGCTAATAAAATACTAACGTTAATAAAAATT TGGAATATTATTTCATTTTTTATCCTATTAATAGGCCGGTGTTAAAGCTTACGAACTAAG AACCAAATCCAAGGAACAATTGGCTTCTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGA ATTGAAGGTCCAAAAGTTGTCCAGACCATCTTTGCCAAAGATCAAGACCGTCAGAAAGAG TATCGCCTGTGTCTTGACCGTCATCAACGAACAACAAGAGAAGCTGTTAGACAATTATA CAAGGGTAAGAAGTACCAACCAAAGGACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAG TTTCCCACAAAGAAAGTACGCTATTAAGGCTTAA

YDL191W, 120 aa (SEQ ID NO 50) MAGVKAYELRTKSKEQLASQLVDLKKELAELKVQKLSRPSLPKIKTVRKSIACVLTVINE QQREAVRQLYKGKKYQPKDLRAKKTRALRRALTKFEASQVTEKQRKKQIAFPQRKYAIKA

CCTCCTCTACATTTTCGTTCTCACCCAAATCTAGGGTCACTTCTTCAAACTCTTCTGGCA ATGAAGACGGTAACCTAATGAATACACCTTCTACGGTTTCCACTGATTATTTGCCACAAC ACCCTCACAGAACATCGTCTTTGCCAAGACCTAATTCCAATCTCTTTCACGCAAGTAATA GTAACCTATCCCGAGCAAATGAGCCCCCAAGGGCCGAAAATTTATCAGATAATATACCAC CCAAGGTCGCTCCATTTGGCTATCCAATACAAAGAACCTCTATTAAAAAATCCTTTTTGA ATGCTTCTTGTACGTTATGTGACGAGCCTATTTCTAACAGAAGAAAGGGAGAAAATTA TAGAGCTTGCATGTGGCCACTTAAGTCACCAAGAATGTCTTATTATCTCTTTTTGGCACCA CTTCAAAGGCAGACGTTCGTGCGCTATTTCCTTTTTGTACCAAATGTAAAAAAGATACTA ACAAAGCCGTTCAATGCATTCCAGAAAATGATGAACTAAAGGATATTCTAATTTCTGATT TTTTGATTCATAAGATTCCTGATTCTGAGTTATCAATCACACCTCAGTCCCGCTTTCCTC CTTATTCACCACTCTTGCCTCCTTTTGGGTTATCCTATACACCTGTTGAAAGACAAACGA TATATTCTCAAGCTCCAAGTCTAAACCCAAATCTCATATTGGCTGCACCCCCAAGGAAA GAAACCAAATTCCACAAAAAAAATCAAACTATACATTTTTACATTCACCCCTGGGGCACA GAAGAATTCCGTCCGGAGCAAACTCTATCTTAGCAGACACCTCTGTAGCGTTGTCAGCTA ATGATTCTATTTCTGCTGTTTCCAATTCGGTAAGAGCAAAGGATGACGAAACCAAAACAA CGTTGCCGCTGTTAAGGTCATATTTTATTCAAATTCTTTTGAACAATTTCCAGGAAGAAT TGCAGGATTGGAGAATAGACGGGGACTATGGATTACTAAGGTTGGTAGACAAATTGATGA TTTCCAAAGATGGTCAGAGATATATACAATGCTGGTGTTTCTTATTTGAAGACGCATTTG TAATAGCAGAAGTGGATAACGATGTTGATGTTTTGGAAATTAGACTAAAGAATTTAGAAG TATTTACACCTATTGCCAACTTGAGAATGACTACACTCGAAGCTTCAGTACTCAAATGCA CCTTAAATAAACAACATTGCGCCGATTTATCAGATCTTTACATTGTTCAGAATATAAATT CTGACGAAAGCACAACTGTACAGAAATGGATATCAGGTATATTGAATCAGGATTTTGTAT TCAATGAGGACAATATCACTTCGACCCTGCCTATTCTTCCCATTATAAAGAACTTTTCAA AAGTTGTTGAAGTTGGAAATGTGCACGATAATGATACTGTAATCATAAGGAGGGGATTCA CCTTAAATTCAGGAGAATGTTCTAGGCAGAGTACTGTCGACAGTATACAATCTGTTCTAA CCACGATAAGCTCAATTCTTTCCCTTAAACGAGAAAAACCTGATAATTTGGCAATAATCT TACAGATCGATTTTACGAAATTGAAGGAAGAAGACAGTTTAATTGTTGTTTATAACAGTC TAAAAGCTTTAACCATTAAATTTGCGCGTTTTGCAGTTTTGTTTCGTTGATCGAAATAATT ATGTTCTGGACTATGGATCGGTATTACACAAGATAGATTCACTAGATTCCATCTCAAATC TCAAATCAAAGAGTTCCTCGACACAATTTTCACCTATTTGGTTGAAAAATACTCTATATC CCGAAAATATTCATGAACATTTGGGTATTGTTGCTGTATCAAATAGTAATATGGAAGCAA AAAAATCCATACTATTTCAAGATTACAGATGCTTTACAAGTTTTGGAAGAAGAAGGCCCA ATGAATTGAAGATTAAGGTGGGCTATTTGAACGTTGACTACAGTGATAAAATTGATGAAC TAGTCGAGGCCAGCTCCTGGACTTTTGTTTTAGAAACTCTTTGCTACAGTTTCGGTCTAA GTTTTGATGAACATGATGACGATGACGAAGAGGGATAATGATGATTCGACCGATAATGAAC TTGATAATAGTTCAGGATCACTGTCGGATGCTGAATCTACAACTACTATTCATATTGATT CTCCATTGATAATGAAAATGCTACCGCAAATATGGTGAATGACAGAAACCTTCTCACTG TGATTCCTAATATTAGATTTTCACTTCATTCTGAGGAGGAAGGTACTAATGAAAATGAAA ATGAAAATGATATGCCAGTATTATTACTTAGTGATATGGATAAAGGAATCGATGGCATAA CCAGACGCAGTTCATTCTCGAGTCTTATAGAGAGCGGTAATAACAACTGTCCCCTCCATA **TGGATTATATATAG**

YDR103W, 917 aa (SEQ ID NO 52)

MMETPTDNIVSPFHNFGSSTQYSGTLSRTPNQIIELEKPSTLSPLSRGKKWTEKLARFQR SSAKKKRFSPSPISSSTFSFSPKSRVTSSNSSGNEDGNLMNTPSTVSTDYLPQHPHRTSS LPRPNSNLFHASNSNLSRANEPPRAENLSDNIPPKVAPFGYPIQRTSIKKSFLNASCTLC DEPISNRRKGEKIIELACGHLSHQECLIISFGTTSKADVRALFPFCTKCKKDTNKAVOCI PENDELKDILISDFLIHKIPDSELSITPQSRFPPYSPLLPPFGLSYTPVERQTIYSQAPS LNPNLILAAPPKERNQIPQKKSNYTFLHSPLGHRRIPSGANSILADTSVALSANDSISAV SNSVRAKDDETKTTLPLLRSYFIQILLNNFQEELQDWRIDGDYGLLRLVDKLMISKDGQR YIQCWCFLFEDAFVIAEVDNDVDVLEIRLKNLEVFTPIANLRMTTLEASVLKCTLNKQHC ADLSDLYIVQNINSDESTTVQKWISGILNQDFVFNEDNITSTLPILPIIKNFSKDVGNGR HETSTFLGLINPNKVVEVGNVHDNDTVIIRRGFTLNSGECSRQSTVDSIQSVLTTISSIL SLKREKPDNLAIILQIDFTKLKEEDSLIVVYNSLKALTIKFARLQFCFVDRNNYVLDYGS VLHKIDSLDSISNLKSKSSSTQFSPIWLKNTLYPENIHEHLGIVAVSNSNMEAKKSILFQ DYRCFTSFGRRRPNELKIKVGYLNVDYSDKIDELVEASSWTFVLETLCYSFGLSFDEHDD DDEEDNDDSTDNELDNSSGSLSDAESTTTIHIDSPFDNENATANMVNDRNLLTEGEHSNI ENLETVASSVQPALIPNIRFSLHSEEEGTNENENENDMPVLLLSDMDKGIDGITRRSSFS

SLIESGNNNCPLHMDYI

YDR238C, 3422 bp, CDS: 501-3422 (SEQ ID NO 53) CCGTGTCAAGATCTAACACGGTAGTCAGCTACTACACAAGGTCTCAGAACAGAATGAGAA GTGGAACACTGGATAATGATTACGTGAACAGACAAAAGCTTCCTACACATATCTCTTC AAGATTATCGTGATGCTAATGCTAGAAGTAATATATCGCGTCAGGACTCTGTCTCCACAA CGAACTCTGATGTGGTAGACCTCAGCTATTCTCTGGGGCATGGCTTGCGTGTGGCAAACC CTGATTCAGACCCAGAATGATATCCTTCTCTGTAGTTTTTGTAGATGTCATATATGTACGT CCGTGTACTCGCTACACGTAGAAAGAAATCAGAAAACAACAGCTCGACAAGTGAAATTTG ACGTTCATTAAGACTCAGTTAAGATTGCCTTGAGAATAAACAAAAGTAATCACAGTTAAC TCGATCCTTCTCCGAGTATGGAGACTTACTCGAGTACCGATTTTCAGAAAGCTCTTGAAA AGGGATCTGATGAACAAAAAATTGACACGATGAAATCAATTTTAGTTACAATGCTGGAAG GAAATCCAATGCCTGAATTGTTGATGCACATAATAAGATTTGTCATGCCTTCTAAAAATA AGGAATTAAAAAGCTTTTGTACTTCTACTGGGAAATTGTTCCCAAACTAGCTGAAGATG GAAAATTGAGACATGAAATGATTCTTGTCTGTAATGCCATTCAACACGATTTGCAACATC CTAATGAATATTAGAGGTAACACATTAAGGTTTTTAACGAAATTGAGAGAGGCCGAAC TCTTAGAACAGATGGTTCCCTCTGTCTTAGCGTGCTTGGAATACCGTCATGCATATGTTC GTAAGTATGCAATCCTAGCAGTTTTCTCCATTTTCAAGGTCAGCGAACATTTACTTCCCG ATGCTAAAGAATCATCAATTCGTTCATAGTAGCTGAAACTGATCCAATATGTAAAAGAA ATGCATTTATTGGGTTAGCTGAATTAGATCGTGAAAATGCCTTACACTATTTAGAGAACA ATATTGCTGATATAGAAAACCTAGACCCTTTATTACAAGCTGTCTTTGTTCAATTTATCA GACAAGATGCAAACAGGACCCCTGCTTTGAAAGCCCAATATATCGAATTATTGATGGAAC TGCTTTCGACCACGACTTCCGATGAAGTCATCTTCGAGACCGCATTAGCCCTAACTGTGT AGGTTTCTGATAATAACATTAAGTTAATTGTTCTAGACCGTATTCAAGACATCAATGCTA ATAACGTAGGTGCTTTGGAAGAGTTAACCCTGGATATTTTGAGAGTCTTGAATGCAGAAG ATTTAGACGTTCGTTCAAAGGCGCTTGATATTTCAATGGACTTGGCCACATCCAGAAATG CTGAAGATGTTGTTCAGCTTTTGAAGAAAGAGCTGCAAACAACCGTAAATAACCCAGATC AAGACAAGGCAATGCAGTACAGACAATTGTTAATAAAAACTATTCGTACCGTGGCTGTAA ACTTTGTAGAAATGGCAGCAAGTGTTGTTTCGCTATTATTAGATTTCATCGGTGATTTAA ACTCGGTTGCCGCCAGTGGTATCATTGCCTTTATCAAAGAAGTGATCGAAAAATACCCAC AACTTAGAGCCAATATCCTTGAAAACATGGTTCAAACGCTAGACAAAGTGAGATCTGCTA **AAGCTTACCGCGGTGCATTATGGATTATGGGTGAGTATGCTGAAGGAGAAAGTGAGATAC AACATTGTTGGAAGCACATTCGTAACAGCGTAGGTGAAGTTCCTATCCTTCAATCAGAAA** TCAAAAAGTTAACACAAAACCAAGAACACCGAAGAAAATGAGGTTGACGCTACCGCCA AGCCAACTGGTCCAGTTATTCTACCAGACGGTACGTATGCCACTGAAAGCGCTTTCGATG TGAAGACTTCTCAAAAGTCAGTTACCGATGAAGAACGTGATTCTAGACCTCCAATTCGCC GGTTTGTTTTAAGTGGTGATTTCTACACAGCTGCCATTCTGGCCAACACCATCATTAAAC TTGTTTTAAAATTCGAAAACGTTTCCAAGAACAAAACTGTCATCAATGCTCTAAAGGCGG AAGCTTTACTAATTTTAGTTAGTATTGTAAGAGTGGGTCAAAGCTCTTTGGTGGAGAAAA AAATTGATGAAGATTCTTTAGAGAGAGTTATGACATCTATTTCTATTTTATTGGATGAAG TTAATCCTGAGGAAAAGAAGGAAGAAGTTAAACTTCTGGAGGTTGCATTCCTGGACACCA CCAAATCCTCATTCAAGAGACAAATTGAAATTGCAAAGAAGAACAAGCATAAGAGAGCAT CTGGTGTGGATTCTACTAATGTGCAAAAAGATAGTATTGAAGAAGATTTACAACTGGCAA TGAAAGGAGATGCAATCCACGCTACTAGCAGCTCTAGTATTTCGAAGCTGAAGAAGATAG ATGTGCAATTTGCAACTCTTGGTGATTTGAAGATTATTGACACACCACAGAAGACCAACG TGATTCCTCATGGCTTCCACAAATTCACTGTTACTGTCAAAGTTTCCTCTGCTGACACAG GTGTCATTTTCGGTAATATTATTATGATGGTGCGCATGGTGAAGATGCTCGTTATGTTA TTTTAAACGACGTTCATGTTGACATTATGGATTATATCAAACCAGCCACTGCTGACGATG **AACATTTCCGTACCATGTGGAATGCATTTGAGTGGGAGAACAAAATATCGGTCAAATCAC AACTACCAACATTGCATGCTTATTTGAGAGAACTGGTCAAGGGAACTAATATGGGTATTC** TAACACCATCAGAGTCGTTGGGAGAAGATGATTGTAGGTTCTTAAGTTGTAATCTGTATG CGAAGTCGTCCTTTGGTGAAGATGCCCTAGCCAACTTGTGTATCGAAAAGGATTCCAAAA CCAATGATGTCATAGGTTATGTTCGTATCCGATCAAAGGGACAAGGTTTGGCTCTGTCCC

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YDR238C, 973 aa (SEO ID NO 54) MTSLSSQPAYTLVFDPSPSMETYSSTDFQKALEKGSDEQKIDTMKSILVTMLEGNPMPEL LMHIIRFVMPSKNKELKKLLYFYWEIVPKLAEDGKLRHEMILVCNAIQHDLQHPNEYIRG NTLRFLTKLREAELLEQMVPSVLACLEYRHAYVRKYAILAVFSIFKVSEHLLPDAKEIIN SFIVAETDPICKRNAFIGLAELDRENALHYLENNIADIENLDPLLQAVFVQFIRQDANRT PALKAOYIELLMELLSTTTSDEVIFETALALTVLSANPNVLVPAVNKLIDLAVKVSDNNI KLIVLDRIQDINANNVGALEELTLDILRVLNAEDLDVRSKALDISMDLATSRNAEDVVQL LKKELQTTVNNPDQDKAMQYRQLLIKTIRTVAVNFVEMAASVVSLLLDFIGDLNSVAASG IIAFIKEVIEKYPQLRANILENMVQTLDKVRSAKAYRGALWIMGEYAEGESEIQHCWKHI RNSVGEVPILQSEIKKLTQNQEHTEENEVDATAKPTGPVILPDGTYATESAFDVKTSQKS **VTDEERDSRPPIRRFVLSGDFYTAAILANTIIKLVLKFENVSKNKTVINALKAEALLILV** SIVRVGQSSLVEKKIDEDSLERVMTSISILLDEVNPEEKKEEVKLLEVAFLDTTKSSFKR OIEIAKKNKHKRALKDSCKNIEPIDTPISFRQFAGVDSTNVQKDSIEEDLQLAMKGDAIH ATSSSSISKLKKIVPLCGFSDPVYAEACITNNQFDVVLDVLLVNQTKETLKNLHVQFATL GDLKIIDTPQKTNVIPHGFHKFTVTVKVSSADTGVIFGNIIYDGAHGEDARYVILNDVHV DIMDYIKPATADDEHFRTMWNAFEWENKISVKSOLPTLHAYLRELVKGTNMGILTPSESL GEDDCRFLSCNLYAKSSFGEDALANLCIEKDSKTNDVIGYVRIRSKGQGLALSLGDRVAL **IAKKTNKLALTHV**

YDR259C, 1652 bp, CDS: 501-1652 (SEQ ID NO 55) AAACTTTGTTCAAGATTATGCTTTCTTTGTAATTTTAAACATAGTCTTGCACTTATTTTT ACTGCATGTGGATAAAAGTTTTTCGAATCGTTTGCAGGCAAATGTAAACTATTACTTTTT AATGATTTCTGATACTCTTTGATTCCATTCTGTCATACTTTTTTCTGCATTTGAAACGCT TTTAATTTCTGGAGAATCTCTTTTTTTGTTATTTTGTTAACACAGTTAGTGGAGCCTTG TAGTATCGAGAGTAGACTATCTTTGGAAAGCAATGCGAGTTGAGAGATTGTGGAGTGTAC TACAGAACCAATATTAAACACAATCTTTCCTCAAACTGTAACACCGAGTTTTTTTCCCCA CCAATCGTGAATCCGATAGCATATACTTTTGTCTAGAAATTTCAATAAACAACAGAATAA CGAAGAGTGCTAAGGGACAAATGCAAAACCCTCCGTTGATTCGTCCCGATATGTATAATC AGGGAAGCAGCTCAATGGCTACTTATAATGCCTCTGAGAAGAATCTAAATGAGCATCCTT CTCCGCAAATTGCACAGCCCAGCACGTCCCAAAAGTTACCTTATAGAATAAATCCTACAA CCACTAATGGGGACACCGACATATCTGTTAACAGCAATCCTATCCAGCCTCCTTTGCCAA ACTTGATGCATCTATCTGGTCCGTCTGACTATAGATCGATGCATCAAAGTCCTATACATC CATCTTATATCATCCCTCCGCATTCAAATGAAAGAAAACAATCAGCTTCTTACAACAGAC CTCAAAATGCTCATGTTAGTATTCAACCTTCCGTGGTATTCCCCCCTAAAAGTTATTCCA TATCTTATGCACCTTATCAAATAAATCCCCCTTTACCAAATGGACTTCCGAACCAGAGCA TATCTTTGAATAAGGAGTATATTGCAGAGGAGCAACTATCAACCCTCCCATCTCGCAATA CCAGTGTTACTACTGCACCTCCTTCTTTTCAAAACAGTGCTGATACCGCTAAAAAATTCAG CTGATAATAATGATAATGATAATGTAACCAAACCTGTTCCTGATAAAGACACCCAAC TCATAAGTAGTTCAGGCAAAACTTTAAGAAATACTAGAAGAGCTGCTCAAAATAGAACCG CTCAAAAGGCATTTAGACAAAGGAAAGAAAAATACATCAAGAATCTCGAACAAAAATCAA AGATATTTGACGATTTACTAGCAGAAAATAATAACTTCAAATCATTAAACGATTCATTAA GAAATGACAACATTTTAATAGCTCAGCATGAAGCTATAAGGAATGCAATTACTATGT TAAGAAGTGAGTATGATGTCTTATGTAACGAAAACAACATGTTGAAGAATGAGAATAGTA TAATAAAAATGAACACAACATGTCAAGAAATGAAAATGAAAACCTAAAACTTGAGAATA TAGTAGGGAGACACTCGGATAGTGCCACGTAA

YDR259C, 383 aa (SEQ ID NO 56)
MQNPPLIRPDMYNQGSSSMATYNASEKNLNEHPSPQIAQPSTSQKLPYRINPTTTNGDTD
ISVNSNPIQPPLPNLMHLSGPSDYRSMHQSPIHPSYIIPPHSNERKQSASYNRPQNAHVS
IQPSVVFPPKSYSISYAPYQINPPLPNGLPNQSISLNKEYIAEEQLSTLPSRNTSVTTAP
PSFQNSADTAKNSADNNDNNDNVTKPVPDKDTQLISSSGKTLRNTRRAAQNRTAQKAFRQ
RKEKYIKNLEQKSKIFDDLLAENNNFKSLNDSLRNDNNILIAQHEAIRNAITMLRSEYDV
LCNENNMLKNENSIIKNEHNMSRNENENLKLENKRFHAEYIRMIEDIENTKRKEQEQRDE
IEOLKKKIRSLEEIVGRHSDSAT

YDR294C, 2270 bp, CDS: 501-2270 (SEQ ID NO 57) CCGACAGTACGACTTAAAAAACAAAACAACGTCCAGGTGGAAAAAGCTGCCGCAAATGG TACACGGTTTAGATCAACAAGATCCAATACCCCTAATTACACATGAATGTGACGTTTCCT **AAAAGAAGTAGCCTGTATAATATAGAGAGATTTTATATACTTTCTTAATGAATTAGACTG** TTTCTACAAGTATTTGACACTGGAAAAAAAGAGAAAGTACATAGAGATTGGCCAAATATT TAAATCTACACAGTTGCCTATCGTTTATCGCCTTATTCTTCAGAAACATTTCATCAACTA TGATTGAAAAAATTGGTATATTTTCAGTACACATATAAAATAAAACCCTCAATTTGCCTCT CCAACCGTTATAACTATTCCAGATCCTCTTTACCGAGCAAGTAGGCTAGCTTCTGTAAAG GGATTTTTCCATCTAATACAATGAGTGGAGTATCAAATAAAACAGTATCAATTAATGGTT GGTATGCCAATTCATTTACTAAGGGAAGAAGCCGACTTTGCCCAGTTTATGATTC TAACCATCAACGAATTAAAAATAGCCATACATGGTTACCTCAGAAATACCCCATGGTACA ATCTGTTGAAAGTTTATGGGCCGGTGAGGTTAGCAGTGAGAACATACGAGCATAGTTCCA GAAGATTGTTTCGTTGGTTATTGGACTCACCATTTTTGAGGGGTACCGTAGAAAAGGAAG TCACAAAGGTCAAACAATCGATCGAAGACGAACTAATTAGATCGGACTCTCAGTTAATGA ATTTCCCACAGTTGCCATCCAATGGGATACCTCAGGATGATGTTATTGAAGAGCTAAATA ACCACGGTGGTGATGATTTGATCCACTTACAAACAATCGCATACGAAAAATATTGCGTTG CCAATCAATTACATCCCGATGTCTTTCCTGCCGTACGTAAAATGGAATCCGAAGTGGTTT CTATGGTTTTAAGAATGTTTAATGCCCCTTCTGATACAGGTTGTGGTACCACAACTTCAG GTGGTACAGAATCCTTGCTTTTAGCATGTCTGAGCGCTAAAATGTATGCCCTTCATCATC GTGGAATCACCGAACCAGAAATAATTGCTCCCGTAACTGCACATGCTGGGTTTGACAAAG CTGCTTATTACTTTGGCATGAAGCTACGCCACGTGGAGCTAGATCCAACGACATATCAAG TGGACCTGGGAAAAGTGAAAAATTCATCAATAAGAACACAATTTTACTGGTCGGTTCCG CTCCAAACTTTCCTCATGGTATTGCCGATGATATTGAAGGATTGGGTAAAATAGCACAAA AATATAAACTTCCTTTACACGTCGACAGTTGTCTAGGTTCCTTTATTGTTTCATTTATGG AAAAGGCTGGTTACAAAAATCTGCCATTACTTGACTTTAGAGTCCCGGGAGTCACCTCAA TATCATGTGACACTCATAAATATGGATTTGCACCAAAAGGCTCGTCAGTTATAATGTATA GAAACAGCGACTTACGAATGCATCAGTATTACGTAAATCCTGCTTGGACTGGCGGGTTAT ATGGCTCTCCTACATTAGCAGGGTCCAGGCCTGGTGCTATTGTCGTAGGTTGTTGGGCCA CTATGGTCAACATGGGTGAAAATGGGTACATTGAGTCGTGCCAAGAAATAGTCGGTGCAG CAATGAAGTTTAAAAAATACATCCAGGAAAACATTCCAGACCTGAATATAATGGGCAACC CTAGATATTCAGTCATTTCATTTCTTCAAAGACCTTGAACATACACGAACTATCTGACA GGTTGTCCAAGAAAGGCTGGCATTTCAATGCCCTACAAAAGCCGGTTGCACTACACATGG CCTTCACGAGATTGAGCGCTCATGTTGTGGATGAGATCTGCGACATTTTACGTACTACCG TGCAAGAGTTGAAGAGCGAATCAAATTCTAAACCATCCCCAGACGGAACTAGCGCTCTAT TAGACGCATTATACAAGTTGGGTCCAGGAGAGGATACCGCCACCAAGTAG

YDR294C, 589 aa (SEQ ID NO 58)
MSGVSNKTVSINGWYGMPIHLLREEGDFAQFMILTINELKIAIHGYLRNTPWYNMLKDYL
FVIFCYKLISNFFYLLKVYGPVRLAVRTYEHSSRRLFRWLLDSPFLRGTVEKEVTKVKQS
IEDELIRSDSQLMNFPQLPSNGIPQDDVIEELNKLNDLIPHTQWKEGKVSGAVYHGGDDL
IHLQTIAYEKYCVANQLHPDVFPAVRKMESEVVSMVLRMFNAPSDTGCGTTTSGGTESLL
LACLSAKMYALHHRGITEPEIIAPVTAHAGFDKAAYYFGMKLRHVELDPTTYQVDLGKVK
KFINKNTILLVGSAPNFPHGIADDIEGLGKIAQKYKLPLHVDSCLGSFIVSFMEKAGYKN
LPLLDFRVPGVTSISCDTHKYGFAPKGSSVIMYRNSDLRMHQYYVNPAWTGGLYGSPTLA
GSRPGAIVVGCWATMVNMGENGYIESCQEIVGAAMKFKKYIQENIPDLNIMGNPRYSVIS
FSSKTLNIHELSDRLSKKGWHFNALQKPVALHMAFTRLSAHVVDEICDILRTTVQELKSE
SNSKPSPDGTSALYGVAGSVKTAGVADKLIVGFLDALYKLGPGEDTATK

CAAGCAATTGTAATCAATAAGCCACCAATTAGAAGGCTACTCAAAAGAATAAAGTTACTA TAAAATATACTGCGGTATATATGTTGCGGTTTCAGCGATTTGCGTCCTCGTATGCCCAAG CACAGGCCGTTAGAAAATATCCAGTTGGAGGTATATTCCATGGTTATGAAGTGAGAAGAA TTCTACCGGTTCCGGAGCTGAGACTCACTGCGGTAGATTTGGTGCACTCCCAGACAGGAG CCGAGCATTTGCATATTGATAGAGACGACAAGAATAATGTGTTCAGCATTGCTTTTAAAA CCAACCCTCAGATTCCACTGGGGTCCCTCATATTCTAGAGCATACAACGTTGTGTGGGT TCATGAACGCTATGACAGGTCCAGATTATACATTTTTTCCCTTTTCCACTACGAACCCTC AAGATTTCGCTAATTTAAGAGGTGTTTATTTAGACTCCACCTTGAATCCGCTACTTAAAC AAGAAGATTTTGATCAGGAGGGTTGGAGGTTGGAGCATAAAAACATCACAGACCCGGAGA GTAACATTGTTTTCAAAGGTGTTGTCTATAACGAAATGAAAGGTCAAATATCAAATGCCA ATTACTATTTCTGGAGTAAATTTCAACAGTCTATTTATCCTTCCCTGAATAACTCCGGCG GAGATCCTATGAAAATTACAGACTTGAGATACGGCGATCTCTTGGATTTCCATCACAAAA ATTACCATCCCTCCAATGCAAAAACTTTCACGTACGGTAACTTGCCATTGGTGGATACGT TAAAGCAATTAAATGAGCAGTTCAGTGGTTACGGGAAGAGAGCTCGAAAGGATAAGTTGT TAATGCCTATTGATTTAAAAAAAGACATAGATGTCAAGTTACTGGGTCAAATAGATACTA TGCTTCCACCGGAGAAGCAGACAAAAGCCTCAATGACGTGGATTTGTGGAGCGCCACAGG CTGTAATGTATCAAAAATTAATAGAATCAGGAATTGGTTTGGAGTTCTCCGTAAATTCAG TTGAAATATTTAAAGACACTGTAAATAATATTTTTCAAAAACCTGTTGGAAACAGAACATC CTTTTGACCGCAAGCGTATCGATGCCATAATTGAACAATTGGAATTATCTAAGAAGGATC TCGATCCTTTTGAGAGCTTGTTTTGAGGACGTTTTGCAAAGATTTAGAGGTGACTTAG AAACGAAAGGTGATACTTTATTCCAAGATTTAATCCGTAAATATATCGTTCATAAACCTT GTTTCACGTTTTCCATTCAGGGATCTGAAGAGTTCTCTAAATCTTTGGATGATGAAGAAC AAACAAGACTGAGAGAAAAAATTACTGCCTTGGATGAACAAGACAAGAAAAACATCTTTA AACGTGGTATACTGTTACAGGAGAAACAAAATGAAAAAGAAGATTTATCCTGTTTACCTA CCTTACAAATAAAAGACATCCCAAGAGCTGGTGATAAATATTCAATCGAACAGAAGAATA ATACAATGTCTAGGATTACTGATACCAATGGTATCACATATGTCAGAGGTAAACGTTTAC TAAATGACATAATACCCTTTGAACTCTTCCCATACTTACCTTTATTTGCTGAATCGTTAA CTAACCTAGGGACAACAACAGAATCCTTCAGTGAAATAGAAGATCAGATAAAATTACATA CGGGTGGTATATCAACACATGTAGAGGTTACATCTGACCCTAACACCACAGAGCCTCGCC GGTCTAAGATCTTACTAGAAACTGATTTCCATAAAAACAGCGATAAATTGAAAGTTCTTA TCCGCTTATTAGCATCTTCAAACACATCTTCTGTAGCAGATGCCGGTCATGCATTTGCAA GGGGCTATTCTGCCGCACATTATAGATCAAGTGGAGCTATAAATGAGACCCTCAATGGTA TTGAGCAACTACAATTTATAAATAGATTGCACAGCTTGTTAGACAATGAAGAAACTTTCC AAAGAGAAGTTGTCGACAAGCTAACTGAATTGCAAAAGTACATTGTTGATACCAATAACA TGAATTTTTTTATCACCTCAGACTCTGATGTTCAAGCGAAAACAGTAGAAAGCCAAATTT CAAAATTCATGGAGAGATTACCTCATGGCAGCTGCTTGCCCAATGGACCAAAGACTTCAG ATTATCCTCTTATTGGATCCAAATGTAAACATACTTTGATAAAATTTCCTTTCCAGGTCC ATTACACATCCCAAGCTTTATTGGGTGTGCCGTATACACATAAGGATGGCTCTGCACTTC AAGTTATGTCAAATATGCTAACATTCAAACATTTGCACAGAGAAGTCAGAGAAAAGGGTG GTGCTTATGGTGGTGCTTCTTATAGCGCCTTAGCGGGTATTTTCAGTTTCTATTCCT ATAGGGATCCTCAGCCTTTGAAGAGTTTAGAAACCTTCAAGAATAGCGGGCGTTATATAC TGAACGATGCCAAGTGGGGCGTCACAGACCTTGATGAAGCTAAATTGACAATATTTCAAC AAGTAGACGCACCTAAAAGTCCCAAAGGAGAGGCGTGACGTATTTCATGAGCGGTGTTA CAGACGATATGAAACAAGCAAGAAGGGAACAACTCTTAGACGTATCTCTCCTGGACGTTC ATAGAGTCGCCGAAAAATATCTACTAAACAAAGAAGGGGTGAGTACGGTCATTGGACCTG GAATCGAGGGAAGACTGTTTCACCAAATTGGGAGGTGAAGGAACTGTAG

YDR430C, 989 aa (SEQ ID NO 60)
MLRFQRFASSYAQAQAVRKYPVGGIFHGYEVRRILPVPELRLTAVDLVHSQTGAEHLHID
RDDKNNVFSIAFKTNPPDSTGVPHILEHTTLCGSVKYPVRDPFFKMLNKSLANFMNAMTG
PDYTFFPFSTTNPQDFANLRGVYLDSTLNPLLKQEDFDQEGWRLEHKNITDPESNIVFKG
VVYNEMKGQISNANYYFWSKFQQSIYPSLNNSGGDPMKITDLRYGDLLDFHHKNYHPSNA
KTFTYGNLPLVDTLKQLNEQFSGYGKRARKDKLLMPIDLKKDIDVKLLGQIDTMLPPEKQ
TKASMTWICGAPQDTYDTFLLKVLGNLLMDGHSSVMYQKLIESGIGLEFSVNSGVEPTTA
VNLLTVGIQGVSDIEIFKDTVNNIFQNLLETEHPFDRKRIDAIIEQLELSKKDQKADFGL

QLLYSILPGWTNKIDPFESLLFEDVLQRFRGDLETKGDTLFQDLIRKYIVHKPCFTFSIQ GSEEFSKSLDDEEQTRLREKITALDEQDKKNIFKRGILLQEKQNEKEDLSCLPTLQIKDI PRAGDKYSIEQKNNTMSRITDTNGITYVRGKRLLNDIIPFELFPYLPLFAESLTNLGTTT ESFSEIEDQIKLHTGGISTHVEVTSDPNTTEPRLIFGFDGWSLNSKTDHIFEFWSKILLE TDFHKNSDKLKVLIRLLASSNTSSVADAGHAFARGYSAAHYRSSGAINETLNGIEQLQFI NRLHSLLDNEETFQREVVDKLTELQKYIVDTNNMNFFITSDSDVQAKTVESQISKFMERL PHGSCLPNGPKTSDYPLIGSKCKHTLIKFPFQVHYTSQALLGVPYTHKDGSALQVMSNML TFKHLHREVREKGGAYGGGASYSALAGIFSFYSYRDPQPLKSLETFKNSGRYILNDAKWG VTDLDEAKLTIFQQVDAPKSPKGEGVTYFMSGVTDDMKQARREQLLDVSLLDVHRVAEKY LLNKEGVSTVIGPGIEGKTVSPNWEVKEL

YDR438W, 1613 bp, CDS: 501-1613 (SEQ ID NO 61) CTTTTCTCAGCACCTGTCCAGAGACATAACATCACAATCACATCGCCCCAGTAAATGCA TACGCAAGATAAGATACAAACTGGCTACGGGAACACTACGCCAACGTGATTGGCAATTGT GCTCTAATAGTTACTCTATTATTGCTGTTAATTGACAATGTTTAGTCACGTGCAACACAA TTCAAGTCACGTGGAAAGGCCTTCACATGGTGATCCATCTTCTACATCTTCATCGGTCCT GCATAAAGTCATAATATGGGGCTACTGGAATGTATGCACTTAACAGTACTATTATATGGT GAGGCTGTAATGCTTACCGTTTTGTGGCTATTCTCGTATTCTGTAGGCCCCCCCATACAC ATTTTTCGGTAACTGCGGCATATAGATGAAAGTTGAAATGAATATTCAAAAGAATATATA TAATAATGCAGGAGATCAAGGAAGAATTAGATATGTATAAGAGTGATGGTAGAGGCAAAA **AATAAAAAGTAAGCAGGAGAATGAATCGTGTTGGTATAGACGTAGATCATATGATAGGGG** TCCTGCTTCTGGCCGTAGTGGTGGTGTTTTGGGTTGGCGCTTCGTGTTTGACTAATGAAT AGGAACGGACAGAACATTACCTATTCACACACAGAATCTTTTTCAGAGTTCCTAC CTTTACTATCTTCAACTCCTTCTACTTCTTCAAATTTGTCTTCGATAGCGGACACGAAAG TGAAGGATACAATGAGGTTGAGTCTGCTATTTTGCGTCTTGTGGTTCGTGGCAAATTTGG CGGCTAACGCTGCTTTGTCGTATACCACAGTGGCTTCGTCAACAATTCTTTCATCGACAT CCTCATTTTTACCTTATTTCTTGCCACTAGTCTAGGAATAGAAACTTTTTCGACAAAAA AACTGCTGGGGTTATTTGTGTCTTTGTTTTGGAATTATCTTAATTGTGATGCAATCCTCGA GGTCATTGGGTTACAGTGTCTATACAACCCTTTTGAAATACGAAATATCATCCAAAGGTC TCAGACTAGACATTCAGATGTTTCTTGGTTATGTTGGTATCTTCACGTTTCTGTTGTTTT GGCCAATTTTAATAATCCTGGATATAACACATATGGAAACTTTTGAACTACCAAGTAACT TCCACATTTCTTTCTTGTCATGTTAAATTGTATCATTATCTTTGTTAGTGACTATTTTT GGTGTAAAGCCCTCATTTTGACATCACCCTTGGTGGTTACCGTTGCCTTAACTTTTACTA TCCCGTTAGCCATGTTCGCTGATTTTGTATGGCGAGAGGCATTTTTTACGCCTTGGTATA TCATTGGTGTTATTTTCATTTTTGTTTCATTCTTTCTAGTTAACCATCGGGGAGAATCTG CTGTTGAAAAGGACTGTGCTGCGGTTGAAAAAGGACCTATCTTGGATGCCTAA

YDR438W, 370 aa (SEQ ID NO 62)
MNRVGIDVDHMIGVLLLAVVVVFWVGASCLTNELLETNAYNKPFFLTYLNISSFALYLTP
DLWRIIQSRRKSLQERTERTLPIHTQESFSEFLPLLSSTPSTSSNLSSIADTKVKDTMRL
SLLFCVLWFVANLAANAALSYTTVASSTILSSTSSFFTLFLATSLGIETFSTKKLLGLFV
SLFGIILIVMQSSKQQDSVSASSFLVGNTLALLGSLGYSVYTTLLKYEISSKGLRLDIQM
FLGYVGIFTFLLFWPILIILDITHMETFELPSNFHISFLVMLNCIIIFVSDYFWCKALIL
TSPLVVTVALTFTIPLAMFADFVWREAFFTPWYIIGVIFIFVSFFLVNHRGESAVEKDCA
AVEKGPILDA

YDR450W, 146 aa (SEQ ID NO 64) MSLVVQEQGSFQHILRLLNTNVDGNIKIVYALTTIKGVGRRYSNLVCKKADVDLHKRAGE LTQEELERIVQIMQNPTHYKIPAWFLNRQNDITDGKDYHTLANNVESKLRDDLERLKKIR AHRGIRHFWGLRVRGOHTKTTGRRRA

YDR486C, 1289 bp, CDS: 501-1289 (SEQ ID NO 65) ACTGCATACACAATAACTGTAGATGTAGCCCAAGGCACTACCACAGGTATTTCTGCTCAC GACAGGTCGATGACTTGTAGGGCTCTTGCAGACTCTTCCTCTACGCCAAAATCATTTTTA AAACCAGGGCACATCTGTCCCTTGAGAGCCGCTGATGGCGGTGTTTTGCAGAGAÄGAGGC ${\tt CACACTGAGGCCGGTGTCGATTTGTGTAAACTAAGTGGACTAAGTCCCGTCGCTGTTATT}$ GGCGAATTGGTTAACGATGACGAACAAGGAACTATGATGAGATTAAATGACTGCCAAGCG TTTGGTAAGAAACATGGCATTCCTTTGATCTCCATCGAAGAATTGGCCCAATATTTGAAG **AAATAATCTGGTGAACATTTTCTCCATTCATTCATCACAACAGACTCACACATATATAC** ATGTATATTTGTAACTTTGTATATATCTTTTGTTTTTTGACCTTTTTCTTCCTCTATG TTTTTCAGCCATACAAAAATATGGGATTTTTAGCAAGAGAAAAAGTACATCTAAAAAAAG TAGTAATAGGAGGAAGCCAAGATTGGTTGAAACACAGTTATAAACTCTTCAAGGCAATTA TGAACAGGATTTTCGGATATGGGAACAAAAAGAGCCATGATCAGCTCTTACAAGAGTCGA ATCAGTCCATGAATCAGGCCCAACAATCACTATCGAACAGAATATCCCAGTTAGATACTC AAATCGCCCAGTTAAACTTCCAGCTGCAAAATATTCAAAAGAATTTGCAAAGATCAAACA AAAATATGAAGGATTCTTTAGATTCTCAATCCTGGTCCATGACGCAAGCCCAGTTAACAA ATGATAACTTACAGAACACAATGATCACTATAAACGCACTAAAGCAAACAACAACGCA TGAAGGCTCAATACGGCAAGATAAATATCGACAAACTACAGGACATGCAGGATGAGATGC TGGATTTAATAGAACAAGGGGATGAGCTGCAAGAAGTCTTGGCAATGAATAATAACAGTG GCGAGCTCGACGACATTAGTGATGCAGAGCTGGATGCAGAGCTGGATGCTCTGGCACAAG TAGGTGCGAATGCGCCACCGGCTTTTATTGATGAAGAGCCAAACTTAGATACTGAAGACA AAAATAAAGCTTTAGAAAGCGCTCAGTGA

YDR486C, 262 aa (SEQ ID NO 66)
MGFLAREKVHLKKVVIGGSQDWLKHSYKLFKAIMNRIFGYGNKKSHDQLLQESNQSMNQA
QQSLSNRISQLDTQIAQLNFQLQNIQKNLQRSNNKQPSLRKQALKILNKRKQLENMKDSL
DSQSWSMTQAQLTNDNLQNTMITINALKQTNNAMKAQYGKINIDKLQDMQDEMLDLIEQG
DELQEVLAMNNNSGELDDISDAELDAELDALAQEDFTLPTSENSLGNDMPSYLLGANAPP
AFIDEEPNLDTEDKNKALESAQ

YDR471W, 136 aa (SEQ ID NO 68) MAKFLKAGKVAVVVRGRYAGKKVVIVKPHDEGSKSHPFGHALVAGIERYPSKVTKKHGAK KVAKRTKIKPFIKVVNYNHLLPTRYTLDVEAFKSVVSTETFEQPSQREEAKKVVKKAFEE RHQAGKNQWFFSKLRF

YDR499W, 2744 bp, CDS: 501-2744 (SEQ ID NO 69) TAACAATAGAAAAAATACACACACTAGATTGGAATTAGAGCTTAAGTGGTACAAACT AGGGCTAATAAAGAGGTAACGGTCGGTTCTCTACTAAGGTTCGTATTGTGTGGCACCGAT GTTAAGCACTTTTAAGCGGAATAACTCGAGTGGAAATTTTATGTTTAGTTTAGGTTTTACC AGCAAAGCAGTAAAAAGTCTCTGAATAAGGATAGTAACCTGTAGTAACTCCAAAATTTAT CTTACAAAGAGCTATTAGTATCTTGGTTCTTCTATTTTCTTCGATTATTGGTGATTTTTC CCGCCTCTAGCCAAATCCGAGCGTTCCATCGATTTTTTGGGGAAAACAGCACATGCAATA AAATAAAAAGCAAACAAATACGCGATAGTGCACGAAACGTCAACACAATCATCAAACTCT . ATGATGATATTCTTTTGGAATTAGGCACCAGGCCTCCAAGGTTTACTCAAATACCGCCAT CATCAGCAGCATTACAAACACAAATTCCCACTACTTTGGAGGTTACAACGACCACATTAA ACAATAAACAGAGTAAAAATGATAACCAACTGGTTAACCAACTGAATAAAGCTCAAGGTG **AAGCAAGCATGCTTCGTGATAAAATAAACTTTTTGAACATTGAAAGGGAAAAGGAAAAGA** ATATTCAAGCCGTCAAAGTTAATGAATTGCAAGTCAAGCATCTTCAAGAGTTGGCTAAAT TAAAACAAGAATTACAGAAACTGGAAGATGAGAAGAAGTTCTTACAGATGGAAGCGAGAG GAAAATCGAAAAGGGAAGTTATTACGAATGTAAAAACCACCGTCAACAACATTATCAACAA ACACAAACACTATAACGCCAGATTCGTCCTCAGTTGCAATCGAAGCAAAACCTCAATCAC ACCCAAATAGGATTATTCCCGATGAAACGAGTTTATTTCTAGAGTCAATATTACTTCATC **AAATAATAGGCGCTGACCTGAGCACAATAGAATATTAAATAGATTGAAGCTTGACTACA** TCACAGAGTTTAAATTTAAGAATTTCGTCATTGCTAAAGGAGCCCCCATAGGGAAGTCCA TAGTTTCTCTACTTTTGCGATGTAAAAAGACGTTGACCCTCGACAGGTTCATAGATACTT TGCTAGAGGATATAGCTGTTTTGATCAAGGAAATATCAGTTCATCCAAATGAATCGAAAT TAGCTGTCCCATTTCTCGTTGCATTGATGTATCAGATTGTACAATTTCGTCCTAGTGCCA CTCATAATTTAGCACTGAAGGATTGTTTTCTTTTTATTTGCGATTTAATAAGAATCTATC **ATCATGTATTGAAAGTACCGATACATGAATCAAATATGAATTTGCATGTAGAACCTCAGA** TTTTCCAATATGAACTGATAGACTATTTGATAATTTCGTATTCCTTTGATCTCCTAGAAG GTATATTAAGGGTACTGCAGTCGCATCCTAAGCAAACTTATATGGAATTTTTTGATGAAA ATATTCTAAAATCATTTGAATTTGTCTACAAACTAGCACTAACCATTTCATACAAGCCAA TGGTAAATGTAATATTTAGTGCAGTCGAGGTCGTTAATATTATCACTAGTATAATATTAA ATATGGACAATTCCTCAGATCTGAAATCCTTGATAAGCGGTAGTTGGTGGAGAGATTGTA TTACAAGATTATACGCTCTTTTGGAAAAGGAAATTAAGAGTGGCGACGTATATAATGAAA ATGTGGATACTACAACTCTTCATATGTCGAAGTACCATGACTTTTTTGGGTTAATCCGAA **ATATAGGTGATAATGAATTGGGAGGATTGATATCAAAGCTGATTTATACTGACCGATTGC** CCCCTATAATAGGTTACAAGATGGAAAAATGGCTTTTGAAGTTAAAAGATGAAGTTTTAA ATATTTTTGAAAATTTATTAATGATCTATGGAGACGATGCGACCATAGTAAATGGAGAAA TGCTCATCCACTCCTAAATTCTTATCCAGGGAGCAAGCGTTAATGATAGAAAGGTACG

TGGGACAAGACTCCCCGAACTTGGACCTCAGATGCCATCTTATTGAACATACTTTAACCA
TAATATATAGGCTATGGAAGACCATTTCAAACAATTGCGTGAAGAACAAATCAAGCAGG
TAGAAAGCCAATTGATTATGTCACTATGGAGGTTTCTCGTATGCCAAACCGAAACTGTGA
CAGCAAACGAAAGAGAAATGAGAGATCATCGACACCTTGTAGATAGTTTGCATGATCTGA
CGATAAAGGATCAAGCCTCTTATTACGAAGATGCCTTTGAGGATTTACCAGAATATATCG
AAGAAGAATTGAAGATGCAATTGAATAAAAGAACGGGGAGAATAATGCAAGTAAAGTACG
ATGAGAAATTTCAAGAAATGGCAAGAACTATTCTTGAGTCAAAATCATTCGATCTAACCA
CACTAGAGGAGGCCGATTCATTATATATCTCAATGGGACTGTAA

YDR499W, 747 aa (SEQ ID NO 70)
MRRETVGEFSSDDDDDILLELGTRPPRFTQIPPSSAALQTQIPTTLEVTTTLNNKQSKN
DNQLVNQLNKAQGEASMLRDKINFLNIEREKEKNIQAVKVNELQVKHLQELAKLKQELQK
LEDEKKFLQMEARGKSKREVITNVKPPSTTLSTNTNTITPDSSSVAIEAKPQSPQSKKRK
ISDNLLKKNMVPLNPNRIIPDETSLFLESILLHQIIGADLSTIEILNRLKLDYITEFKFK
NFVIAKGAPIGKSIVSLLLRCKKTLTLDRFIDTLLEDIAVLIKEISVHPNESKLAVPFLV
ALMYQIVQFRPSATHNLALKDCFLFICDLIRIYHHVLKVPIHESNMNLHVEPQIFQYELI
DYLIISYSFDLLEGILRVLQSHPKQTYMEFFDENILKSFEFVYKLALTISYKPMVNVIFS
AVEVVNIITSIILNMDNSSDLKSLISGSWWRDCITRLYALLEKEIKSGDVYNENVDTTTL
HMSKYHDFFGLIRNIGDNELGGLISKLIYTDRLQSVPRVISKEDIGMDSDKFTAPIIGYK
MEKWLLKLKDEVLNIFENLLMIYGDDATIVNGEMLIHSSKFLSREQALMIERYVGQDSPN
LDLRCHLIEHTLTIIYRLWKDHFKQLREEQIKQVESQLIMSLWRFLVCQTETVTANEREM
RDHRHLVDSLHDLTIKDQASYYEDAFEDLPEYIEEELKMQLNKRTGRIMQVKYDEKFQEM
ARTILESKSFDLTTLEEADSLYISMGL

YDR507C, 3929 bp, CDS: 501-3929 (SEQ ID NO 71) CTCTTTAAATATTCTATGTACTTTGTGCAAACATCATTGTCATCACATAAATGCATTCCT ACTATTACTAACTTGAACTTCACTTCACTGGAAGAACTGGGTTATTCAAGGTAAAGAAAT CATTTGTTTTGCGCCAAGTTTCGTCTGACAAGAATTTTTTATTATTATTTCCCACTTTTC ATCGAAGGAAACGCGTCAAATCCATTCGTTACTACGCGCAATCTGCGTTATTTCCTTTTT CGGCATACCATCGCGAAATATCAACGGCCACACCATAGATTCCTTTTGATGTTAAATTAA TTTGCTTTCTCTCTGTCGACACGTCTCAACTGTACTCACCATTAGTATTCTCGAAGGC **ATACAATAATAACATTCAAAATGGCAATCAATGGTAACAGTATTCCTGCCATAAAGGATA** ATACCATCGGTCCATGGAAACTAGGTGAAACTCTCGGTCTAGGGAGCACTGGTAAAGTCC AGCTTGCTCGTAATGGATCCACAGGACAAGAGGCGGCAGTTAAGGTAATATCAAAAGCAG TATTCAATACCGGTAATGTCAGCGGTACTTCGATTGTTGGCTCCACCACCCCAGATGCTC TACCATATGGTATAGAACGCGAAATAATCATTATGAAGTTGTTAAACCACCCAAATGTGT TACGTTTATATGATGTCTGGGAAACAAATACAGATTTATACCTTGTTTTAGAATACGCGG AGAAAGGTGAGTTGTTCAACTTATTGGTTGAGAGAGGTCCTCTGCCAGAGCATGAAGCTA TCAGGTTTTTTAGACAAATTATTATTGGTGTGTCGTACTGTCATGCGTTGGGTATTGTCC **ATCGTGATCTAAAACCGGAAAATCTATTATTAGATCATAAATATAACATCAAGATTGCAG** ATTTTGGTATGGCTGCTTTGGAAACTGAAGGAAAGCTACTGGAGACGTCGTGCGGATCAC CACATTATGCTGCACCAGAAATTGTATCTGGTATACCGTATCAAGGTTTCGCAAGTGATG TGTGGTCATGCGGTGTGATCCTATTCGCCCTTCTTACTGGTCGGTTACCCTTTGACGAGG **AAGATGGAAATATAAGAACACTATTACTTAAAGTTCAAAAAGGTGAGTTCGAAATGCCTT** CTGATGATGAAATTTCGCGTGAAGCTCAGGATTTGATTAGAAAAATCTTAACCGTTGATC CTGAAAGAAGAATCAAGACCAGAGATATACTCAAACATCCGCTATTACAAAAATATCCAA TATCAGAAAGTAATTCTTCTATTGACGCTACGATTTTGCAAAATTTAGTAATATTATGGC ATGGAAGAGATCCTGAAGGAATTAAGGAAAAACTAAGAGAACCTGGCGCTAATGCAGAAA AGACATTATATGCACTACTGTATAGATTTAAGTGTGACACTCAAAAAGAGCTTATTAAGC AACAGCAAGTTAAGAAGAGGCAGTCAATTAGTAGCGTTTCTGTTTCCCCATCTAAAAAAG TATCGACAACTCCACAACGCAGAAGAAATAGAGAATCTTTAATTAGTGTAACATCTTCTC GTAAAAAGCCAATATCCTTCAACAAATTCACTGCCTCCAGTGCCTCCTCCAGCAATCTAA CTACACCCGGTTCTTCAAAACGCCTTTCAAAAAACTTCTCTTCAAAGAAGAAATTATCTA CAATCGTTAACCAATCTTCTCCAACACCAGCATCACGTAATAAAAGAGCTTCGGTTATAA ATGTGGAAAAGAATCAAAAAAAGAGCCTCTATCTTTTCTACTACCAAGAAGAACAAAAGAT CTTCTAGATCTATCAAGAGAATGTCATTGATACCAAGCATGAAACGTGAATCGGTGACAA CAAAATTAATGTCAACATATGCGAAATTGGCAGAGGATGACGATTGGGAATACATTGAGA

CAAAATTCTTGGGTTCATCATTTAATATCGATAAAGAGTTGAAATTGTCTAAAATGGAAT ATCCAAGTATAATTGCACCACAAAGATTGTCAGAGGAGCGAGTGGTGTCAGATTCTAATG ATGGATATGAATCTTTGATCCTCCCGAAGGATGGGAATGGCGTATCTCAATTAAAGGATA GTACCGCAACAACTGCTCCCGTCTCTGATGGTAGGTTGAGGAAGATCTCTGAAATTAGAG TACCACAATTTACTAGAAAATCAAGGCATTTTAGTGAGTCCAATAAAAGGCTATCTGTCC TGTCGATGTACTCTACCAAGGAGTCGTTTACCAACTTGGTTGATATTTTGAAAAACGGTA ACCTTGATGTCAATAACCAACAAGCCAAGAATTCCAACACCAAGAAGTGCGGATGATT CAGAATTTCTTTTGAAACTGTCAACGAAGAAGCTGAATATACAGGAAATAGTTCGAACG ATGAGAGATTGTACGATGTCGGTGATTCCACTATCAAAGACAAATCCGCGTTAAAGCTGA CGATCCTTCCTCCGCTTAATGGTGACAATGAATTGCGTAAACAGAATAGCCAAGAGGGTG ACCAGGCACATCCAAAGATTAAATCGATGATACCAGAATCAGGCTCTTCTTCACATACTG AGGATCAAGAAAAAGAGAGAAAGTAGTAGATGATATGGAGCCACCATTGAACAAATCTG TGCAAAAAATTAGGGAAAAAATGCTGGCTCGCAGGCAAAGGATCATTCAAAAGATCACT TAAAAGAGCATAAGCAGGATAAAAATACAGCAATTGGAAATGGTTCCTTCTTTAGAAAAT TCTCAAAATCTTCGGACAAAACAATGGAATTGTATGCCAAGATTTCTGCAAAACAATTGT TTAATGGTTTAGAGAAGCTGTTGCGTGGTTGGACTCAGTATGGTTTAAAAAATATAAAAAT CGCACCCCAACAATCTGACCTTAACGGGTAAACTATCGAGTGATAATATATTCTCACTAC GTTCAACACTCTTTGAGGTTAATATTTATCCGAGAGGTAAGATGAGCGTTGTGCAGTTCA AGAAAGTTTCTGGTTCATTCAAAGCTGTCAAAAAGTTGGTCAATGAAGTTGAGAACGTCC TGAATAAGGAAGGCGTTCTACAAAAATAG

YDR507C, 1142 aa (SEQ ID NO 72) MAINGNSIPAIKDNTIGPWKLGETLGLGSTGKVQLARNGSTGQEAAVKVISKAVFNTGNV SGTSIVGSTTPDALPYGIEREIIIMKLLNHPNVLRLYDVWETNTDLYLVLEYAEKGELFN LLVERGPLPEHEAIRFFRQIIIGVSYCHALGIVHRDLKPENLLLDHKYNIKIADFGMAAL ETEGKLLETSCGSPHYAAPEIVSGIPYQGFASDVWSCGVILFALLTGRLPFDEEDGNIRT LLLKVOKGEFEMPSDDEISREAODLIRKILTVDPERRIKTRDILKHPLLQKYPSIRDSKS IRGLPREDTYLTPLSESNSSIDATILONLVILWHGRDPEGIKEKLREPGANAEKTLYALL YRFKCDTQKELIKQQQVKKRQSISSVSVSPSKKVSTTPQRRRNRESLISVTSSRKKPISF NKFTASSASSSNLTTPGSSKRLSKNFSSKKKLSTIVNQSSPTPASRNKRASVINVEKNQK RASIFSTTKKNKRSSRSIKRMSLIPSMKRESVTTKLMSTYAKLAEDDDWEYIEKETKRTS SNFATLIDEIFEYEKYEOIRKEKEELERKVREAKAREELERRRRKOEEKERARKLLEKED LKRKQEELKKQIEIDISDLEQELSKHKEEKLDGNIRSISAPMENEEKNINHLEVDIDNIL RRRNFSLQTRPVSRLDPGIMFSSPTEEVSPVEPKRTENERLTTEKKILETIRRSKFLGSS FNIDKELKLSKMEYPSIIAPQRLSEERVVSDSNDGYESLILPKDGNGVSQLKDSTATTAP VSDGRLRKISEIRVPQFTRKSRHFSESNKRLSVLSMYSTKESFTNLVDILKNGNLDVNNQ QSQRIPTPRSADDSEFLFETVNEEAEYTGNSSNDERLYDVGDSTIKDKSALKLNFADRFN GSNEAKOTDNLHLPILPPLNGDNELRKONSOEGDOAHPKIKSMIPESGSSSHTEKEEENE EKEEKKPEQHKQEEDQEKREKVVDDMEPPLNKSVOKIREKNAGSQAKDHSKDHLKEHKQD KNTAIGNGSFFRKFSKSSDKTMELYAKISAKQLFNGLEKLLRGWTQYGLKNIKSHPNNLT LTGKLSSDNIFSLRSTLFEVNIYPRGKMSVVQFKKVSGSFKAVKKLVNEVENVLNKEGVL

YDR515W, 1844 bp, CDS: 501-1844 (SEQ ID NO 73)
GAGTTGAATCTATGCGTAACCATTTTGACTACCGCTTCGTATGCTTTCTTGCACTTTGTG
GAGCTACTCATACAATAGCTTATAATCTGTGTAGTCAAACTATATACTAGGCAAATTACT
AGTAAATGCAGTATTCATATGTCCTCAAACCGTTTTTTTGCAGTATGTTATTGATCCATCG
AATCAAAATTTTTCACCGCCAAGAGAAAAAAGATCTTACTATTTTTGTGCTTATGAAAAAA

TTAGTAAAAGTAAAGCTGGAAGCACATACAAGCGCAGCTGAATCACAAAGGAAAATTGGC ACATCCTTGGTTGACACTTGTCTATTTATTAAAAAGGTTTTAAAAAGTAGTGTTCAGCAGT TCTATCATATTTTTTTATTTAAAAAAAAATACTGAGAGGAAGCGTATTGTTAAGACACAA TTTAGGGTGGCGTTAAATAAACGAGAGGCCCAAAAATATAACCAAGATAAAGAAAATCA ATCATAAAGTGAATTCAAAAATGTCATCGCAAAACCTCAATGATAATCCAAAAAATACAA CCTCAGCAGCTGAAGATAAGAAGAAACAAACTTCATCCTTAAAGTTGGCACCAATACCAA

CCACATCGCCATGGAAATCATCTTCGCCAGATAGCAATACAGTAATTCCTGTAGAGGAAC TAAGAGATATATCAAAGACTGCAAAGCCAAGTAAAAATGGTTCGGGGTCAATTAAATTAA CAAGCAATACCAAATGGACTCCAATTACGCCGTCTGTTATAATCTCAGGTTCCAAGGACA CAAATTCAAAGTCAGGAAAGAACTCTAAAAATTCTAAGACTAATAAAAAAATGAAAAAGC GTGGCAAATATAACGATATCAATAAAAAGGACTTTAACGGTCAAACCAACAGTACAT CGGAAATAAGTAACGTTTCCAATCTTGAATCCAAACCTTTAGATGCTAACGCTAAAGTAA ACATACATTCAAGCTCAGGAGCAACTGCCAATGGGAATATAAAGAGGGATAACAACAACA ACAATTCAACCAACGGTAGACAATCAAGAAATTATCAAAACAGGAATGGCAAAACAAGAT ACAACAACAATAGTAGACACAGTCAGGCGGCTAATAATGCCATCTCCTTCCCAAATAATT ATCAGGCTAGACCTGAATATATTCCCAATGCCAGCCACTGGTTGAACAACAATTCAAGAA ATAGCTATAAACAACTGTCATACTTCCGTCAACAGCAGTATTATAATAACATCAACTATC AACAACAATTGCAAACACCATATTATTACTCAATGGAACCTATTTTTAAATCTATCGAAA GTATCAAAAACCAAATTGAATTCTATTTTAGTGAAGAGAACTTGAAAACAGATGAATTTT TAAGATCTAAAATTCAAAAAAGCCAATGACGGATTTATCCCCATGAGTTTGATAGGGAAAT TTTACCGTATGGTTAATTTATCTCTTGGTGGAGACCCAAATTTAATTTTGGCATCTATGA GAGAAGTTTTACAACATAAAGAAACAAACCATTTGGAAATTGCCCTTGGAAGCATAGAAG GTGCTCAGAAGAACATGGCAGATGATTTCAATCCATTGGAAAACTATTTTATTAGGCGCG AAAATTGGGCTGAATACGCTATGGAAAGTAATTTTGATGAAAATGATGACGAAACTGAAA **AATACAACATTGAGAAACTATTGGGACCGAACGATTTAGACAATTATTCTTATATGGGCT** ATCCAAACTTCTTTCCCAGTAATGAAAATGGGAAAAAGAGTCAGAGCTATGACCAAGGTG AAATTAGCAGGCAGTTTGAACAAAACTTACAAATAAATGATTAA

YDR515W, 447 aa (SEQ ID NO 74)
MSSQNLNDNPKNTSSAAEDKKKQTSSLKLAPIPTTSPWKSSSPDSNTVIPVEELRDISKT
AKPSKNGSGSIKLTSNTKWTPITPSVIISGSKDTNSKSGKNSKNSKTNKKMKKRGKYNND
INKKDFNGQTNSTSEISNVSNLESKPLDANAKVNIHSSSGATANGNIKRITNNNNSTNGR
QSRNYQNRNGKTRYNNNSRHSQAANNAISFPNNYQARPEYIPNASHWLNNNSRNSYKQLS
YFRQQQYYNNINYQQQLQTPYYYSMEPIFKSIESIKNQIEFYFSEENLKTDEFLRSKFKK
ANDGFIPMSLIGKFYRMVNLSLGGDPNLILASMREVLQHKETNHLEIALGSIEGAQKNMA
DDFNPLENYFIRRENWAEYAMESNFDENDDETEKYNIEKLLGPNDLDNYSYMGYPNFFPS
NENGKKSQSYDQGEISRQFEQNLQIND

YDR518W, 2054 bp, CDS: 501-2054 (SEQ ID NO 75) GCAGCAGGGCAAGATGACAACCCTGTTCCTGTTCCTGTTCCAGTAGAATCTGAGACGGC AAAGGGTACCCAGCCATTGGCAATGGATGACTATTTTAATGAAGGCAGAGATAAGTCATC TACCGCTGCGAAGTCAGCAGAATCTGACATCCTCGCCCCACCACCACAAAAACAGTCATC CTCTGATTAACTTTCCTGGTTAGTCTTTTGGTTTTGTTTCATAGCAAAATTAAATATATA TATATAAGCTTGCTTTCCCTTCAAAACACGTAAACGATAGTTGGCAATGTACGAAAAGTA CCGAGACTTTTTTCAAAGGCACGCGTGTCCTTTTTTGTTAAGACAATAGATATTTTAGC ATTCAGAAAGTTTCAATTTCCAAGACTTGACGTTTCAATTATATGGCAATCTCCCAACAA GCACCCGCTCATATAATACCATGCAAGTGACCACAAGATTTATATCTGCGATAGTCTCGT TTTGCCTGTTTGCTTCTTTCACGTTGGCTGAAAACAGCGCAAGAGCTACGCCGGGATCAG ATTTACTCGTTCTAACAGAGAAATTTAAATCATTCATCGAATCTCATCCGTTAGTCC TCGTCGAGTTTTTTGCTCCATGGTGTTTGCATTCTCAGATCTTACGCCCTCACTTAGAAG ACAGTATGGTTTGCCTGCAACAAACTATAAATACCTACCCAACCTTGAAAATCTTTAAAA ATGGTCGTATTTTTGATGGTCAAGTCTATCGCGGTGTCAAGATCACCGATGAAATCACTC **AACCATACTTGGAAAATGCAACTTTACCAGTAGTAATAAACAGAGGCTTGACAGGCTTGA** ATGAAACGTATCAAGAAGTCGCACTGGACCTTGCTGAGGATTACGTCTTTTTATCCCTTC TAGATTCAGAAGATAAGTCATTATCAATCCACTTGCCAAACACTACAGAACCAATTCTGT TTGATGGAAATGTAGACTCTTTGGTCGGAAATTCCGTTGCTCTAACTCAGTGGTTAAAAG

YDR518W, 517 aa (SEQ ID NO 76)
MQVTTRFISAIVSFCLFASFTLAENSARATPGSDLLVLTEKKFKSFIESHPLVLVEFFAP
WCLHSQILRPHLEEAASILKEHNVPVVQIDCEANSMVCLQQTINTYPTLKIFKNGRIFDG
QVYRGVKITDEITQYMIQLYEASVIYLNSEDEIQPYLENATLPVVINRGLTGLNETYQEV
ALDLAEDYVFLSLLDSEDKSLSIHLPNTTEPILFDGNVDSLVGNSVALTQWLKVVILPYF
TDIEPDLFPKYISSNLPLAYFFYTSEEELEDYTDLFTQLGKENRGQINFIALNSTMFPHH
VRFLNMREQFPLFAIHNMINNLKYGLPQLPEEEYAKLEKPQPLDRDMIVQLVKDYREGTA
KPIVKSEEIPKEQKSNVYKIVGKTHDDIVHDDDKDVLVKYYATWCIHSKRFAPIYEEIAN
VLASDESVRDKILIAEVDSGANDILSFPVTGYPTIALYPAGNNSKPIIFNKIRNLEDVFE
FIKESGTHHIDGQAIYDKLHQAKDSEVSTEDTVHDEL

YDR519W, 908 bp, CDS: 501-908 (SEQ ID NO 77) GGGGCAAATGATATCTTAAGTTTTCCTGTGACAGGATATCCAACCATTGCTTTGTATCCT GCCGGAAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAAATTTGGAAGATGTTTTC GAATTTATCAAGGAATCAGGTACACATCACATTGACGGCCAGGCAATTTATGATAAATTG CACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTACATGATGAATTATAATCA ATAAATAAAGCATATATAATGCACATTTTTAACATCTGATTACTCGCATCGTTTCTGGAA GAAAATAGCTAATATTCGTTATTTATGGCATCACGATTATTCTCACCAGTTACCCGTTTA TGCTCTTGAAGAGATTTAGCATTACTGCCAGCGCATCTTCAAATACAGGTTTATATGAGA CCCATTACTATAACCCTAAGAAGAGAAAAAGGAGTGCTTTCGTTTTCAATCACATTCTAG CCATTCTTGCAGGTTCCCTGTCAGATTTGGAAATCGGTATTATCAAGAGAATACCGGTAG AAGATTGCTTAATTAAGGCAATGCCAGGTGATAAAGTTAAGGTTCATTATACAGGATCTT TATTAGAATCGGGAACTGTATTTGACTCAAGTTATTCAAGAGGCTCTCCTATCGCTTTTG **AACTTGGCGTTGGCAGAGTAATTAAAGGTTGGGATCAAGGTGTTGCCGGCATGTGCGTTG** GCGAAAAAAGAAGCTGCAAATTCCAAGTTCTTTGGCCTACGGAGAAAGAGGTGTCCCAG GCGTCATTCCTCCAAGTGCTGATTTGGTGTTTGATGTCGAATTGGTAGACGTGAAATCAG CCGCCTAG

YDR519W, 136 aa (SEQ ID NO 78) MMFNIYLFVTFFSTILAGSLSDLEIGIIKRIPVEDCLIKAMPGDKVKVHYTGSLLESGTV FDSSYSRGSPIAFELGVGRVIKGWDQGVAGMCVGEKRKLQIPSSLAYGERGVPGVIPPSA DLVFDVELVDVKSAA

YER102W, 1103 bp, CDS: 501-1103 (SEQ ID NO 79)
CGAGCTTGCCAGCATTCCAATGCCCATCGTATTGTACTCAATGGTGAAACTTACCACCAT
ATTGTTAAAAGCTATTATTTATGATTTTTACCTACCAAACATTGAAAGGAGAACTGAACAC
ACCACGATAAAACGTATGTTCTGATACCCAGCAAATGAGAAAGTAGAAGGAGAAACCTAA
AAACCTGTGGCGGTCAAGACTGCTAGCAAGATGGATATTTAGATCATAAATTCTAACGCA
TGCATCCTGAGCAATGAAATCATGCAACCTAACATTTGAGGTTAATATATAGAGAATTAAC
TAGCGTTGAGGAGGTACTGCAATTTAAAAGACCGAAGAATTATCGATGCAAGGAAAAATG
GGTCTAGGATGAATACGAGCAATTGAAATACATTTGGAATACCTTGTGAAAATATCACAT
ACTTTCGCCTTCTATCTCGATGCGTTATTACAAGAAAATAGTTTTACTAACAAATTAACA
AAAATTAAAATAGTGTAAAAAATGGGTATTTCTCGTGATTCCGTCACAAAAGATCAGCCA

PCT/BE00/00077

CTGGTGCTAAACGTGCTCAATTCAGAAAGAAGAAAGTTCGAATTAGGTCGTCAACCAG CCAACACAAAATTGGTGCTAAGAGAATCCACTCTGTCAGAACTAGAGGTGGTAACAAGA AATACAGAGCTCTAAGAATTGAAACCGGTAACTTTTCTTGGGCTTCTGAAGGTATCTCCA AGAAGACCAGAATTGCTGGTGTTGTTTACCATCCATCCAACAATGAATTGGTTAGAACTA ACACTTTGACCAAGGCTGCCATTGTCCAAATTGATGCTACTCCATTCAGACAATGGTTCG AAGCTCACTACGGTCAAACCTTGGGTAAGAAGAAGAAGAACGTCAAGGAAGAAGAACTGTTG CCAAGAGCAAGAACGCTGAAAGAAAGTGGGCTGCTAGAGCTGCTTCTGCCAAGATCGAAT CTTCCGTTGAATCTCAATTCAGCGCCGGTAGATTATACGCTTGTATCTCTTCCAGACCAG GTCAATCCGGTAGATGTGATGGTTACATCTTGGAAGGTGAAGAATTAGCTTTCTACCTAA GAAGATTGACTGCTAAGAAATAG

YER102W, 200 aa (SEQ ID NO 80) MGISRDSRHKRSATGAKRAQFRKKRKFELGRQPANTKIGAKRIHSVRTRGGNKKYRALRI ETGNFSWASEGISKKTRIAGVVYHPSNNELVRTNTLTKAAIVOIDATPFROWFEAHYGOT LGKKKNVKEEETVAKSKNAERKWAARAASAKIESSVESQFSAGRLYACISSRPGQSGRCD GYILEGEELAFYLRRLTAKK

YER153C, 1265 bp, CDS: 501-1265 (SEQ ID NO 81) ACCCTATATGGGAGGACAACTCGCCCACTGTTTGGGTCGTGTTAGCGATAAGGTCCGAAG TAGAAGCGGAAAGAAGAGGCTGAAGAGGTTAATTCATCGATGGAAGGCAACTGGGTTT GGATTTCCGAGACATCGTTGGCATTTGGGCCCGTCGAATTAAATCTTTTGGCCTGAAAAG AGATCCATGACGGATGGGGCCGGGCAATACTATGGTTCGAGCGGTGGCCAGTCTGGAAG AGGCAGCAAACCTTGACGTGACGAGTCGAGAGGTGAGTTTGAACATCGTCGGGGAGGTTA TTCTGTGGCTCCGCTTGTACGTGAACAGATACGTATAGAGGGCGAGCCACTGGTTAAATT TTTCATGGCTCGGATTACTTCCGTACTGCTGGCTAAAATCGAAATCTCGGCCTGCTGAGA GTGTTTTGAGCAATCAAGGGAACATCTGAACGTGGAAGAGCAGACGAGGCATTAGCTCGA ACATAAGAACGGAACACGTCATGTTGACTATCACGAAAAGACTGGTGACCACCGATGTGC GGTCGCGAATACTGTTAAGCAGTTTAAACGGGAAAATGTCCGATGCACTGGCGCTGCTGC GTCAGCAGCAGCAGCCAGCGTGGATGTGGAGCTGCTGCACACGATGCTAGCGCGAGCCG CTGCGCTTGCCCATGCCGACACTATAGCATACATGTGGTATCAGCATGTGATGCCACGCC GGCTCTTCTTACCCGCGCAGTTCCTCCAGCACTACCAGGCGATGAATCGCGATCGTCGCA CCAGCCCAGAAGATGAACTGATTGAGTATGAGCTTAGACGGATTAAAGTCGAAGCGTTTG CGCGTGGCACAATGCACTCCACGGCGCTCAGGGAAAAGTGGAAGGTATTCTTGCAGGAGA TGGATACGCTACCAGGGCAGCCGCCATTAAGGCTGCGCGACTTCCCGCAAATGACCAAGG CTATGGGCATAGCATTGATGCAGCAAGATGAGCAAGCAGCTGCCCTGGCGTTGTTTGGAC GGCATGTTCCCGGCCCAGCGCAGGCGCGACGTGTGCTGGCGGAGTTCCGTCAAAGTTATC

YER153C, 254 aa (SEQ ID NO 82) ${\tt MLTITKRLVTTDVRSRILLSSLNGKMSDALALLRQQQQTSVDVELLHTMLARAAALAHAD}$ TIAYMWYQHVMPRRLPVEGRLLCEMAGVALYQDRLFLPAQFLQHYQAMNRDRRTSPEDEL IEYELRRIKVEAFARGTMHSTALREKWKVFLQEMDTLPGQPPLRLRDFPQMTKAMGIALM QQDEQAAALALFGRQPLVIKNEWSLPLLLAGVLWHVPGPAQARRVLAEFRQSYRGLPLLD AELVIKRRGFEINT

YFL014W, 830 bp, CDS: 501-830 (SEQ ID NO 83) GGACTAGAAGCCAAAAGCCAGAGGCGGTAAAAATAGCAAGACTAGAATATTGCTGGCATC TGTTAAGGGGATATGTTGCAACTTGCAGGGGGGGGCGCACAAATAACATAGAAACGTAGTA AAGAGGGGAAAAGGAAAAGGAAAAGGAAAAAAAAACCCATTGACGTAGAAAT TGAAAGAAGGAAAGGTATACGCAAGCATTAATACAACCCACAAACACAGACCAGAAGCAC TCTAGACGGAGAGTAACTAGATCTACAGCCCCTGGAAAATCGTTTGGTCAACTTTGAGGT TCCGGTCGTCCCCCTCTTGATCTGAAAGGTCTTTCTCTAAATCTATATTAAAACGTATAA TAATATATAGAAAAAAAACCATCTGATTATTCGATAATCTCAAACAACAACTCAAAAC AAAAAAAACTAAATACAACAATGTCTGACGCAGGTAGAAAAGGATTCGGTGAAAAAGCTT CTGAAGCTTTGAAGCCAGACTCTCAAAAGTCATACGCTGAACAAGGTAAGGAATACATCA CTGACAAGGCCGACAAGGTCGCTGGTAAGGTTCAACCAGAAGACAACAAGGGTGTCTTCC

YFL014W, 109 aa (SEQ ID NO 84) MSDAGRKGFGEKASEALKPDSQKSYAEQGKEYITDKADKVAGKVQPEDNKGVFQGVHDSA EKGKDNAEGOGESLADOARDYMGAAKSKLNDAVEYVSGRVHGEEDPTKK

YFL015C, 995 bp, CDS: 501-995 (SEO ID NO 85) GACCTTCAGCGTTATCCTTGCCTTTTTCGGCAGAGTCGTGGACACCTTGGAAGACACCCT TGTTGTCTTCTGGTTGAACCTTACCAGCGACCTTGTCGGCCTTGTCAGTGATGTATTCCT TACCTTGTTCAGCGTATGACTTTTGAGAGTCTGGCTTCAAAGCTTCAGAAGCTTTTTCAC ATAAGATCAAACGCAATTGAGGAAGTAGAACGCAATTCACCGTCCTATTTATACGTTTTA ATATAGATTTAGAGAAAGACCTTTCAGATCAAGAGGGGGACCGCCGGAACCTCAAAGTTG ACCAAACGATTTTCCAGGGGCTGTAGATCTAGTTACTCTCCGTCTAGAGTGCTTCTGGTC TGTGTTTGTGGGTTGTATTAATGCTTGCGTATACCTTTCCTTCTTTCAATTTCTACGTCA ATGTTATTTTGTGCCGCCCCCTGCAAGTTGCAACATATCCCCTTAACAGATGCCAGCAAT ATTCTAGTCTTGCTATTTTTACCGCCTCTGGCTTTTGGCTTCTAGTCCTTGTCCCAAGAG CCAAGGGCCCGTCAACACGTCGTCATTGCTACCGCCAGCTGGCACCCACACATCACCGAC CTTGGATTTGCGCGTCCCCTTTTTTTCTTCATTCTCTGACTCCCCCTACCTTCTCCCACT TTTCTGTGTATCAAGAGGAAAAGAAGGAGAAAAGGAGAACTCCGAAAAATACCGAACAAG AGGGTAACAGAATGTGCATTTGGATGAGCGGGTAA

YFL015C, 164 aa (SEQ ID NO 86) MLAYTFPSFNFYVNGFFSFLFLFLFLFPSLLRFYVILCRPLQVATYPLNRCQQYSSLAIF TASGFWLLVLVPRAKGPSTRRHCYRQLAPTHHRPFFSIFGWAVSGIRPLPEIFTWICASP FFLHSLTPPTFSHFSVYQEEKKEKRRTPKNTEQEGNRMCIWMSG

YFR022W, 2702 bp, CDS: 501-2702 (SEQ ID NO 87) CTGCCTTCCGTACGTCACAACGCATACACAATATAGTTTATATAAACTCCTGCGTATAAT AATAGAACTCGCCTAAAGGGGAAATTTTCGATATAAAAATTCAAAAAAATGGCTTTCATG GATCGAGTATTTGTTGTCGAAAAAGGATCACTGGAGTGACGTTACTACGCTACGAAGCC TCCTTCCGGCTTAGCCCTGTTGATTACGAATTTGGATCAGTTGGTATTTGATTCCTCGGA AGAGTTAACTTCACGCGGGTAAATCACTTGTGATGCGGTATATTCTCTATACGGCTAATA GATGAATCAGGGTGTTTTAAAGTGCGTATAAACCCTTTTGCTATTTTCGTTTATAATATT GGCGTTGATAAAGAGCCAATATCTATTGTTGCTACATAGAGGCAGCTCTCTTAGCAAAAT AAAAATACAAAAAGTTCGACATGGGCTTCAGTAGCGGTAAATCAACTAAGAAAAAGCCTC TGCTTTTCGATATCAGACTTAAAAATGTTGACAACGATGTAATACTCCTCAAAGGTCCTC CAAACGAGGCCCCTCGGTGCTTTTATCTGGTTGCATCGTTTTATCGATTAACGAACCCA TGCAGATCAAAAGCATATCATTGAGACTTTATGGGAAGATACAAATAGACGTACCATTAG AGAGGCCCCAGGACGCTAGTTCTTCGTCGTTGTCTTCATCGCCGCCAAAGATCAGAAAGT ACAACAAAGTTTTTTATAATTACGCATGGGATAATGTTAACCTCAAGGAGTATCTGAGTG GTTTAAGAGGGCAATCTGGCCTTGCGGGCAGTAGCTCATCAAGTAATATCTTGGGCACTC GCCAAAGAGCTCAGTCCACAAGTTCCTTGAAGTCTTTAAAGGGGTCCTCCTCACCCTCTT CATGTACTTTAGATAAGGGCAACTACGATTTTCCCTTTAGTGCTATTTTGCCTGGTTCGT TACCAGAGAGCGTAGAATCTTTGCCAAATTGCTTCGTGACATATAGCATGGAATCCGTTA TTGAACGCAGCAAAAATTATAGTGATTTGATCTGTAGGAAAAATATTAGAGTTCTGAGAA CCATTCACCCGCAGCAGTGGAGTTATCAGAAACTGTTTGTGTAGATAACTCATGGCCCG ACAAAGTGGATTATTCTATTTCAGTACCCAACAAAGCCGTAGCTATTGGTTCAGCCACCC TATTATTTGAGAATTATCAATATTGTGACCCCTTCCCTCCAGTAATTTCTGAAAATAGGC AAGTGACAGAACTAAATCTTGAAGATCCCTTGAACGAGTCATCTGGAGAATTTAATGGTA

AGATTGATACCATCCTGCAAATCCCGAACAGCTTATCAAACTGTGTGCAAGATTGTGATG TCCGCTCTAACATTAAGGTTCGCCATAAGCTCAAATTTTTCATCATCCTAATTAACCCAG ATGGTCATAAATCTGAGTTAAGAGCGTCCTTACCGATTCAACTTTTTATTTCACCATTTG TGGCACTTTCAATAAACCATTGTCATCCTCGAATTTGTATTCGCTTTTTAGCACCACTA ACCAGAAAGACGAAAACTCATCACAAGAAGAGGGAAGAGGGAATATCTGTTTTCTAGATCAG CATCAGTCACAGGGTTGGAATTATTAGCGGATATGCGTAGCGGTGGCTCTGTTCCTACCA TTTCAGACTTGATGACGCCCCCAAATTATGAAATGCACGTATATGATCGTCTTTATAGCG GTTCTTTCACTCGCACGGCTGTGGAAACGTCTGGAACATGTACTCCTTTGGGAAGCGAAT GTTCGACTGTCGAGGATCAGCAACAGGATTTAGAAGATTTACGTATACGGTTGACAAAAA TTAGAAATCAACGTGACAATCTAGGGCTACCACCGTCTGCCTCGTCTGCCGCTTCCA GATCGCTATCTCCATTACTAAACGTTCCAGCACCAGAGGATGGCACGGAGAGAATCTTAC CTCAGAGTGCTCTTGGTCCCAATAGTGGCTCTGTGCCAGGAGTACATAGTAACGTATCAC CTGTTTTACTTTCAAGATCCCCAGCCCCAAGCGTGTCAGCCCATGAAGTGTTACCAGTGC CCTCGGGCTTAAATTATCCAGAGACTCAAAACCTGAACAAGGTTCCATCGTATGGCAAGG ATGTGCAACCAAGAAAACCCAGTAGGGTACATTCCAGGAACTCTTCGACAACATTGTCAT CTTCTATACCAACTAGCTTTCATTCCTCTAGTTTTATGAGTAGCACTGCTTCCCCTATTT CCATAATTAATGGCTCTAGAAGTAGTTCTAGTGGGGTATCTCTTAATACACTTAATGAGT TAACTTCGAAAACTTCGAATAACCCATCCAGTAATAGTATGAAAAGGTCACCAACAAGAC GGAGGCTACTTCTTAGCTGGGTTTATGGGAGGTTTTCTATCAAAGGGTAACAAACGAT

YFR022W, 733 aa (SEQ ID NO 88)
MGFSSGKSTKKKPLLFDIRLKNVDNDVILLKGPPNEAPSVLLSGCIVLSINEPMQIKSIS
LRLYGKIQIDVPLERPQDASSSSLSSSPPKIRKYNKVFYNYAWDNVNLKEYLSGLRGQSG
LAGSSSSSNILGTRQRAQSTSSLKSLKGSSSPSSCTLDKGNYDFPFSAILPGSLPESVES
LPNCFVTYSMESVIERSKNYSDLICRKNIRVLRTISPAAVELSETVCVDNSWPDKVDYSI
SVPNKAVAIGSATPINISIVPLSKGLKLGSIKVVLFENYQYCDPFPPVISENRQVTELNL
EDPLNESSGEFNGNGCFVNNPFFQPDHSFQDKWEIDTILQIPNSLSNCVQDCDVRSNIKV
RHKLKFFIILINPDGHKSELRASLPIQLFISPFVALSIKPLSSSNLYSLFSTTNQKDENS
SQEEEEEYLFSRSASVTGLELLADMRSGGSVPTISDLMTPPNYEMHVYDRLYSGSFTRTA
VETSGTCTPLGSECSTVEDQQQDLEDLRIRLTKIRNQRDNLGLPPSASSAAASRSLSPLL
NVPAPEDGTERILPQSALGPNSGSVPGVHSNVSPVLLSRSPAPSVSAHEVLPVPSGLNYP
ETQNLNKVPSYGKAMKYDIIGEDLPPSYPCAIQNVQPRKPSRVHSRNSSTTLSSSIPTSF
HSSSFMSSTASPISIINGSRSSSSGVSLNTLNELTSKTSNNPSSNSMKRSPTRRRATSLA
GFMGGFLSKGNKR

YGL011C, 1259 bp, CDS: 501-1259 (SEQ ID NO 89) AGACAATAAAATATGGAAAATAAAACGCTTAGCACAGCAGTCAATGAAATACTCTGATAT ATTTTGACTCTGTGGAGCATACAGCTACCACTAAATAGGATTGTGGGGACAAATATGGAA TGGATCAAAACGTTCTTAGGATTGTGGTGGTAAAACTTGTAAAATCCAAGCTGAGATCTT AAATCCAGCAAACCTTCGCCCATATTTATTCTTTTATAACAGAAGAAGAGACTATATTCT CAAAACCTCGTATATTTATATACATATCCTCCAAACAACTCCCAAGTTTCACTTTCCTG GATTTACCTTGGCATTCCTTTTCCCCATCCTCTTATAATGGTAATCGCGATCCTTAATTA TGATATCACAATAGACGAAGGGCACACACCAATTTGCCACCGTAAGGATAGAGTAAGTTA AATGGCTAACTCATTATAATCTTCATGCTAAATCATATAAGGGCAGAGACGAAGCAAAGC GAAAAAACATATTACAATCATGTCGGGTGCTGCTGCTGCTGCTGCTGCTTATGACA GGCACATCACTATCTTTTCCCCCGAGGGTCGTTTATATCAAGTAGAATATGCCTTTAAAG CGACTAATCAAACTAACATAAACTCACTAGCGGTCAGAGGTAAAGATTGTACAGTGGTGA TAAGTCAGAAAAAGGTCCCTGATAAACTGTTGGATCCAACTACTGTTTCGTATATTTTTT GTATTTCAAGAACAATTGGTATGGTAGTGAACGGACCAATACCGGATGCAAGAAATGCGG CCCTAAGAGCCAAGGCTGAGGCTGCAGAATTCCGTTATAAATATGGTTATGATATGCCAT GCGATGTATTGGCTAAGAGAATGGCTAACCTTTCCCAAATCTATACTCAAAGAGCATATA TGAGACCATTAGGTGTTATACTCACATTTGTTTCGGTAGATGAAGAATTGGGTCCCTCCA TTTACAAAACTGACCCTGCAGGTTATTACGTTGGCTACAAAGCTACTGCGACAGGACCAA AACAACAGGAGATCACAACAAACTTAGAAAACCATTTCAAAAAGAGTAAAATCGACCATA

TTAATGAAGAATCATGGGAGAAGGTGGTAGAATTTGCTATTACTCATATGATTGACGCAC TGGGTACCGAATTTTCAAAGAATGACTTGGAAGTCGGTGTCGCTACAAAGGACAAATTCT TTACCTTGAGTGCTGAGAACATCGAAGAAAGGCTAGTAGCAATTGCTGAACAAGATTAA

YGL011C, 252 aa (SEQ ID NO 90)
MSGAAAASAAGYDRHITIFSPEGRLYQVEYAFKATNQTNINSLAVRGKDCTVVISQKKVP
DKLLDPTTVSYIFCISRTIGMVVNGPIPDARNAALRAKAEAAEFRYKYGYDMPCDVLAKR
MANLSQIYTQRAYMRPLGVILTFVSVDEELGPSIYKTDPAGYYVGYKATATGPKQQEITT
NLENHFKKSKIDHINEESWEKVVEFAITHMIDALGTEFSKNDLEVGVATKDKFFTLSAEN
IEERLVAIAEOD

YGL031C, 968 bp, CDS: 501-968 (SEO ID NO 91) CCAAGTTAAGCAAGACACCAAGACAATAACTTGAGAGGTATGTCCCTATATGATGATGAT TCATAATTAATGGCGACCGAGGGCAGCGTTGTGCTAGAAAGCAATGTATTAATATATGAG AGAGCTTCAGATAGCCAATACACCGGAATTTAGACTTTGACAGGATTGTGGCTTGTTCCA GTATAACTTATAATATATGTCAACCTTTGAGCAGGAAACCCAATGAAAATGCTTCATTAC ATATATACGATATGGAGAAGCATGAAAAATAACAGCGTGAGATGTTATCCATGTTGCAAG AACCTAGTAAAATGAATTCTGAATTTGCAAAAAGTCCATATTTCCACGTTCTCCTCTTCC TGGATTAATATAGTGATAAAATGAAGGTTGAAATCGATTCTTTTTCAGGTGCCAAAATCT ACCCAGGCAGAGGTACCTTGTTTGTCCGTGGTGACTCCAAAATCTTCAGATTCCAAAACT CCAAATCTGCCTCTTTGTTCAAGCAAAGAAGAACCCAAGAAGAATCGCTTGGACTGTCT TATTCAGAAAGCATCACAAGAAGGGTATCACCGAAGAAGTTGCTAAGAAGAGATCTAGAA AAACCGTTAAGGCCCAAAGACCAATTACCGGTGCTTCTTTGGACTTGATCAAGGAAAGAA GATCTTTGAAGCCAGAAGTTAGAAAGGCTAACAGAGAAAAAAATTGAAGGCCAACAAAG AAAAGAAGAAGGCTGAAAAAGGCTGAAAAGGCTAAAAGGCTAAGTCTGCTGGTACTC AAAGTTCTAAGTTCTCCAAGCAACAAGCTAAGGGTGCTTTCCAAAAGGTTGCTGCTACTT CTCGTTAA

YGL031C, 155 aa (SEQ ID NO 92) MKVEIDSFSGAKIYPGRGTLFVRGDSKIFRFQNSKSASLFKQRKNPRRIAWTVLFRKHHK KGITEEVAKKRSRKTVKAQRPITGASLDLIKERRSLKPEVRKANREEKLKANKEKKKAEK AARKAEKAKSAGTQSSKFSKQQAKGAFQKVAATSR

YGL032C, 87 aa (SEQ ID NO 94) MQLLRCFSIFSVIASVLAQELTTICEQIPSPTLESTPYSLSTTTILANGKAMQGVFEYYK SVTFVSNCGSHPSTTSKGSPINTQYVF

TGCTTCGAATGACAACGCCTTTTTGATATATAATATCCAATTTCATTATAGGGAAATTTT CAACTCTTACCCGCCCCACTGTGCTGATATGACCAAGTGATCACTCGATGATGGGACTAC GTATTGAAAAATATTGAATGAAAAATTACTCAAGCAGCAGAACATTCACAGTGTAGTCAG TCCGCATAAGAGCATTCATCATGGATAGTAAGGAAGTACTGGTACATGTTAAGAATCTAG AAAAGAACAAAAGTAATGATGCTGCAGTTCTAGAAATCTTACATGTCTTGGATAAAGAAT TCGTCCCCACTGAAAAGTTACTGAGAGAAACAAAAGTTGGTGTGGAAGTCAACAAGTTTA AAAAATCCACTAATGTAGAGATCAGCAAACTCGTGAAGAAAATGATTAGCTCTTGGAAAG ACGCAATTAATAAAAATAAGCGTTCCAGGCAAGCACAGCAGCATCATCAAGATCATGCGC CAGGCAATGCAGAGGACAAGACAACTGTAGGTGAGTCCGTGAATGGTGTTCAACAGCCGG CCTCCTCCCAGTCAGATGCCATGAAACAAGACAAGTACGTCAGCACTAAACCAAGAAATA GTAAGAACGATGGTGTGGATACAGCTATATACCACCACAAATTACGTGATCAGGTACTAA AAGCACTCTACGACGTTTTGGCCAAGGAAAGTGAGCATCCACCTCAATCTATTTTGCATA CTGCAAAGGCCATAGAAAGTGAAATGAATAAAGTTAACAACTGTGACACCAACGAAGCCG CTTACAAAGCCAGGTATCGTATAATTTATTCAAACGTCATATCAAAGAATAACCCAGATC TCAAACATAAAATTGCCAACGGTGATATAACACCTGAATTCTTAGCTACATGCGATGCCA AGGATCTGCCACCGCCCTTAAAGCAAAAGATAGAAGAAATTGCCAAGCAAAACTTAT ACAACGCACAGGGTGCCACCATAGAAAGGTCACCGATAGATTTACATGTGGTAAAT GTAAAGAGAAGGTATCTTACTATCAATTGCAAACAAGATCTGCGGATGAACCATTGA CCACTTTCTGTACATGTGAAGCATGTGGTAACAGATGGAAATTCTCTTAG

YGL043W, 309 aa (SEQ ID NO 96)
MDSKEVLVHVKNLEKNKSNDAAVLEILHVLDKEFVPTEKLLRETKVGVEVNKFKKSTNVE
ISKLVKKMISSWKDAINKNKRSRQAQQHHQDHAPGNAEDKTTVGESVNGVQQPASSQSDA
MKQDKYVSTKPRNSKNDGVDTAIYHHKLRDQVLKALYDVLAKESEHPPQSILHTAKAIES
EMNKVNNCDTNEAAYKARYRIIYSNVISKNNPDLKHKIANGDITPEFLATCDAKDLAPAP
LKQKIEEIAKQNLYNAQGATIERSVTDRFTCGKCKEKKVSYYQLQTRSADEPLTTFCTCE
ACGNRWKFS

YGL102C, 929 bp, CDS: 501-929 (SEQ ID NO 97)
TGTTACGATCAACATTCTTGTCCGTAATCAGCATGGTAGTTAAACCCATTCTGTACATAT GGTCAGATATACTTTCGCATGGGTCAATACCATGGTCAACCCAACCAGTTCTTCTTTGCG TTTTCAAAAGTTGTATAATATTCAAAAACGCTAACTGATAATTTGGGTGAGGTTTCGAAA GAATTGCCAAAATCTCCCTAGGTATATTATCTTCTGGCTTCCAGATGTTAACTGCAGTCA TTTTGTTTTCCTGGTCTTTACCTCGAATAGGTTTTCTTGTTTTGTTATTTGTTTTCTTT TTGGACCCTATGTTTATATATGGATTTTGAAAATCTTTTAAAAAAGCGATAAAAGCGTTG GGATCTGCCACTGGTAACTTCAAAATAGACAAGACGAAAAAACGGTGAAAATGGGTGATA GAAATAATACAGAAGTAGATGTTGAATTAGATTAAACTGAAGATATATAATTTATTGGAA AATACATAGAGTTTTTGTTGATGCGCTTAAGCGATCAATTCAACAACACCACCAGCAGCT CTGATTTTTCTTCAGCCAACTTGGAGACGAATCTAGCTTTGACGATAACTGGAACATTT GGAATTCTACCCTTACCCAAGATCTTACCGTAACCGGCTGCCAAAGTGTCAATAACTGGA GCAGTTTCCTTAGAAGCAGATTTCAAGTATTGGTCTCTCTTGTCTTCTGGGATCAATGTC CACAATTTGTCCAAGTTCAAGACTGGCTTCCAGAAATGAGCTTGTTGCTTGTGGAAGTAT CTCATACCAACCTTACCGAAATAACCTGGATGGTATTTATCCATGTTAATTCTGTGGTGA TGTTGACCACCGGCCATACCTCTACCACCGGGGTGCTTTCTGTGCTTACCGATACGACCT TTACCGGCTGTACAAAAAAAATATTGTAA

YGL102C, 142 aa (SEQ ID NO 98)
MRLSDQFNNTTSSSDFFFSQLGDESSFDDNWNIWNSTLTQDLTVTGCQSVNNWSSFLRSR
FQVLVSLVFWDQCPQFVQVQDWLPEMSLLLVEVSHTNLTEITWMVFIHVNSVVMLTTGHT
STTGVLSVLTDTTFTGCTKKIL

TTTGCTTTCTCCGTTGATTTTTTTCCTTCTTAGTGATTTTTTTGCATTAAATCCCAGAAC **AATCATCCAACTAATCAAGAATGCCTTCCAGATTCACTAAGACTAGAAAGCACAGAGGTC** ACGTCTCAGGTATGTAGTTCCATTTGGAAGAGGGAATGAAAGAACCAAGACGGTGACTTT TTTTTTAGTGTTGTGCAACCAATATGTCGTGTGTATATCATGGTACAGGAGAATGTCAAT CAGCTAAGTGTACTCAACATATTTCTTTGTGTTTTGATTGCGAACTTTGTATTACCATCT CACTGTTGAGACGGCTTATTTGAGGTAATAGCTCGAGTAAATGTACTCTTCCATCGCAAA CTGAGCAAAAAGAAGTGTGCATAGCCTTTGTCATACTTCTCCTTTATTATACCATGATA TTCAGAACAGTCATACTGTCTACTCATTTTACGGCTATAAAAGGTAACTTTCATTTAGAT TATGGAAAGCACTAATTATCGCTGTATCAAATGGTTGTAGAGAGCGCAATTATGAAAAAG AGTTACCACGTTTCTTTTGTTTCGATAAAATGTCCAGTTGAAAACCTGTTTTACTAACGA TTTAAAAATTGTATTTCATTACAATATTTTTTTTTGTACAGCCGGTAAAGGTCGTATCGGT AAGCACAGAAAGCACCCCGGTGGTAGAGGTATGGCCGGTGGTCAACATCACCACAGAATT AACATGGATAAATACCATCCAGGTTATTTCGGTAAGGTTGGTATGAGATACTTCCACAAG CAACAAGCTCATTTCTGGAAGCCAGTCTTGAACTTGGACAAATTGTGGACATTGATCCCA GAAGACAAGAGAGACCAATACTTGAAATCTGCTTCTAAGGAAACTGCTCCAGTTATTGAC ACTTTGGCAGCCGGTTACGGTAAGATCTTGGGTAAGGGTAGAATTCCAAATGTTCCAGTT ATCGTCAAAGCTAGATTCGTCTCCAAGTTGGCTGAAGAAAAAATCAGAGCTGCTGGTGGT GTTGTTGAATTGATCGCTTAA

YGL103W, 149 aa (SEQ ID NO 100) MPSRFTKTRKHRGHVSAGKGRIGKHRKHPGGRGMAGGQHHHRINMDKYHPGYFGKVGMRY FHKQQAHFWKPVLNLDKLWTLIPEDKRDQYLKSASKETAPVIDTLAAGYGKILGKGRIPN VPVIVKARFVSKLAEEKIRAAGGVVELIA

YGL130W, 1880 bp, CDS: 501-1880 (SEQ ID NO 101) TTTTGGTACTTGAATTTCTCGTTTCTACTAGCTGGATTGCTTGTCCTTTTTACAATTCCTG GGAGTTTGGCTATTGCTACCCTTGGTCTTAGCACCACTTTTTTCCGCTATTTGTATTTGT TGAACTAATTTAGTATCTATTTCCATTTCATTATAATTCACGTTTTTAGCAGCCTCTCTT CTTCTAGGTAATTGGAAATCTTCTTCTTTAGGCATAGCGTGACCAGCTGAAAGGCAGATG ATCTCAATATGTCCCGATAGGCCAATTTTGCCACCAGATAGTTCGATGGCATTTTATTTT TAGTCCTTTTGAAAGCAATATCATAAAATATATATATATCTCCATGATGTTCGGGTCAGT CGCTCCGAAGCGTAACCTAGTATAATAATAGTTCATTGCAGAAAATAACGAAAGAATG CGACCGCTAATTTAACAAATATGGTTTTAGCAATGGAAAGTAGAGTGGCACCGGAAATTC CTGGGCTCATTCAACCTGGGAATGTCACGCAAGACTTGAAGATGATGGTCTGTAAATTAT TGAATTCCCCAAAACCTACGAAAACATTCCCTGGTTCCCAGCCTGTGTCCTTTCAGCATT CTGATGTGGAAGAGAGCTGCTTGCGCATGATTACTACGTTTGTGAGAAAACAGATGGTC TGCGGGTGTTGATGTTTATAGTGATAAATCCTGTGACGGGTGAGCAAGGATGCTTTATGA TTGATAGGGAAAATAACTATTATCTGGTTAATGGATTTAGGTTTCCCAGATTACCCCAAA AGAAGAAGAAGAGCTGCTAGAGACTCTTCAAGATGGCACCTTATTAGATGGTGAACTTG TCATACAAACTAACCCAATGACAAAATTACAAGAGTTGCGTTATTTAATGTTCGATTGTC TTGCTATCAATGGTAGATGTCTCACACAATCACCAACAAGTTCTAGACTAGÇCCACCTTG GAAAAGAATTTTTTAAACCATACTTCGATTTAAGAGCAGCGTACCCTAATCGTTGTACTA CTTTTCCGTTCAAAATTTCCATGAAACATATGGATTTCAGTTACCAATTAGTAAAAGTTG CTAAAAGTTTAGATAAACTACCACATCTTTCTGATGGTCTGATATTTACTCCTGTGAAGG CACCTTACACTGCCGGCGGAAAAGATTCATTGTTATTAAAATGGAAGCCAGAACAAGAAA ACACCGTGGACTTCAAATTGATTTTAGATATCCCAATGGTGGAGGATCCTTCTTTGCCTA AAGATGATCGGAACAGGTGGTATTACAATTATGACGTTAAGCCAGTTTTCAGCTTATATG TCTGGCAAGGCGGAGCTGATGTCAATTCACGTTTAAAACATTTCGACCAGCCTTTCGATA GGAAGGAATTTGAAATATTAGAAAGAACATACAGAAAATTTGCAGAGTTGAGCGTTTCAG ATGAGGAATGGCAAAATTTGAAGAACCTAGAACAGCCATTAAATGGTAGAATAGTAGAGT GCGCAAAAAACCAAGAGACTGGGGCGTGGGAAATGTTAAGATTCAGGGATGATAAGTTAA ATGGTAATCATACATCGGTGGTCCAGAAAGTTTTGGAGAGTATCAACGATTCAGTTTCAT ATATGGCTGGTGGTAGTGGGAGACCACTACCGTCTCAAAGTCAAAATGCGACATTATCTA CCTCTAAGCCAGTCCATTCACAGCCCCCAAGTAATGATAAGGAGCCAAAATATGTAGACG AGGATGATTGGTCGGATTAG

YGL130W, 459 aa (SEQ ID NO 102) MVLAMESRVAPEIPGLIQPGNVTQDLKMMVCKLLNSPKPTKTFPGSQPVSFQHSDVEEKL LAHDYYVCEKTDGLRVLMFIVINPVTGEQGCFMIDRENNYYLVNGFRFPRLPQKKKEELL ETLQDGTLLDGELVIQTNPMTKLQELRYLMFDCLAINGRCLTQSPTSSRLAHLGKEFFKP YFDLRAAYPNRCTTFPFKISMKHMDFSYQLVKVAKSLDKLPHLSDGLIFTPVKAPYTAGG KDSLLLKWKPEQENTVDFKLILDIPMVEDPSLPKDDRNRWYYNYDVKPVFSLYVWQGGAD VNSRLKHFDQPFDRKEFEILERTYRKFAELSVSDEEWQNLKNLEQPLNGRIVECAKNQET GAWEMLRFRDDKLNGNHTSVVQKVLESINDSVSLEDLEEIVGDIKRCWDERRANMAGGSG RPLPSQSQNATLSTSKPVHSQPPSNDKEPKYVDEDDWSD

YGL147C, 1076 bp, CDS: 501-1076 (SEO ID NO 103) CAATATTATAGTTACTACCTATTTGATTATTAAGATCAAAAGTAATCCTTCATCTCATAT CAAAAAGAAAGGTTTGTAAAAAGAGCATTGGGCAGAGAGTATTTGTCCTGCGTATAGAGGA TTTCCAGAAATGTTTGGGTTTATTTTTTAATTTTTTGAAACATTTTTTTCATCCTTTCTC ATTTTGTCATTTCTGTGGAAAATTTCACTGACGCGAAGAAGCGATGAAATTTC GAGGTCAGAGGCAATGTGGCAGAGACGCTGGCGCGCCTGTATTGTATAATAGTATATTT ACACTCAATTCAATTTTTGATATTAAATTAGTGTGTAAAAAGCTTCTGAAATCAAGAAG CCCGTACCAGAAGTTCAATCATGAAATACATCCAAACTGAACAACAAATCGAAGTCCCAG **AAGGTGTCACTGTCAGCATCAAGTCCAGAATCGTCAAGGTTTGTTGGTCCAAGAGGTACTT** TGACCAAGAACTTGAAGCACATTGATGTTACCTTCACCAAGGTCAACAACCAATTGATCA AGGTTGCTGTTCACAACGGTGGCAGAAAGCACGTTGCTGCTTTGAGAACCGTCAAGTCTT TGGTTGACAACATGATCACTGGTGTCACCAAGGGTTACAAGTACAAGATGAGATACGTCT ACGCGCATTTCCCAATCAACGTCAACATTGTTGAAAAGGATGGTGCCAAATTCATTGAAG TCAGAAACTTTTTGGGTGACAAGAAGATCAGAAACGTTCCAGTTAGAGATGGTGTTACTA TCGAATTTTCCACCAACGTTAAGGACGAAATTGTCTTGTCAGGTAACTCTGTCGAAGACG TTTCCCAAAACGCTGCTGACTTGCAACAATCTGTCGTGTCAGAAACAAGGATATCCGTA AATTTTTGGACGGTATCTACGTTTCTCACAAGGGTTTTATTACTGAAGATTTATAA

YGL147C, 191 aa (SEQ ID NO 104) MKYIQTEQQIEVPEGVTVSIKSRIVKVVGPRGTLTKNLKHIDVTFTKVNNQLIKVAVHNG GRKHVAALRTVKSLVDNMITGVTKGYKYKMRYVYAHFPINVNIVEKDGAKFIEVRNFLGD KKIRNVPVRDGVTIEFSTNVKDEIVLSGNSVEDVSQNAADLQQICRVRNKDIRKFLDGIY VSHKGFITEDL

YGL213C, 1694 bp, CDS: 501-1694 (SEQ ID NO 105) AATCAAAACGATCGTTATACAATTCATTGAGGAACCTCTCTAGTCCGATCCGTCTTTCAT CGATCATTTCCGGATCATCATATCTTCTTTGCCACCTCCTGTCCAATACACCGGGCTTTT CAGGGAAGTCATATGGGATGGTGCTTCCTACATCTCTCCCAATCGTGTCTTCAGTTTCC AAAACTCGGAATACCTTTTGTAAAGGCGCTTGTTTGGTGTACTAACACCGTATAAAACAT ACTTGGGGTTGATTTTAACATCGTCCACCTTGATTCTTAACTTTTCACTCATTTTCCCTA CAGAATTAGCTGCCATCAATATCAATTATCAACCCTTATATGACTTTATTGTTTTTGTTT GAAGGAAAAATTAGGCGATATTAAAACAAATCTAAAATAAAGACAAGAAACGAAAAAGAG GTTAATCAAGTATTGGAAAAATGTCCAAAGTGTTTATTGCCACAGCAAATGCAGGTAAAG CTCATGACGCTGATATTTTCTCGGTTTCTGCTTGCAATTCATTTACGGTAAGTTGTTCAG GTGACGGTTACTTAAAGGTGTGGGATAATAAGCTGTTAGATAATGAAAATCCAAAAGATA AGTCATATTCTCACTTTGTCCATAAGTCCGGATTGCACCATGTCGATGTCTTGCAAGCTA TTGAGAGAGATGCATTTGAATTATGCCTTGTTGCTACCACTTCATTTTCTGGCGATTTAC TCTTCTATCGTATCACTAGAGAGATGAGACTAAAAAAGTTATATTCGAGAAATTGGATC TTCTAGACTCAGACATGAAAAAGCATTCCTTTTGGGCATTAAAATGGGGTGCCTCAAATG ACAGACTACTTTCCCATAGGCTGGTTGCTACAGACGTCAAAGGGACCACTTACATTTGGA AGTTTCACCCGTTTGCAGATGAGTCAAATTCTTTAACACTAAATTGGAGCCCCACGTTAG AATTACAAGGCACTGTCGAATCGCCTATGACTCCAAGTCAATTTGCCACTTCTGTGGATA TCTCTGAACGAGGACTAATTGCCACAGGTTTTAATAATGGAACAGTACAAATTTCAGAAC TATCTACATTACGCCCGTTGTACAATTTTGAATCTCAGCATTCTATGATTAATAATTCGA ATTCCATCAGATCGGTGAAATTTTCTCCTCAAGGATCCTTATTAGCCATTGCTCACGATT CAAATTCATTTGGTTGCATCACTCTATATGAAACTGAATTTGGTGAAAGAATAGGCTCCT TATCCGTACCAACCCATAGCTCGCAGGCAAGTCTGGGTGAATTTGCACATTCTAGCTGGG TCATGAGTCTATCGTTTAATGATTCTGGTGAAACATTATGCAGTGCCGGATGGGATGGTA AATTGAGATTTTGGGATGTAAAAACAAAGGAAAGAATCACTACATTGAATATGCATTGTG

YGL213C, 397 aa (SEQ ID NO 106)
MSKVFIATANAGKAHDADIFSVSACNSFTVSCSGDGYLKVWDNKLLDNENPKDKSYSHFV
HKSGLHHVDVLQAIERDAFELCLVATTSFSGDLLFYRITREDETKKVIFEKLDLLDSDMK
KHSFWALKWGASNDRLLSHRLVATDVKGTTYIWKFHPFADESNSLTLNWSPTLELQGTVE
SPMTPSQFATSVDISERGLIATGFNNGTVQISELSTLRPLYNFESQHSMINNSNSIRSVK
FSPQGSLLAIAHDSNSFGCITLYETEFGERIGSLSVPTHSSQASLGEFAHSSWVMSLSFN
DSGETLCSAGWDGKLRFWDVKTKERITTLNMHCDDIEIEEDILAVDEHGDSLAEPGVFDV
KFLKKGWRSGMGADLNESLCCVCLDRSIRWFREAGGK

YGL235W, 1037 bp, CDS: 501-1037 (SEQ ID NO 107) CTGGTTCCAACCATATCTTATGGGAAGATCTATCAGGAAACCTTAGAATCTTAGCTTCGA TGGAGGGACAATAGCGGGGCCTTTGATGGTCGTGTCCTGAATATGAATGGATTGATGCA AGTTATTGCGCAAAAAGTCGTGCATTTGAGGTGTGGTATGTGTGCCAAAGCAATCCAGTT GCTTCGTGGGTTCGACTGACACGGTTTCATTCAGAAAACTCATAGGGACAGGCAACGCAT CTCCCTTCTGGACCTCCAGAGCGCTGAAATCAATGGATTCCTTGGCCAGCCTAGCCGGAG TGCCTGTTTTCAAACGCCCTAACTGAAAGCCCACCTCATTTTGTAGAGTATTGCTGATCC CATATGTTGGCTGCTCGCCAATTCTTCCTGCTGCAATACGCTTGTCGCCGATGTGAATTT CTGCACTGAGAAACGTACCTGTAGTGATTATGACCTGATCTGCCCCAACCTGGGTACCGT CATCCAGAACCACACCTTTGATGACCTTGTGGCCACATCCGGGGTCATACAAGATCAAGT CAGCAACTTTGTTCTGCAGCAGAGACAAGTTGGGGTGTGCTTTCTTGTCGGAAAGTTCCC TTTGCATGTATTTCTTATATAACTCTCTGTCTATCTGGGCTCTGGGCCCCCACACAGCAG GACCCTTGCTTCTGTTCAGCATTTTGAATTGCACTCCAGCGAGATCAGTTACTTTGCCCA TCAGCCCATCGAGAGCGTCGATTTCCTTTACAAGGATGCCCTTACCCACTCCACCAATAG AGGGGTTGCACGAACACTTACCAATATCTGTTAACGATGGTGTAATGAGAGTAGTATGCG CACCAGTCCTAGATGACGCAGCTGCAGCTTCGCAGCCTGCATGTCCAGCACCGATGACCA CGACCTGTGTCTTGGTTGTGGGAAGCTTGTCAAAGAAGATATGGTCAACCGCCTCC TGAGGACCTGTAAGGGAAATGAAGTACACGAAGACGCCAAGGTTGTTACACGCAGCATCG TTCTTTGGGGCGTTTAG

YGL235W, 178 aa (SEQ ID NO 108) MTLWPHPGSYKIKSATLFCSRDKLGCAFLSESSLCMYFLYNSLSIWALGPHTAGPLLLFS ILNCTPARSVTLPISPSRASISFTRMPLPTPPIEGLHEHLPISVNDGVMRVVCAPVLDDA AAASQPACPAPMTTTCVLVVGWKLVKEDMVNRLLRTCKGNEVHEDAKVVTRSIVLWGV

YGL260W, 76 aa (SEQ ID NO 110) MEMLLFLNESYIFHRLRMWSIVLWHSCVFVCAECGNANYRVPRCLIKPFSVPVTFPFSVK KNIRILDLDPRTEAYC

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 111)
TCCTTACTTTAGTCTATTATCAATATCTCTTCCCCCTCTAAATATGTACTCTTTATTT

TTTTTAATTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTTCCT GTCGTATAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTCAGGACA TTTTAAACATCCGTACAACGAGAACCCATACATTACTTTTTTAATATTCTTTTTGTTTT CACCGCCTTCTTTTATTTTATCCGAAGATCTTTTGGAACCCGCTCTGCGAATAGCGAA GCTAGGATACCAAATTGAAACTTGGACATAACTCATCATTAAAGAAGTATACTGTTAAGA GAGGCATTCATTTCGTGTATTATAACGTTTAGCATCAGTTACCCTTGAAAGCCCAACATA TACAAAAATACGCGTCCAAGATGTCTACTAAAGCCCAAAACCCTATGCGTGATTTGAAGA TCGAGAAATTGGTCTTGAACATCTCCGTTGGTGAATCTGGTGACAGATTAACCAGAGCCT CCAAGGTTTTAGAACAATTATCTGGTCAAACTCCAGTTCAATCCAAGGCCAGATACACTG TCAGAACTTTCGGTATCAGAAGAAACGAAAAAATTGCTGTTCACGTTACCGTCAGAGGTC CAAAGGCTGAAGAAATTTTGGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA GAAACTTCTCTGCTACCGGTAACTTCGGTTTCGGTATTGACGAACACTTGACTTGGGTA TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTTCTATGTCGTCATGAACAGAC CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGGTACTGTTGGTAACTCCCACAAGA CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAAGTACGACGCTGATGTGCTCGATA AATAA

YGR085C, 174 aa (SEO ID NO 112) MSTKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIR RNEKIAVHVTVRGPKAEEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI GIFGMDFYVVMNRPGARVTRRKRCKGTVGNSHKTTKEDTVSWFKQKYDADVLDK

1258 bp, exon1: 501-565, intron1: 566-885, exon2: 886-1258 (SEQ ID NO 113) AGCCATGTCGGTCGCACTAGACTTTCTTCTCACTGTCACTTACCTGTTTGAAATCATGT CCTTTTTTTTTTGCCATTCTTATACATTTTCTTTCCTTCTGAAATTAACTGTACACCCA TACCCTATATACACCCATACCCTATTTTTAAATATAAAAAGTAAACTTCATTTTGAAAGA CCACTCTGCATCAGCACGCGGCTCTGGAAGGAAGAAATGACGTTTCGGCGGAATACCCT TTCAGAAGGTCTGCTCTTGTGGCTGGTTCATGGGAGACACCCAGCGGAGCTCCTCCCGAG AAAGGCCCCTTCATCTCTGCCGATTGCTGACGGAAAGCAGTAGCGGAGGTTTGAGTTCTC TACGCCGAGAGTACACTGCCGTAATATCACAATGTTTCGACTAACGGTTACAGTACGTTA **AATTAGATACTGCCTATGAATTGACATATTAGATAATGTCAAATTTTACAAAAACCTAAG** ACAACAGGAAATAAACAAAGATGGGTAAAGGTAAGCCAAGAGGTTTGAACTCTGCTAGAA **AACCCCCTATTGTGATATCGTTTTAGGTGAAGGAAATGTTGTGAGCTCTGGAGTGATAAA** TTTATCAAGTAACATATCCTGGCGCAAATCAGTTTGGAGAGGCTTAAAATGACACGTCAC AGTGATAAAAAGTAATGAATAGTGAACGGTCAGCTTCGGCCATTCTTCCCAATCTATAGT GTGGAAAATAAACCTTTTCTTCCCAAAATAACTCAGAAAGTCACAGGAGGCCGTTTTTTA CAACGGAATCATTTTTTACTAACAGTTTTTTTTTTTATTATTAGCCGTTGGGCCGAAAA CAACTACAAGAAGAGATTGTTGGGTACTGCCTTCAAGTCTTCTCCATTCGGTGGTTCTTC TCATGCCAAGGGTATCGTCTTGGAAAAATTGGGTATCGAATCCAAGCAACCTAACTCTGC TATCAGAAAGTGTGTTAGAGTTCAATTAATCAAGAACGGTAAGAAGGTCACTGCTTTCGT TCCAAACGATGGTTGTTTGAACTTTGTCGACGAAAATGATGAAGTCTTGCTAGCAGGTTT CGGTAGAAAGGTAAAGCTAAGGGTGATATTCCAGGTGTTAGATTCAAGGTCGTTAAGGT CTCTGGTGTCTCCTTGTTGGCTTTGTGGAAAGAAAGAAGGAAAAGCCAAGATCATAA

YGR118W, 145 aa (SEQ ID NO 114) MGKGKPRGLNSARKLRVHRRNNRWAENNYKKRLLGTAFKSSPFGGSSHAKGIVLEKLGIE SKQPNSAIRKCVRVQLIKNGKKVTAFVPNDGCLNFVDENDEVLLAGFGRKGKAKGDIPGV RFKVVKVSGVSLLALWKEKKEKPRS

YGR142W, 1733 bp, CDS: 501-1733 (SEQ ID NO 115) GGACTACTTTACAGGGTAATGAATATTTGGGCGTTTTTCGCTATTTTAGCATGCTGTAGT GACACTCGGTGGAGCTCGAGAGTTGTATCCAGTTTTCTTGTTCGGCGATATTCCGAACCA GGTCGGGTTGGGCTAACAGCCGCCCAGGATGGAAGAATTAAGAATTTCATAGAAGCCTTC_ AGTTCTTGGCGAAGTAAAGTGGCAAAACAAATGGAAGATCTATTGCATTACATATATAAA

CTTCTTGAAAGAAATATCAGTATTACAATCATAACAACAACCAAAAGAAAATAACTAATA GACCCCATTACAATATAGAAATGTTTTCCATATTCAATTCACCATGTGTTTTTGAACAGC TGCCATCTTTTAGTCAGCCCCTACATTCGCGTTATTTTGATTGCAGTTCTCCAGTGAGCT GCGATGCAAATTGTTCAGAACCTTTGAGGTATGCACTTGCTGAAACACCAAATGGTTATA CATTAAGCTTGTCTAAGCGGATTCCATATGAACTTTTTTCAAAGTACGTTAATGAGAAAT TAGGTGAGCTAAAGGAGAACCATTACAGACCAACTTACCATGTTGTCCAAGATTTTTTTG GAAACCAGTATTATGTTGAAGATGAAGCGGATGAAGATGCTCTATTGAGATCTGCATTGA AAGATCTGGATTTTAGAGCCATAGGAAAGAAAATTGCTAAGGATCTTTTCCAAGACTACG **AAATAGAATTGAATCATAGAGGTGATGAATTGAGCATATTGAGTAAGAAGGATAAAATCT** TTAAGGAATTCTCTCTAGACCAAGTGTTTGAAGATGTTTTTGTTATTGGCTGTGGAGTTG **AAAACATAGATGATGGCTCGAGAGAAAAATATGCACTTTTAAAGATTGGTTTAGTTAAGC** ATGAGGAAGAATTTCCGAAGGTGGCATCAACGAACCAAAGATGCCAATAATTGAATCCA **AAATAGACGAGTCTCACGATGATGTTAACATGTCTGAATCTTTGAAGGAGGAAGAAGCGG** AGAAAGCGAAAGAACCACTAACCAAAGAAGACCAAATAAAAAAATGGATAGAGGAAGAAA GATTGATGCAGGAGGAAAGCAGAAAATCAGAACAGGAAAAAGCTGCCAAGGAAGATGAAG AAAGGCAAAAGAAAGAAAGGAAGCCAGATTGAAGGCAAGGAAAGAATCTTTGATAAATA AGCAAAAAACCAAGAGGTCCCAGCAAAAAAAAATTGCAAAATTCCAAATCATTGCCTATCT CTGAGATTGAGGCCAGCAATAAAAATAATAATAGCAATTCTGGTTCAGCAGAAAGTGATA ATGAAAGTATAAACAGTGATTCTGATACGACTTTGGATTTCTCTGTGTCTGGTAATACAC TAAAAAACACGCTTCACCCCTATTAGAAGACGTTGAGGATGAGGAAGTTGACAGATACA ACGAGTCCCTAAGCAGATCTCCCAAGGGAAACTCTATTATTGAGGAGATATAA

YGR142W, 410 aa (SEQ ID NO 116)
MFSIFNSPCVFEQLPSFSQPLHSRYFDCSSPVSYYPECKRRKAIKANLRAPKKSDANCSE
PLRYALAETPNGYTLSLSKRIPYELFSKYVNEKLGELKENHYRPTYHVVQDFFGNQYYVE
DEADEDALLRSALKDLDFRAIGKKIAKDLFQDYEIELNHRGDELSILSKKDKIFKEFSLD
QVFEDVFVIGCGVENIDDGSREKYALLKIGLVKHEEEISEGGINEPKMPIIESKIDESHD
DVNMSESLKEEEAEKAKEPLTKEDQIKKWIEEERLMQEESRKSEQEKAAKEDEERQKKEK
EARLKARKESLINKQKTKRSQQKKLQNSKSLPISEIEASNKNNNSNSGSAESDNESINSD
SDTTLDFSVSGNTLKKHASPLLEDVEDEEVDRYNESLSRSPKGNSIIEEI

YGR236C, 890 bp, CDS: 501-890 (SEQ ID NO 117) CAAAAAAGTTTTCGGATGAACCGGATTAATACAAGTAAAATCAGCAAAGATATAGAAGAC AAAATAAGCGTGAAAACAATCATAAACCACTCACAACGGGGTTTTCAGCTGTTACTCCT CCATACATACATTTGATAAAGATATAATGTTATATTTCTTTTCGTAATTTTGTTTTACT TCGGTTTGCTCTATAGATTTCATCAGCCGCACCGAAAAGGGAGATCAATAAGGTACCCTT TAAAAGGGATAAGAAGCCTACATCACCCCAATAAATGGAGTAATGGCCAGCATTGGATGA AGAGAAGAATTACGGGATACTGGGATAACACTGTTAAAAAAATGCTTCGCGACGTGAGGGT CTTCTTCATATAAATTGAACTGCCAAATCTCTTTCACATTATCCAGGATAGTTTGGAATG TGTGTTACTGAAGGATCAGAATCAATAAATACAATCAATACAATATTTAGCGCATAAAA TTCAAACAAAGTTTACTGAAATGAAGTTAGATTCAGGAATATACTCAGAGGCACAAAGAG TTGTGAGAACTCCAAAGTTTAGATATATTATGTTAGGGCTGGTGGGCGCTGCTGTGGTAC CGACCGCATACATGAGGAGAGGCTATACGGTTCCTGCACATAGCTTAGACAACATCAACG GCGTAGACACCAACTAAGGCGTCTGTTATGGGTACAGAACAGAGAGCAGCTATGACGAAGG **GTAAGAGTTTACAAGAGATGATGATGATGAAGTAACGTATTTGATGTTCCTCTTCA** ATCATGTAAGGGAATTTGTACTTGGTTCCCTGCATTTATGTTCTTTGCATTTTGTTTTCG CATTTAATCATAGTACGACAAACGGGGAAGGGGATTGTGATTTTACATAA

YGR236C, 129 aa (SEQ ID NO 118) MKLDSGIYSEAQRVVRTPKFRYIMLGLVGAAVVPTAYMRRGYTVPAHSLDNINGVDTTKA SVMGTEQRAAMTKGKSLQEMMDDDEVTYLMFLFNHVREFVLGSLHLCSLHFVFAFNHSTT NGEGDCDFT

YGR277C, 1418 bp, CDS: 501-1418 (SEQ ID NO 119)
AATCTTTGCGATTGAATTGCTGCACGAACATTAACATTAGTTCTTTTGCTAAAGTTTCTC
CAATATCTGGAATATCAGAATTTAGCAAGGCAATCAAAGCGGATAAAGCAGGGATTAGCC
TGCCATTCTGTTTGTTCAGAGTAAAATCCACAACATTTTTACAAATTATGTTGCGGCCAA
TAAGTATATTGACTTGAAATAAGTCTCTGTGCGATTCCTGTAAGTTGTCCATTGTTAAAT
TGGATATTATGGGTGAAACGTGTGACCTTATCATTTCCCAGTTTTCTCTGAAATTTAA

TGTCTTCATCCTGTATGGTAGCGGTAGACATGCTGGTTTGTAGCCTTTTTATTCCTTTTT AGGTTTCTTACTCACAATGCCAAAATAAATATCAGTGTAATATAATTTTTCAAGAGTACG TAATGGAAAAAGATAAAAATAAGGACCGTCATAAAAAGAGACGTGATTAAACCTAAAAAT CTAAAGTAAAGAAGTGTAAGATGGTTGAGGAAAATTCCAGAGTTTTGATTGTTCCTT ATACACCGCCTAGTGCTACTTTGCAGAGGATTATAGGGCAAACTATTCCGTTCTTAAGAG **AATGTCAAAGTCAACTAGACATCGTGATTGTACCTGAATTCAAAACCTCATTCCAGTTGG ATTCTGCGCTAGGGAAGATGTACAGTATTACCAGGGATGTCCTTTTTGGGCTATGGAATGA** TCAACAGCGGAATCAACATCATATTCAACAATATTCATTTCGTCGAGAGTAATTTGCAAT GGAAAGTGGTTTTATTGCCACAGGAATCCACTTTTGAAACTTGGAAGCTAGAGTTGGGAC **AAGGACAATACCATAGTATAGAACATTATGCATTACACGATAATATAATGGAAGAGATAG** AAGGTCCCÁAAGATGCTAACAAATTTCATGTCACCGCATTGGGCGGAACGTTCGACCACA TTCACGATGGACATAAAATATTGTTGAGCGTCTCTACATTCATCACGTCACAAAGGTTAA CTTATGATACACGATGCAGGCACGTACATCAATTCATCAAGTTGTTAAAACCGGATCTCT CCGTAGAACTAGTTCCCTTAAGGGACGTGTGCGGCCCCACAGGGAAAGTACCCGAGATAG **AATGTTTAGTTGTGAGTAGAGAAACCGTCAGTGGGGCAGAGACTGTGAATAAGACTAGGA** TTGAAAAAGGCATGAGCCCATTGGCAGTACATGTGGTTAATGTACTTGGAGGAAGGGAGG AAGACGCTGGAGCGAGAAGTTAAGCAGCACGGAAATCAGACGCCTACTTAAGTCCTCTG CTTCGCCAACGTGCACTCCACAAAACCCTTGCGTATAA

YGR277C, 305 aa (SEQ ID NO 120)
MVEENSRVLIVLPYTPPSATLQRIIGQTIPFLRECQSQLDIVIVPEFKTSFQLDSALGKM
YSITRDVLLGYGMINSGINIIFNNIHFVESNLQWKVVLLPQESTFETWKLELGQGQYHSI
EHYALHDNIMEEIEGPKDANKFHVTALGGTFDHIHDGHKILLSVSTFITSQRLICGITCD
ELLQNKKYKELIEPYDTRCRHVHQFIKLLKPDLSVELVPLRDVCGPTGKVPEIECLVVSR
ETVSGAETVNKTRIEKGMSPLAVHVVNVLGGREEDGWSEKLSSTEIRRLLKSSASPTCTP
ONPCV

YGR284C, 1433 bp, CDS: 501-1433 (SEQ ID NO 121) AGAGAGCCATCCGTAACTCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGGCCA CCACGATTGACGAACAAGTTGGTTTGATCGTTGACAGTTTGAATGACGAAGAGTTAGTGT CCACCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAGGAAGTTTTGAAGGAATCTG CAAAGACTATTGTCGATTCTGGCAAACTACCATCCAGCTTGTTGTCCTACTTCGTGTGAA TACCGTAAGAAATGGAATAGAATATATACGAATGTATACGAATATTATAGAGAACGTTCT CTTTTATTCTATAATGAATAGGTTCGGGTAACGGTTCCCTTTTTAGGTATTTCTAGAAG ATGAGAGAGAGGGAATAATGAGAAAGGCGAAAAATAAAGGACACCTTTAACGAAAGATC AAAGGTGTCCTTATTTACTTACAATAGCTGCAATTAGTACGACTCAAAAAAAGTGAAAAC AAAACTGAAAGGATAGATCAATGTCTTACAGAGGACCTATTGGAAATTTTGGCGGTATGC CAATGTCATCATCGCAAGGACCATACTCTGGCGGTGCACAATTCAGATCAAACCAGAACC AATCCACTTCTGGCATCTTAAAGCAATGGAAGCATTCTTTTGAAAAGTTTGCCTCCAGAA TTGAGGGGCTCACTGACAATGCAGTTGTTTATAAATTGAAGCCTTACATTCCAAGTTTGT CAAGATTTTTCATTGTGGCCACCTTTTATGAAGATTCGTTTAGGATCTTATCACAATGGT CAGATCAAATTTTTTATCTGAATAAGTGGAAGCATTACCCATACTTCTTTGTCGTTGTGT TTCTAGTGGTTGTTACCGTTTCCATGTTGATTGGCGCCAGTTTGTTAGTTTTAAGAAAGC AAACCAATTATGCCACCGGTGTGTTATGTGCTTGCGTTATTTCTCAAGCATTAGTTTATG GGTTGTTTACGGGTTCATCATTTGTCCTAAGAAACTTTAGTGTTATTGGTGGGTTGTTAA TTGCATTCAGCGATTCAATTGTTCAAAACAAGACAACATTCGGTATGCTTCCTGAATTAA ACAGCAAAAACGACAAAGCGAAGGGTTACCTGTTGTTTGCTGGTAGAATTTTAATTGTTT TAATGTTTATCGCTTTCACTTTCAGTAAATCATGGTTTACTGTTTTTTGACCATTATCG GCACAATATGTTTCGCCATTGGTTACAAGACAAAATTCGCATCCATTATGTTGGGTTTGA TACTAACTTTTTACAATATCACGCTAAACAACTACTGGTTTTATAACAATACTAAGAGAG ATTTCTTGAAGTATGAGTTTTACCAGAACTTAAGCATCATTGGTGGGCTTCTATTAGTTA CTAATACTGGCGCTGGTGAATTATCCGTTGATGAAAAGAAGAAGATTTACTAG

YGR284C, 310 aa (SEQ ID NO 122)
MSYRGPIGNFGGMPMSSSQGPYSGGAQFRSNQNQSTSGILKQWKHSFEKFASRIEGLTDN
AVVYKLKPYIPSLSRFFIVATFYEDSFRILSQWSDQIFYLNKWKHYPYFFVVVFLVVVTV
SMLIGASLLVLRKQTNYATGVLCACVISQALVYGLFTGSSFVLRNFSVIGGLLIAFSDSI
VQNKTTFGMLPELNSKNDKAKGYLLFAGRILIVLMFIAFTFSKSWFTVVLTIIGTICFAI
GYKTKFASIMLGLILTFYNITLNNYWFYNNTKRDFLKYEFYONLSIIGGLLLVTNTGAGE

LSVDEKKKIY

YGR285C, 1802 bp, CDS: 501-1802 (SEQ ID NO 123) CATTTAGTTCTGATTACAGCAGAAATCGTAGCGCGATGAGACATTTCATCAAATGGCCTT TTTTTTTGGGCAATTTTTTATATCTTGAAATGATAGTTGCCTTGTACTTTCAACCGTT AACTATAAATATGTCAAAGAAACCATACAATCATAGATTTATAACTATCTTTTTGGATGAC ATTAATGAACATAACGCTCCTAATACAAATGTCCAAAAAATATTACCCGCAAATACGAAT CTTTTTTTTTCTCGATGAAATTTTGCAAAGAGTTCGAAATTTTTATTTCAAGAGCTGGT AGAGAAAATTTCATAAGGTTTTCCTACCGATGCTTTTATAAAATCTTCGTTTTGTCTCAC ATATACCAACAAGAGTAACGATGTTTTCTTTACCTACCCTAACCTCAGACATCACTGTTG AGTTCTTTTTGCAACATGCTCAAAGAACTTTGAGAAACCACACCTGGTCTGAATTTGAAA GAATTGAAGCTGAAAAGAACGTCAAAACCGTTGATGAATCCAATGTCGACCCAGATGAGT TGTTATTCGACACTGAATTGGCCGATGAAGATTTACTGACTCATGATGCTAGAGACTGGA AAACTGCCGATTTGTATGCTGCTATGGGTTTGTCTAAGTTGCGTTTCAGAGCTACTGAAA GTCAAATCATCAAGGCTCACAGAAAACAAGTTGTCAAGTACCATCCAGACAAGCAATCTG CTGCTGGTGGTAGTTTGGACCAAGATGGCTTTTTCAAGATTATTCAAAAGGCCTTTGAAA CTTTGACTGATTCCAACAAGAGAGCTCAGTACGACTCATGTGATTTTGTTGCCGATGTTC CTCCTCCAAAGAAGGGTACCGATTATGACTTTTATGAAGCTTGGGGCCCCGTTTTCGAAG CTGAAGCTCGTTTTTCTAAGAAGACTCCTATTCCTTCTCTAGGTAACAAAGATTCTTCCA AGAAGGAAGTTGAACAATTCTATGCTTTCTGGCACAGATTTGACTCCTGGAGAACCTTTG AGTTCTTGGACGAAGATGTCCCAGATGACTCTTCTAACAGAGACCACAAGCGTTACATTG AAAGAAAGAACAAGGCCGCAAGAGACAAGAAGAAGACTGCTGATAACGCTAGATTGGTCA AACTTGTTGAAAGAGCTGTCAGTGAAGATCCCCGTATCAAAATGTTCAAAGAAGAAGAGA AGAAGGAAAAGGAAAGAAAATGGGAAAGAGAGCCGGTGCCAGAGCTGAAGCTGAAG CTAAGGCCAAGGCCGAAGCTGAAGCCTAAAGCTGAATCTGAAGCCAAGGCTAACG CCTCCGCAAAAGCTGACAAAAAGAAGGCTAAGGAAGCTGCTAAGGCCGCCAAGAAAAAGA ACAAGAGAGCCATCCGTAACTCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGG CCACCACGATTGACGAACAAGTTGGTTTGATCGTTGACAGTTTGAATGACGAAGAGTTAG TGTCCACCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAGGAAGTTTTGAAGGAAT CTGCAAAGACTATTGTCGATTCTGGCAAACTACCATCCAGCTTGTTGTCCTACTTCGTGT

YGR285C, 433 aa (SEQ ID NO 124)
MFSLPTLTSDITVEVNSSATKTPFVRRPVEPVGKFFLQHAQRTLRNHTWSEFERIEAEKN
VKTVDESNVDPDELLFDTELADEDLLTHDARDWKTADLYAAMGLSKLRFRATESQIIKAH
RKQVVKYHPDKQSAAGGSLDQDGFFKIIQKAFETLTDSNKRAQYDSCDFVADVPPPKKGT
DYDFYEAWGPVFEAEARFSKKTPIPSLGNKDSSKKEVEQFYAFWHRFDSWRTFEFLDEDV
PDDSSNRDHKRYIERKNKAARDKKKTADNARLVKLVERAVSEDPRIKMFKEEEKKEKERR
KWEREAGARAEAEAKAKAEAEAKAKAESEAKANASAKADKKKAKEAAKAAKKNKRAIRN
SAKEADYFGDADKATTIDEQVGLIVDSLNDEELVSTADKIKANAAGAKEVLKESAKTIVD
SGKLPSSLLSYFV

41/161

ATTCATATTCATTGAGCTATACGAGGCAGTGGAAGGGTTATCAAAAAGTTGTAATTTAAA AGAAAAAGCATCAATAGCCACCAAATAAGATGGTGAAAGTTCCGCGATATATTTGCTAA CCCTATTAAAAATTCGTGGGCCTATGATAATTTTTCTCTCCCTAGTATTGAAGAACAAAA TTTTTTACACAGCTGTCGTTGTCCGTGGTCGTTACGCCGGTAAGAAGGTTGTTATCGTTA **AACCACATGATGAAGGTTCCAAGTCTCACCCATTTGGTCACGCTTTTGGTTGCCGGTATTG** AAAGATACCCATTGAAGGTCACCAAGAAGCACGGTGCCAAGAAGGTTGCTAAGAGAACCA AGATCAAGCCTTTCATCAAGGTCGTCAACTACAACCATTTATTGCCAACCAGATACACTT TAGATGTTGAAGCTTTCAAATCCGTTGTTTCTACTGAAACTTTCGAACAACCTTCCCAAC ACCAATGGTTCTTCTCTAAGTTGAGATTTTAA

YHR010W, 136 aa (SEQ ID NO 126) MAKFLKAGKVAVVVRGRYAGKKVVIVKPHDEGSKSHPFGHALVAGIERYPLKVTKKHGAK KVAKRTKIKPFIKVVNYNHLLPTRYTLDVEAFKSVVSTETFEQPSQREEAKKVVKKAFEE RHQAGKNOWFFSKLRF

YHR021C, 1299 bp, exon1: 501-503, intron1: 504-1053, exon2: 1054-1299 (SEQ ID NO 127) TTACTTACGTCTATTATAACCTTCCGCGTAAAAAAGAAATATTGACATCCTTTCTTGTAT TTAGCCCATACATTTTCACCCATGCACCATTGGATTATAAAGAAAAAAATTTAATAAAAA TCTGCCGGGGAAATTTCAGAAGAAAAAGGAAGGTGTGTTCGCATTTAACACGGGCCACC ATAAACTTTTGTTTGCCACCCATCTAGACGGGATCCGCCCCGCCCAAGGCTCTCTTCCTC TAGCTAGGCAATGTGGCTCTCGGAAAGGAAACTCCCACCAGGACGTGGTGGGAAATGCAG **AAAAGTTCTATATAGCATTTGCTTTTATTTAGAGAATACGAAAACACCAGCAGATAATTAG** TGCATATATATAGATCAATATGGTATGTGAAAGAGATATTAAACATAAGATGTGAAGGA **AACAGAAGAGAACAATATTTGAGGAATGAATTCGGATGAAATTCTAGTAGAAGAAAAAAG** CCTAAAATAAAAGAAAGAAAGGAAAATAAAGCAGTAATCAACCTCTGACATTTGATAGG AGTATGCGTTTCCGCAAAATCAACAAATCATGCATTAAACTGGTAACGGAGACTTTAAAG ACGTGCAAAGAAAGCAATTAATTTTTAGATAGGGAATTGAAAGGCTCTGTATAGCAGAAA **ATTTGAGATCTACTGTGGAGATAAGCATATGGTGTTGAGTTATGGGTAATCTAACAATAA** TAGAAACTTATAGCAGTTGAAGATGGCGGATCATGATGCCGGATACTGCTGGGTAATGAT TTATCCTTCTTTTTTGGAGCACAAATGCTCACTTTTTCCTGTCTCCTCTAACTTTTCTG CTTTCGTTTTCGTTTCTATTTATTTCATTACAGGTTTTAGTTCAAGATTTGTTGCACCCA ACTGCTGCTTCTGAAGCCAGAAAGCACAAGTTAAAGACTTTGGTTCAAGGCCCAAGATCC TACTTCTTGGATGTCAAATGCCCAGGTTGTTTGAACATCACCACTGTTTTTTCTCATGCT CAAACTGCTGTCACTTGTGAATCATGCTCTACTGTCTTATGTACTCCAACCGGTGGTAAG GCCAAATTATCTGAAGGTACTTCTTTCAGAAGAAAGTAA

YHR021C, 82 aa (SEQ ID NO 128) MVLVQDLLHPTAASEARKHKLKTLVQGPRSYFLDVKCPGCLNITTVFSHAQTAVTCESCS TVLCTPTGGKAKLSEGTSFRRK

YHR141C, 1262 bp, exon1: 501-504, intron1: 505-945, exon2: 946-1262 (SEQ ID NO 129) TAAAACATGGCATTTTAAATAGTACTGCCAAAATTTAATGCAATGGCAATTAGTTGGCTA TGTTGCTACATATTATTTTCCATAGCATTCTCTGTCACAAACTTCAAAATAAAAGACAGT TCTTGATACAAAAAAGATCGCTGTCAAAAATGCGGCCAGACTGCCGCTGCATCGTACCA ACCAAGAGAGGTAAAATTATTCGTCGAAATGAACTCAGAGATACATCCATATTGTTGACA ATGTATATCTTAATTGATGTGGTATTTTCACTGTTTTAACGTAAATTGAAGGAGATTAAG CAAAAAACAATCAGTAATAATGGGTATGTGGACGATTAGGAATAGACAAACCATGTTAT TTATCTCCATTAGGGCGTGAGAGTGTAATTAGTACACAGGTACTACTAGAATGCTAAAGA

YHR141C, 106 aa (SEQ ID NO 130) MVNVPKTRKTYCKGKTCRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGFGGQTKPVFHK KAKTTKKVVLRLECVKCKTRAOLTLKRCKHFELGGEKKQKGQALQF

YHR217C, 962 bp, CDS: 501-962 (SEQ ID NO 131) TCCATGGTGCACAGTATCTTAACTATCTGCTTAGTCGAGGAGAACCAGGATTCTGTTCGT TGCTCAGCCGCTTCGTGGATATTCTCTTGGATACTTTAAACATGGACCTACGTTCCGCTC TCGAAAAGACCAATATAATAAAAAGTTATAAATTACATTTCCTTATTAGGTATACGACCT AACTTCCCCCAAAAATGTATTACCCCGCCGAATAAGAAAACAGACCCATTCACCCACGAC GTATCAAGTTACTTCCTTGGTGCAATGTCCCACTATAAAAAATTCCTTGACGCTAGATC GTTGGACTAAAATCTGCGTCACAATCGCCTAAACAGGAAATATTGCCTATTTTCGTACAA GGTTACTTCCTAGATGCTATATGTCCCTACGGCCTTGTCTAACACCATCCAGCATGCAAT ACCTGTCTCTTAACCTACCCTCACATTACCCTACCTCCCCACTCGTTACCCTGCCCCACT TCATACCGTTACCCTCCAATTACCCATATCCAACTCCACTACCATTACCCTGCTATTAC CCTACCATCCACCATGTCCTACTCACTGTACTGTTGTTCTACCCTCCATATTGAAACGTT

YIL112W, 3752 bp, CDS: 501-3752 (SEQ ID NO 133) TTCCATAGGGCTTATTTTCCAGTTGATGGAATGGGAGGTTGCTCTTAACGCGAAGACTAA TTCCGTATTTCTTCGCTTTGTTTCATGCTCTGTTCTGAGCTTTTAGTTTCTCTTATTGAG AGCCTTTTCCAAATCAAGGCTCAGGAAGTGACTCGTCCTTAGAAGAACAAGGTTTGGATT TGGTAGGGTTCTTGTACGAAGTTCTCAATATAATTTGCGCATTTACTGTACGGTTCATAC TAGTTTATTCCGGGTAACAAGTTTTCTTGTGATGCTAAATCAATGTGTATATTGAGAAAA CTATGTAGTAAGTTACACAAAGCAACAAAGGATATTATTATATGTGACAGAGAAGAATTG CTGTAGAGATTCATGACAATATGAATGAGACTACTACAAAACAGCCGCTAAAGAAAAGGT CCCTGAGCAGCTATCTTTCAAACGTGAGCACGAGACGGGAGGAGCTGGAAAAGATTTCTA AACAAGAAACATCCGAAGAGGAAGATACTGCCGGCAAGCATGAACAAAGGGAAACACTGT CGGAAGAAGTAAGTGATAAGTTTCCAGAAAATGTTGCATCGTTTCGCTCACAGACTACAA GCGTTCATCAAGCCACCCAAAATAACCTGAATGCAAAGGAATCCGAAGACCTGGCCCATA AGAATGATGCGAGTTCACACGAAGGAGGGTTAATGGGGACAGCCGTCCGGACGATGTTC CTGAAACGAATGAAAAAATAAGCCAAGCAATACGAGCGAAAATTTCGTCATCATCATCAT CACCCAATGTACGTAATGTTGATATCCAAAACCATCAACCTTTTTCGAGAGACCAACTTC GAGCGATGTTGAAAGAACCAAAAAGGAAAACTGTTGATGATTTCATAGAAGAAGAGGGGTT CAGAAAATGTGGAAAAAGATATAGAGTATAGCGACTCAGATAAGGACACAGACGATGTGG 43/161

GAAGCGATGATCCCACGGCACCCAACTCACCAATAAAACTTGGTCGTCGCAAACTGGTTA GAGGTGACCAACTTGATGCAACAACAAGTTCCATGTTTAATAACGAATCAGATTCTGAAT TATCAGATATCGATGATAGCAAGAATATTGCTTTATCCAGTAGCCTATTTAGAGGCGGTT CTTCACCTGTGAAAGAGACAACAACAACCTTTCAAATATGAATTCTTCACCAGCACAAA ATCCAAAAAGGGGTTCTGTCTCCAGGAGTAATGATAGTAACAAGAGTTCTCATATAGCTG TTTCCAAGCGCCCCAAACAGAAGAAGGGCATATATAGGGATTCTGGTGGTAGAACAAGAC TACAGATTGCCTGTGACAAGGGCAAATATGATGTAGTCAAAAAAGATGATTGAAGAAGGAG GTTACGATATTAATGACCAAGACAATGCTGGTAATACAGCATTGCATGAAGCGGCGTTGC AAGGTCATATTGAGATTGTGGAACTGTTGATAGAAAATGGTGCAGATGTAAATATCAAGT CTATTGAAATGTTCGGCGATACTCCCTTGATCGATGCTTCCGCCAATGGACACTTGGATG TTGTCAAGTATCTTCTTAAAAACGGTGCGGACCCAACTATACGTAACGCTAAAGGGTTAA CTGCGTTTGAATCTGTCGATGATGAATCTGAATTTGATGATGAAGAAGACCAAAAGATTT TGCGTGAAATAAAAAAAGGTTGAGTATAGCCGCTAAAAAATGGACTAACAGAGCAGGAA TTCATAATGACAAATCTAAAAATGGCAATAATGCTCACACAATAGATCAGCCACCTTTTG ATAATACCACAAAAGCCAAAAACGAAAAGGCCGCTGACTCACCTTCAATGGCTTCCAATA TTGATGAGAAAGCTCCGGAAGAGGAATTCTATTGGACAGATGTTACTTCTAGAGCGGGAA AAGAAAACTGTTTAAAGCTTCGAAGGAGGGCACATTTACCATACGTTGGTACGTATGTAG AAAATGGTGGTAAGATAGACTTAAGGTCATTTTTCGAAAGCGTTAAGTGTGGCCATGAAG ATATTACAAGTATCTTTTTGGCATTCGGATTTCCCGTAAATCAAACTTCAAGGGATAATA **AAACATCCGCTTTAATGGTAGCTGTAGGTCGTGGCCATCTTGGAACTGTTAAACTGCTAT** TAGAGGCAGGTGCAGATCCAACCAAAAGAGATAAAAAGGGTCGTACCGCTTTGTACTATG TAAATAACTATTTGAAGAAGCACTCTGAAGATAATAATGATGATGATGATGATGATGATGATA **ATAATAATGAAACATATAAACATGAAAAAAAGAGAGAGAAAACGCAATCACCCATATTAG** CAAGCCGAAGAAGTGCCACTCCTAGAATTGAAGACGAAGAGGACGATACGAGGATGCTCA ATCTGGCAGACGATGACTTTAATAACGATCGTGATGTCAAGGAATCTACAACTTCGGATT CGCGCAAGAGATTGGATGACAATGAAAATGTTGGTACTCAATACTCATTGGACTGGAAAA **AACGTAAAACAAATGCCTTGCAAGATGAAGAAAAATTAAAAAGTATCTCACCACTCTCTA** TGGAACCTCATTCTCCAAAGAAGGCAAAATCTGTAGAGATAAGTAAAATACATGAAGAAA GGATCGAAGAACAGGAGAAGCAGAAAGTCTTAGAAATGGAAAGATTGGAAAAAGCTACTT TAGAGAAAGCAAGAAAAATGGAAAGGGAAAAAGAAATGGAAGAAATCTCTTATAGAAGGG CAGTAAGGGACTTATATCCGTTAGGACTGAAGATTATTAACTTCAACGATAAACTTGATT ACAAAAGATTTTTGCCGCTATATTATTTTTGTAGACGAAAAAAACGATAAATTTGTGCTCG CTTCTGAGAAGATTCCCGTCGATCCCTCGCACCTGACTCCATTGTGGAATATGTTGAAAT TCATTTTCCTGTATGGAGGTAGTTATGATGATAAAAAGAACAACATGGAAAATAAAAGAT ATGTTGTAAACTTTGATGGGGTTGATTTGGACACAAAGATTGGGTATGAGCTTTTGGAGT ACAAAAATTTGTTAGTTTGCCCATGGCGTGGATTAAATGGGATAACGTTGTTATTGAAA ACCACGCAAAAAGAAAAGAAATTGAAGGAAATATGATTCAAATATCAATAAACGAATTTG CACGATGGAGAAACGATAAGCTGAACAAAGCGCAGCAGCCGACGCGCAAACAGCGTTCTC TAAAAATACCTCGAGAGTTACCGGTTAAATTTCAACACCGTATGAGCATATCCTCCGTCC TCCAGCAGACATCCAAAGAACCATTTTGGTAA

YIL112W, 1083 aa (SEQ ID NO 134)
MNETTTKQPLKKRSLSSYLSNVSTRREELEKISKQETSEEEDTAGKHEQRETLSEEVSDK
FPENVASFRSQTTSVHQATQNNLNAKESEDLAHKNDASSHEGEVNGDSRPDDVPETNEKI
SQAIRAKISSSSSSPNVRNVDIQNHQPFSRDQLRAMLKEPKRKTVDDFIEEEGLGAVEEE
DLSDEVLEKNTTEPENVEKDIEYSDSDKDTDDVGSDDPTAPNSPIKLGRRKLVRGDQLDA
TTSSMFNNESDSELSDIDDSKNIALSSSLFRGGSSPVKETNNNLSNMNSSPAQNPKRGSV
SRSNDSNKSSHIAVSKRPKQKKGIYRDSGGRTRLQIACDKGKYDVVKKMIEEGGYDINDQ
DNAGNTALHEAALQGHIEIVELLIENGADVNIKSIEMFGDTPLIDASANGHLDVVKYLLK
NGADPTIRNAKGLTAFESVDDESEFDDEEDQKILREIKKRLSIAAKKWTNRAGIHNDKSK
NGNNAHTIDQPPFDNTTKAKNEKAADSPSMASNIDEKAPEEEFYWTDVTSRAGKEKLFKA
SKEGHLPYVGTYVENGGKIDLRSFFESVKCGHEDITSIFLAFGFPVNQTSRDNKTSALMV
AVGRGHLGTVKLLLEAGADPTKRDKKGRTALYYAKNSIMGITNSEEIQLIENAINNYLKK
HSEDNNDDDDDDDNNNETYKHEKKREKTQSPILASRRSATPRIEDEEDDTRMLNLADDDF
NNDRDVKESTTSDSRKRLDDNENVGTQYSLDWKKRKTNALQDEEKLKSISPLSMEPHSPK
KAKSVEISKIHEETAAEREARLKEEEEYRKKRLEKKRKEQELLQKLAEDEKKRIEEQEK

QKVLEMERLEKATLEKARKMEREKEMEEISYRRAVRDLYPLGLKIINFNDKLDYKRFLPL YYFVDEKNDKFVLDLQVMILLKDIDLLSKDNQPTSEKIPVDPSHLTPLWNMLKFIFLYGG SYDDKKNNMENKRYVVNFDGVDLDTKIGYELLEYKKFVSLPMAWIKWDNVVIENHAKRKE IEGNMIQISINEFARWRNDKLNKAQQPTRKQRSLKIPRELPVKFQHRMSISSVLQQTSKE PFW

YIL115C, 4883 bp, CDS: 501-4883 (SEQ ID NO 135) TTTCAATGCGCTACAACTGACTGAACCAGTCCACAAATTTGGCTGGTCTCTATCGTTCTC GCCCTGAGAGATTTTATTTTCTTATAAATTTTTACTAAATAAGGATTTGTACTTTTGATAG AGTTTTTTTTTTTCTGACGTTTGTTTAGTTAATATTATATAATAGTATTTAGGAAACTA GGTGGGAGGGGACATCGCAACTTTTATCGTGACCTACGACCAGTGTTTTTTCAATTGTTT GATCAAAAGAGAAAAAAAGACAAAGGACCGAAGGATAGTTGCACGCATAAACTGGAGAAA **AAATTGTGTTTGACATCGGCGTTTAGGCTTGTTTGTTCTGTCACACATACGCTGCTTCAC** ACCAATTCATATTTCTCAGGTTAATTTGTCTCCTCTCCAACTTCAATAACGATTTTGCGT GATTACAGAACCATTATAACATGTCTTCTTTGAAGGATGAAGTACCCACTGAGACTTCCG TGCCATTTGCATCTCTACAAAATCTCGATATTTCAAACAGTAAGTCTTTATTCGTTGCTG CCTCTGGTAGTAAGGCGGTGGTCGGCGAATTACAATTACTGAGAGATCATATCACCTCCG ACTCTACTCCGTTAACGTTCAAGTGGGAGAAAGAAATCCCAGATGTAATATTTGTGTGCT TTCATGGTGATCAGGTTTTGGTTTCAACCAGAAATGCATTATATTCGTTAGACTTGGAGG AATTGAGTGAATTTCGAACGGTCACTTCTTTTGAGAAGCCAGTTTTCCAATTGAAGAACG TTAATAACACTTTAGTAATTTTAAATTCAGTCAATGATTTATCAGCACTGGATTTAAGAA CAAAATCGACTAAGCAACTGGCACAAAACGTTACCTCTTTTGATGTCACAAATTCGCAGT TAGCAGTTCTACTAAAAGATAGAAGTTTTCAAAGTTTTGCATGGCGAAATGGCGAAATGG AAAAACAATTTGAGTTCTCTCTACCGTCAGAATTAGAAGAGCTTCCAGTAGAAGAATATT CCCCTTTGAGTGTTACCATTCTCTCTCCACAGGATTTTTTGGCGGTTTTTCGGTAATGTTA TATCAGAGACCGATGACGAAGTTTCATACGATCAAAAAATGTACATTATAAAGCACATAG ACGGCAGCGCCTCATTTCAAGAAACTTTTGATATTACACCTCCATTCGGGCAAATAGTAA GGTTCCCATATATGTACAAAGTTACCTTGTCTGGTTTAATTGAACCTGATGCAAACGTAA ATGTGCTAGCATCATCATGTTCAAGTGAAGTAAGTATATGGGACTCGAAACAAGTTATTG **AACCTTCCCAGGATTCTGAACGAGCAGTATTGCCCATCAGTGAGGAAACAGATAAGGACA** CAAATCCAATAGGTGTGGCAGTTGACGTCGTTACTTCAGGCACTATTCTAGAACCTTGTT CCGGTGTTGATACGATAGAGCGATTGCCGCTCGTTTACATATTGAATAACGAAGGTAGCT TACAGATAGTCGGGTTGTTTCATGTGGCAGCAATCAAAAGCGGCCATTATAGCATAAATC TGGAATCTTTAGAACATGAGAAATCTCTCTCTCCTACATCAGAAAAAATTCCTATTGCTG GACAGGAGCAGGAAGAAAAAAAGAAAAATAATGAATCAAGTAAGGCTTTATCAGAGAATC CTTTCACATCAGCAAATACATCAGGCTTCACTTTTCTTAAAACACAACCAGCCGCTGCCA ATAGCCTGCAGTCTCAAAGTTCTTCAACCTTTGGTGCTCCCTCATTTGGATCATCCGCAT TTAAAATTGACTTGCCATCAGTCTCATCTACCAGTACTGGTGTAGCGTCCAGTGAACAAG ACGCAACAGATCCTGCTTCTGCTAAGCCAGTATTCGGCAAACCCGCGTTCGGAGCTATTG TTGGCTCTGGAAAGTCATCTGTTGAATCGCCTGCCTCCGGATCTGCCTTTGGTAAGCCCT CTGCATTTGGTAAGCCCTCTTTTGGTACTCCTTCCTTTGGCTCTGGAAATTCATCTGCTG AGCCGCCTGCTTCCGGATCTGCCTTTGGTAAGCCCTCTTTTGGTACATCTGCATTCGGAA CTGCATCAAGTAACGAAACTAACTCTGGATCCATATTTGGAAAGGCTGCATTTGGTTCAT CATCTTTTGCACCCGCCAACAATGAACTTTTCGGATCAAACTTTACTATTTCAAAACCTA CAGTTGACAGCCCAAAGGAGGTAGATTCAACGTCACCTTTCCCATCTTCTGGCGATCAAA GTGAAGATGAGTCTAAGAGTGATGTAGACTCTTCTTCGACACCTTTTTGGTACGAAACCTA ACACCTCTACGAAACCAAAGACCAATGCCTTTGATTTTGGGAGTTCTTCCTTTGGATCTG GATTTTCAAAGGCTCTGGAATCTGTTGGTTCCGATACAACTTTTAAATTCGGTACTCAGG CTTCACCTTTCTCTCACAGTTAGGAAACAAATCACCATTCAGTTCCTTCACAAAAGATG ATACTGAAAATGGATCTTTAAGTAAGGGCTCTACCAGTGAAATCAATGACGATAATGAAG AACACGAAAGCAATGGTCCCAACGTAAGCGGTAATGATTTGACAGATTCTACGGTTGAGC AAACATCTTCTACTAGATTACCGGAAACTCCCTCGGATGAAGATGGTGAAGTTGTCGAGG TTGACATGGCTGGTTTAAAAAATCCTGTATTTGGAAATCATGTCAAAGCAAAATCCGAAT CGCCGTTTTCAGCATTTGCAACAATATTACCAAACCAAGCTCTACAACACCTGCTTTTT CGTTTGGTAACTCCACAATGAATAAAAGTAATACATCTACGGTTTCACCAATGGAAGAAG

CTGATACTAAAGAAACTAGTGAAAAGGGCCCCATAACCTTGAAGAGTGTGGAGAATCCGT TTCTACCAGCGAAAGAAGAACTGGAGAAAGTTCTAAAAAGGATCATAACGATGACC CAAAAGATGGTTATGTATCAGGAAGTGAAATATCTGTAAGGACTTCTGAAAGTGCTTTTG ATACCACAGCAAACGAAGAAATTCCAAAGTCACAGGACGTGAACAATCATGAAAAAAGCG AAACAGACCCAAAATATAGTCAACATGCTGTGGTTGATCACGATAACAAGTCTAAAGAAA TGAATGAAACTTCGAAGAATAATGAAAGGAGCGGTCAACCAAATCATGGTGTCCAAGGAG **ATGGAATAGCATTGAAAAAAGACAATGAAAAAGAGAATTTTGATTCAAATATGGCAATAA** GCAGTGAAGTTAAAGAATCAGATGATAACATGTCACTCAACAGTGACCGGGATGAAAGTA TATCTGAGTCCTACGATAAACTGGAAGATATTAATACTGATGAGCTACCTCATGGTGGAG AAGCTTTTAAAGCACGTGAAGTGAGCGCTTCCGCTGATTTTGATGTACAAACTTCATTAG AAGACAATTATGCTGAATCTGGCATACAGACAGACCTTTCAGAAAGTTCCAAGGAAAATG CAGTCGACAATGGTCTGCAAACTGAGCCTGTTGAAACATGTAATTTTTCTGTTCAAACAT TTGAAGGTGACGAAAATTATTTAGCAGAGCAATGCAAACCAAAGCAATTGAAAGAATATT ACACAAGTGCAAAAGTATCAAATATTCCTTTCGTTTCACAAAATTCTACGTTAAGGTTGA TTGAGAGTACATTTCAGACGGTCGAAGCTGAGTTTACTGTTCTGATGGAAAACATCCGGA ATATGGATACTTTTTTTACTGATCAATCGAGCATCCCTTTGGTGAAGCGTACAGTGCGGT CTATCAATAATCTGTATACTTGGAGAATACCAGAGGCTGAAATTCTATTAAATATTCAGA ATAATATCAAGTGTGAACAAATGCAAATAACAAATGCTAACATTCAAGACCTGAAGGAAA **AAGTTACAGATTATGTCAGGAAAGATATTGCACAAATAACTGAAGATGTAGCCAATGCAA** AAGAGGAGTATCTGTTTTTAATGCATTTTGATGATGCTTCGAGTGGATACGTTAAAGATC TCAGCACGCATCAATTTAGAATGCAAAAGACATTACGTCAAAAGCTATTCGATGTCCG CCAAAATTAATCATACTGAAGAGTTGCTGAACATTTTAAAATTGTTCACTGTAAAGAATA AGAGATTGGACGATAATCCATTAGTGGCAAAACTAGCTAAAGAATCTCTTGCACGTGACG GTTTACTAAAAGAAATCAAATTATTGCGTGAGCAAGTGAGTAGGTTACAATTGGAGGAGA AAGGTAAAAAGGCTTCGTCGTTCGATGCATCCTCTTCAATAACAAAGGACATGAAAGGAT TTAAAGTAGTAGAAGTTGGGTTGGCCATGAATACGAAAAAGCAAATTGGTGATTTCTTCA AAAATTTGAACATGGCAAAATAG

YIL115C, 1460 aa (SEQ ID NO 136) MSSLKDEVPTETSEDFGFKFLGOKOILPSFNEKLPFASLQNLDISNSKSLFVAASGSKAV VGELOLLRDHITSDSTPLTFKWEKEIPDVIFVCFHGDQVLVSTRNALYSLDLEELSEFRT VTSFEKPVFQLKNVNNTLVILNSVNDLSALDLRTKSTKQLAQNVTSFDVTNSQLAVLLKD RSFQSFAWRNGEMEKQFEFSLPSELEELPVEEYSPLSVTILSPQDFLAVFGNVISETDDE VSYDQKMYIIKHIDGSASFQETFDITPPFGQIVRFPYMYKVTLSGLIEPDANVNVLASSC SSEVSIWDSKQVIEPSQDSERAVLPISEETDKDTNPIGVAVDVVTSGTILEPCSGVDTIE RLPLVYILNNEGSLQIVGLFHVAAIKSGHYSINLESLEHEKSLSPTSEKIPIAGQEQEEK KKNNESSKALSENPFTSANTSGFTFLKTQPAAANSLQSQSSSTFGAPSFGSSAFKIDLPS VSSTSTGVASSEQDATDPASAKPVFGKPAFGAIAKEPSTSEYAFGKPSFGAPSFGSGKSS VESPASGSAFGKPSFGTPSFGSGNSSVEPPASGSAFGKPSFGTPSFGSGNSSAEPPASGS AFGKPSFGTSAFGTASSNETNSGSIFGKAAFGSSSFAPANNELFGSNFTISKPTVDSPKE VDSTSPFPSSGDQSEDESKSDVDSSSTPFGTKPNTSTKPKTNAFDFGSSSFGSGFSKALE SVGSDTTFKFGTQASPFSSQLGNKSPFSSFTKDDTENGSLSKGSTSEINDDNEEHESNGP NVSGNDLTDSTVEQTSSTRLPETPSDEDGEVVEEEAQKSPIGKLTETIKKSANIDMAGLK NPVFGNHVKAKSESPFSAFATNITKPSSTTPAFSFGNSTMNKSNTSTVSPMEEADTKETS EKGPITLKSVENPFLPAKEERTGESSKKDHNDDPKDGYVSGSEISVRTSESAFDTTANEE IPKSQDVNNHEKSETDPKYSQHAVVDHDNKSKEMNETSKNNERSGQPNHGVQGDGIALKK DNEKENFDSNMAIKQFEDHQSSEEDASEKDSRQSSEVKESDDNMSLNSDRDESISESYDK LEDINTDELPHGGEAFKAREVSASADFDVQTSLEDNYAESGIQTDLSESSKENEVQTDAI PVKHNSTOTVKKEAVDNGLOTEPVETCNFSVOTFEGDENYLAEQCKPKQLKEYYTSAKVS NIPFVSQNSTLRLIESTFQTVEAEFTVLMENIRNMDTFFTDQSSIPLVKRTVRSINNLYT WRIPEAEILLNIQNNIKCEQMQITNANIQDLKEKVTDYVRKDIAQITEDVANAKEEYLFL MHFDDASSGYVKDLSTHQFRMQKTLRQKLFDVSAKINHTEELLNILKLFTVKNKRLDDNP LVAKLAKESLARDGLLKEIKLLREQVSRLQLEEKGKKASSFDASSSITKDMKGFKVVEVG LAMNTKKQIGDFFKNLNMAK

YIL148W, 1321 bp, exon1: 501-508, intron1: 509-942, exon2: 943-1321 (SEQ ID NO 137)
TCGATCAACTCTATCCAACAATTCTATAATATCCACTGTTCATTAACGAATATTGGTCTT

TTTCCCTTATGGTGAAGTAAATTTTCCATGCAATATCCGGGTAAGCTATCGACAAGTTTA TTGACTGCAATTTGAGTTTATTACATCCGTACATTACTAAGATGTATGGTTTTTCTATTT TTGTGCTCCGTGTCGATATTTCGTGGAGCAAACCAGAAAAGATGCGGAACCTCTTAGCAC TCCGCCTGGACATAGGCGGAGCATATTCCTCCTATGGGATGGGTTTTGTTGTACTCTTTT CTCTCTAGACAGGACCTCCGATTGCCTCCCTGAGGGTGAGATGGTTTCCGGCCTCAGGAC **AAATTAAAGGTAGTTGAATCTCTATTTGTTGTTGTTATTACCGCTTATTATCCCATAGTT** GAGACGACCAAGATTCAAACATGCAAATGTATGCACCATATCCATTCTAAACATAGTTTT TCGAACGTTCAGAGCTTAAAGGGACAATTATTTTAGAAACTGAATTTTTACCCAGTGGAA TAACATCGTATCTGTAAAGTCTACAAAATTTTTTATCCATCAAAAATTAAAACAAAGAAA ACTGCCAAACTGAATATGAGGAACTTTCCTCTCTAGGAATGACTTAGTGAATGTACAGTG **ACTTGTGGAAAATATGATTAGATTTTGAGCGGGTGATGCGACTTAACAGTCTCATTGCCT** AAGAAATATCCAAATTTGTGGTTCATGCTCTCCCCCAAGATATGACGATGAGAGCTCGTT TAAAATTTTGTCTTCTTCCGAACAGTTATGAAAAAACTATTACGTGTTTTTATGATATCC TTACTAACTTGTCATTTTTTTATAAAATTATTTTTTTAACAGTTTTGTCAAGACTTTGAC TGGTAAGACCATCACTTTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCAAA GATTCAAGACAAGGAAGGTATCCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCA ATTGGAAGACGGTAGAACCTTGTCTGACTACAACATTCAAAAAGAATCCACTTTGCACTT **AGTCTTGAGATTGAGAGGTGGTATCATTGAACCATCTTTGAAAGCTTTTGGCTTCCAAGTA** CAACTGTGACAAATCTGTTTGCCGTAAGTGTTATGCTAGATTGCCACCAAGAGCTACCAA CTGTAGAAAGAGAAAGTGTGGTCACACCAACCAATTGCGTCCAAAGAAGAAGTTAAAATG

YIL148W, 128 aa (SEQ ID NO 138) MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYN IQKESTLHLVLRLRGGIIEPSLKALASKYNCDKSVCRKCYARLPPRATNCRKRKCGHTNQ LRPKKKLK

YIL150C, 2216 bp, CDS: 501-2216 (SEQ ID NO 139) AATATTCAACCTGAAGTTGCAGTCAAAGCGGCGATTAACTTTTCCAACGTAACCGATCTA ACTAACAATAGCACCGATGGAGCAAAAATAACAGAAATTGGAAGTACATCTAAACGGCCA ATTGAGAGCGGTACATCTTCTGATCCAGACACCAAAAAGGTTAAAGAGAGTCCAGCAAAT GATCAAGCTTCCAACGAGTGATGTAATATTAAACAATGTAATTATAAATATGAAACAT CTACATATTTTAAATGTCACTAATGTCATTACAGAGGACATAAAGTGATTTATGACACAT GTTTCTTGGATGCGCAAACCCACCTTTTCTAACACCCACTAAGAAATATCAACTTTATAGG CCATCGAAGATAAAGGAACGTAAGTTTGTCAATTCAACCTCACATTTTCAACGCACATTA AGCACTTGGTTCGTGGAGAAATGAATGATCCTCGTGAAATTTTTAGCGGTTGATCCGTACA ATAATATTACTTCTGATGAAGAGGATGAGCAAGCCATCGCGAGAGAACTTGAATTTATGG AGGATCCTAATTTTGAAGCCATCGAGGTACCTCAATCTCCTACCAAAAACCGTGTGAAAG TGGGGTCTCATAATGCTACACAACAAGGCACAAAATTCGAAGGTTCGAATATTAATGAAG TAAGGTTATCTCAATTACAGCAGCAACCAAAACCACCAGCTAGTACAACCACATACTTTA TGGAGAAATTTCAAAACGCAAAGAAGAACGAAGATAAACAAATTGCCAAGTTTGAAAGCA TGATGAATGCAAGAGTACATACGTTCAGTACCGATGAGAAGAAATATGTGCCGATAATCA CAAACGAATTAGAAAGCTTTTCAAATCTTTGGGTTAAAAAGAGGTACATACCTGAAGATG ACTTAAAACGGGCTTTGCATGAGATCAAAATCCTTCGGTTGGGCAAACTTTTTGCTAAAA TTCGCCCACCTAAATTTCAAGAGCCTGAATACGCCAACTGGGCCACCGTAGGCCTCATTA GCCACAAATCGGACATCAAATTTACATCATCTGAAAAGCCAGTCAAATTCTTCATGTTCA CCATAACGGACTTTCAGCATACACTAGATGTTTATATCTTCGGGAAAAAGGGTGTAGAAA GATATTATAATCTTCGCCTGGGTGATGTGATAGCAATATTAAACCCAGAAGTACTACCAT GGAGACCCTCAGGGCGAGGAAATTTTATCAAATCCTTCAACCTTCGAATTAGTCATGACT TCAAATGTATCCTGGAGATAGGTTCAAGTAGAGATTTAGGTTGGTGTCCCATAGTGAATA AAAAGACTCACAAAAAATGTGGCTCTCCCATTAACATATCTCTTCATAAGTGTTGCGATT ACCATAGAGAAGTGCAATTTCGTGGAACAAGTGCTAAAAGAATTGAATTAAATGGTGGGT ACGCCTTGGGCGCCCTACGAAAGTGGACTCTCAACCAAGCCTATATAAGGCCAAAGGGG **AAAACGGGTTTAATAATCAAAGGTACTCGTAAGCGCCTGTCAGAAGAGGGGAAAAGAC** TTAAAAAGAGCTCTCACAATTTTACGAATAGTAATTCTGCCAAAGCATTTTTCGACGAGA AATTTCAGAATCCAGATATGCTGGCAAACTTAGACAATAAAAGAAGGAAAATAATAGAAA CTAAGAAATCGACAGCACTGAGCCGCGAACTAGGCAAAATTATGAGAAGGAGGGAATCCA

GCGGATTAGAAGATAAGAGCGTCGGAGAGCGACAGAAAATGAAACGAACCACAGAAAGTG CCCTCCAGACAGGGCTTATCCAACGCCTAGGATTCGATCCCACTCATGGAAAAATTTCCC **AAGTACTCAAGTCTTCTGTATCAGGGAGCGAACCTAAGAACAACTTACTCGGTAAAAAAA AAACTGTTATAAACGATCTCTTGCATTACAAGAAGGAAAAAGTCATTCTCGCACCTTCAA AGAACGAATGGTTCAAGAAAAGAAGCCATCGCGAAGAAGTTTGGCAAAAAACATTTCGGAT** CCAAGGAAACTAAAGAAACTTCTGACGGTAGTGCCAGCGATCTTGAGATAATATAA

YIL150C, 571 aa (SEQ ID NO 140) MNDPREILAVDPYNNITSDEEDEQAIARELEFMERKRQALVERLKRKQEFKKPQDPNFEA IEVPOSPTKNRVKVGSHNATQQGTKFEGSNINEVRLSQLQQQPKPPASTTTYFMEKFQNA KKNEDKOIAKFESMMNARVHTFSTDEKKYVPIITNELESFSNLWVKKRYIPEDDLKRALH EIKILRIGKLFAKIRPPKFQEPEYANWATVGLISHKSDIKFTSSEKPVKFFMFTITDFQH TLDVYIFGKKGVERYYNLRLGDVIAILNPEVLPWRPSGRGNFIKSFNLRISHDFKCILEI GSSRDLGWCPIVNKKTHKKCGSPINISLHKCCDYHREVQFRGTSAKRIELNGGYALGAPT KVDSQPSLYKAKGENGFNIIKGTRKRLSEEEERLKKSSHNFTNSNSAKAFFDEKFQNPDM LANLDNKRRKIIETKKSTALSRELGKIMRRRESSGLEDKSVGERQKMKRTTESALQTGLI QRLGFDPTHGKISQVLKSSVSGSEPKNNLLGKKKTVINDLLHYKKEKVILAPSKNEWFKK RSHREEVWQKHFGSKETKETSDGSASDLEII

YIL167W, 1133 bp, CDS: 501-1133 (SEQ ID NO 141) GACATTTTGAAAAAATTACATTTATAGAAGTTTATTATAACGTAACAGTTAACAACAAAG GCTCATAGTCCGAGATCAATATAATAAATTATTCAAGGTTTAAGGAAGAAGTTACCATGG **AAATGACTTACTATGAAAAGACACCTTTGATTCGTCAATTTTTGAACAATGGTAAGACAA** ATTCGTGGTTTTACGTTAAGCATGAGATGTTACAACCAGGTGGAAGTTTCAAATCGAGAG GAATCGGGCATTTGATAAGGAAGAGTAATGAAGAAGCGCTAAGCGAGGGTTCTGGGAAGC CGATGCCACTTAATTGCAGTGTAGTGGTTCCTAAAACTACAAAACCTAGAATGGTAAAGA **AAATTCAAAGTGCAGGAGCCAAAGTCATTATCCATGGTGATCATTGGGGGGAAGCAGATG AATACTTGAGGCACGAATGAATGGCGCAAGAAAGCCAACATGGTTCGAAGACACTATATG** TGCACCCGTTTGATAACGAGACAATTTGGGAAGGTCATTCTACGATTGTGGATGAAATCA TAGAACAATTGAAGGAAAATGATATATCCTTACCTAGGGTGAAAGCTTTGGTTTGTAGTG TTGGTGGTGGTGGGCTATTTAGTGGCATAATTAAAGGCCTAGATAGGAATCAGCTTGCTG AAAAATTCCGGTCGTTGCTGTAGAAACTGCCGGTTGTGACGTATTGAATAAGTCTCTCA AAAAAGGTAGTCCAGTTACTCTTGAAAAATTGACAAGTGTTGCAACTTCTTTGGCCTCCC CATACATAGCATCATTCGCGTTTGAGAGTTTTAACAAGTATGGATGTAAGTCTGTAGTTT TATCAGATCAAGACGTTCTGGCAACATGCTTGAGATATGCCGATGACTACAATTTTATAG TGGAACCAGCCTGTGGAGCATCCTTACATTTATGTTATCATCCAGAGATTCTTGAAGACA TTCTGGAACAAAAATATATGAGGATGATATCGTTATTATAATCGCATGCGGTGGATCAT GTATGACGTATGAAGACTTGGTGAAAGCGTCGAGCACATTAAACGTATCATAA

YIL167W, 210 aa (SEQ ID NO 142) MAQESQHGSKTLYVHPFDNETIWEGHSTIVDEIIEQLKENDISLPRVKALVCSVGGGGLF SGIIKGLDRNQLAEKIPVVAVETAGCDVLNKSLKKGSPVTLEKLTSVATSLASPYIASFA FESFNKYGCKSVVLSDQDVLATCLRYADDYNFIVEPACGASLHLCYHPEILEDILEQKIY **EDDIVIIIACGGSCMTYEDLVKASSTLNVS**

YJL034W, 2549 bp, CDS: 501-2549 (SEQ ID NO 143) CCATGAACTCAGCATGTGCTACTCCAGTTAATGACTTGTTCGTATCGTTCATGCCATAAG CCATCACCTGGCCAGTTGGCGTATGTACAAAGATGCAAGCTACCGGTGTCTCATCGTGGT CAAGAGCGTATCTAGCCAAACGGACAGCTGTCCTCATATGTTTAATATGCTGCATAGTGT GAGTCCTCTAGTTTTTACCGCAGCCACCAGCCGCTTCTCGAGCAAAGTGTAGATCCCATT AGGACTCATCATCTAATTTTGCTATGTTAGCTGCAACTTTCTATTTTAATAGAACC TTCTGGAAATTTCACCCGGCGCGCACCCGAGGAACTGGACAGCGTGTCGAAAAAGTTGC TTTTTTATATAAAGGACACGAAAAGGGTTCTCTGGAAGATATAAATATGGCTATGTAATT CTAAAGATTAACGTGTTACTGTTTTACTTTTTAAAGTCCCCAAGAGTAGTCTCAAGGGA AAAAGCGTATCAAACATACCATGTTTTTCAACAGACTAAGCGCTGGCAAGCTGCTGGTAC CACTCTCCGTGGTCCTGTACGCCCTTTTCGTGGTAATATTACCTTTACAGAATTCTTTCC ACTCCTCCAATGTTTTAGTTAGAGGTGCCGATGATGTAGAAAACTACGGAACTGTTATCG GTATTGACTTAGGTACTACTTATTCCTGTGTTGCTGTGATGAAAAATGGTAAGACTGAAA TTCTTGCTAATGAGCAAGGTAACAGAATCACCCCATCTTACGTGGCATTCACCGATGATG

AAAGATTGATTGGTGATGCTGCAAAGAACCAAGTTGCTGCCAATCCTCAAAACACCATCT TCGACATTAAGAGATTGATCGGTTTGAAATATAACGACAGATCTGTTCAGAAGGATATCA AAGGAGAAAAGAAGGTTTTTACTCCAGAAGAAATTTCTGGTATGATCTTGGGTAAGATGA AACAAATTGCCGAAGATTATTTAGGCACTAAGGTTACCCATGCTGTCGTTACTGTTCCTG CTTATTTCAATGACGCGCAAAGACAAGCCACCAAGGATGCTGGTACCATCGCTGGTTTGA ACGTTTTGAGAATTGTTAATGAACCAACCGCAGCCGCCATTGCCTACGGTTTGGATAAAT CTGATAAGGAACATCAAATTATTGTTTATGATTTGGGTGGTGGTACTTTCGATGTCTCTC TATTGTCTATTGAAAACGGTGTTTTCGAAGTCCAAGCCACTTCTGGTGATACTCATTTAG GTGGTGAAGATTTTGACTATAAGATCGTTCGTCAATTGATAAAAGCTTTCAAGAAGAAGC ATGGTATTGATGTCTGACAACAACAAGGCCCTAGCTAAATTGAAGAGAGAAGCTGAAA AGGCTAAACGTGCCTTGTCCAGCCAAATGTCCACCCGTATTGAAATTGACTCCTTCGTTG ATGGTATCGACTTAAGTGAAACCTTGACCAGAGCTAAGTTTGAGGAATTAAACCTAGATC TATTCAAGAAGACCTTGAAGCCTGTCGAGAAGGTTTTGCAAGATTCTGGTTTGGAAAAGA AGGATGTTGATGATATCGTTTTGGTTGGTGGTTCTACTAGAATTCCAAAGGTCCAACAAT TGTTAGAATCATACTTTGATGGTAAGAAGGCCTCCAAGGGTATTAACCCAGATGAAGCTG TTGCATACGGTGCAGCCGTTCAAGCTGGTGTCTTATCCGGTGAAGAAGGTGTCGAAGATA TTGTTTTATTGGATGTCAACGCTTTGACTCTTGGTATTGAAACCACTGGTGGTGTCATGA CTCCATTAATTAAGAGAAATACTGCTATTCCTACAAAGAAATCCCCAAATTTTCTCTACTG CCGTTGACAACCAACCGTTATGATCAAGGTATACGAGGGTGAAAGAGCCATGTCTA AGGACAACAATCTATTAGGTAAGTTTGAATTAACCGGCATTCCACCAGCACCAAGAGGTG TACCTCAAATTGAAGTCACATTTGCACTTTGACGCTAATGGTATTCTGAAGGTGTCTGCCA CAGATAAGGGAACTGGTAAATCCGAATCTATCACCATCACTAACGATAAAGGTAGATTAA CCCAAGAAGAGTTGATAGAATGGTTGAAGAGGCTGAAAAATTCGCTTCTGAAGACGCTT CTATCAAGGCCAAGGTTGAATCTAGAAACAAATTAGAAAACTACGCTCACTCTTTGAAAA ACCAAGTTAATGGTGACCTAGGTGAAAAATTGGAAGAAGAAGACAAGGAAACCTTATTAG ATGCTGCTAACGATGTTTTAGAATGGTTAGATGATAACTTTGAAACCGCCATTGCTGAAG ACTTTGATGAAAAGTTCGAATCTTTGTCCAAGGTCGCTTATCCAATTACTTCTAAGTTGT ACGGAGGTGCTGATGGTTCTGGTGCCGCTGATTATGACGACGAAGATGAAGATGACGATG GTGATTATTTCGAACACGACGAATTGTAG

YJL034W, 682 aa (SEQ ID NO 144)
MFFNRLSAGKLLVPLSVVLYALFVVILPLQNSFHSSNVLVRGADDVENYGTVIGIDLGTT
YSCVAVMKNGKTEILANEQGNRITPSYVAFTDDERLIGDAAKNQVAANPQNTIFDIKRLI
GLKYNDRSVQKDIKHLPFNVVNKDGKPAVEVSVKGEKKVFTPEEISGMILGKMKQIAEDY
LGTKVTHAVVTVPAYFNDAQRQATKDAGTIAGLNVLRIVNEPTAAAIAYGLDKSDKEHQI
IVYDLGGGTFDVSLLSIENGVFEVQATSGDTHLGGEDFDYKIVRQLIKAFKKKHGIDVSD
NNKALAKLKREAEKAKRALSSQMSTRIEIDSFVDGIDLSETLTRAKFEELNLDLFKKTLK
PVEKVLQDSGLEKKDVDDIVLVGGSTRIPKVQQLLESYFDGKKASKGINPDEAVAYGAAV
QAGVLSGEEGVEDIVLLDVNALTLGIETTGGVMTPLIKRNTAIPTKKSQIFSTAVDNQPT
VMIKVYEGERAMSKDNNLLGKFELTGIPPAPRGVPQIEVTFALDANGILKVSATDKGTGK
SESITITNDKGRLTQEEIDRMVEEAEKFASEDASIKAKVESRNKLENYAHSLKNQVNGDL
GEKLEEEDKETLLDAANDVLEWLDDNFETAIAEDFDEKFESLSKVAYPITSKLYGGADGS
GAADYDDEDEDDDGDYFEHDEL

YJL035C, 1253 bp, CDS: 501-1253 (SEQ ID NO 145)
TACCTAAGTCAATACCGATAACAGTTCCGTAGTTTTCTACATCATCGGCACCTCTAACTA
AAACATTGGAGGAGTGGAAAGAATTCTGTAAAGGTAATATTACCACGAAAAGGGCGTACA
GGACCACGGAGAGTGGTACCAGCAGCTTGCCAGCGCTTAGTCTGTTGAAAAACATGGTAT
GTTTGATACGCTTTTTCCCTTGAGACTACTCTTGGGGACCTTTAAAAAAACAGTAA
CACGTTAATCTTTAGAATTACATAGCCATATTTATATCTTCCAGAGAACCCTTTTCGTGT
CCTTTATATAAAAAAAGCAACTTTTTCGACACGCTGTCCAGTTCCTCGGGTGCCGCGCGG
GTGAAATTTCCAGAAAGTTCTATTAAAATAGAAAGTTGCAGCTAACATAGCAAAATTAGA
TGAATGATGAGTCCTAATGGGATCTACACTTTGCTCGAGAAGCGGCTGGTGGCTGCGGTA
AAAACTAGAGGACTCACACTATGCAGCATATTAAACATATGAGGACAGCTGTCCGTTTGG
CTAGATACGCTCTTGACCACGATGAGACACCGGTAGCTTGCATCTTTTGTACATACGCCAA
CTGGCCAGGTGATGGCTTATGGCATCAGACCAGTTGGGCTCCCGAGGAGTTGTTG
ACGTGTTCAAAGACATTACTCTATATGTTACTGTAGAACCGTGTATAATGTGTGCATCTG
CTCTCAAGCAATTAGACATTGGAAAGGTGTTTCGGTTTTTTGGAC

GCAACGGTACTGTCTTGTCAGTAAATCATGATACGTGTACATTAGTGCCCAAGAACAATA GTGCGGCAGGGTACGAGAGTATACCGGGGATCTTGAGGAAAGAAGCAATAATGCTGCTGA GATACTTTTATGTAAGACAAAATGAAAGGGCGCCAAAGCCACGGTCCAAGAGTGACAGAG TGTTGGATAAAAACACGTTTCCGCCTATGGAATGGTCAAAGTATCTTAATGAAGAAGCAT TCATTGAGACTTTTGGTGATGATTACAGGACTTGTTTTGCGAATAAAGTTGACTTGTCCA GTAATAGCGTCGATTGGGATTTGATTGACTCCCACCAAGATAATATAATCCAAGAACTGG AAGAACAATGCAAAATGTTTAAGTTTAATGTACATAAGAAATCTAAGGTTTGA

YJL035C, 250 aa (SEQ ID NO 146)
MQHIKHMRTAVRLARYALDHDETPVACIFVHTPTGQVMAYGMNDTNKSLTGVAHAEFMGI
DQIKAMLGSRGVVDVFKDITLYVTVEPCIMCASALKQLDIGKVVFGCGNERFGGNGTVLS
VNHDTCTLVPKNNSAAGYESIPGILRKEAIMLLRYFYVRQNERAPKPRSKSDRVLDKNTF
PPMEWSKYLNEEAFIETFGDDYRTCFANKVDLSSNSVDWDLIDSHQDNIIQELEEQCKMF
KFNVHKKSKV

YJL070C, 3167 bp, CDS: 501-3167 (SEQ ID NO 147) TCCCCTGATGGTCAAATACTGTGCATGGCATCCCGTGCAGTCAAGGATGCTTTGAGACTA GTTCATCTGCCTTCTTGTAGCGTGTTCAGCAACTGGCCTACCAGCGGGACGCCTTTGGGT *AAAGTTACCAGTGTCGCATTTTCGCCATCTGGTGGGCTACTGGCCGTGGGTAACGAACAA* GGTAAAGTGAGGCTCTGGAAATTAAACCACTACTAAATTTCCATTTATAGACAAACTTAG ATATTAAAAGCAATGTACAAATACATACACAAAATATCACTGTAAAAAAATTGCGAAGAA **ACTTGAAATTGAATATGATTCTGCCCACTTTTTTCTTGCTGTCATTTATAGTCAGAAATG** AAAAATTGTCCGAGAAATTAAATATAATATATGGAAAAAAAGGGGACATTGAGTTTAAAG AATTTGATTAAAATGTCCTCTCAATATCCTCTGTAAGAGTTATCTAAATCTCACTTTACT TATTCATCTCGCTGGGAATTATGCAGGCGGTAGAGAGAAGGCCCTCGTTACTCTTTGACG AATATCAAAATTCTGTTACTAAGCCTAATGAGACGAAGAATAAAGAÁGCCAGGGTCTTGT CAGAGAATGACGGTGATGTCTCCCCATCTGTTTTGAAACAGAAGGAAATATCAGTCGATG ATATGGATATGATTTCTTTGCCCACGGAATTTGACAGGCAAATGGTTTTAGGTTCACCTA ATTATGGAAATGGAGAAAGTGACAGCTTTGTCTCATCGTACACGCCCTCAAATCTGAAAA CGGGTGAAGAAACTAAAGATCTTTTCATTAATCCGTTTGAATTGGTTTCTCAAATGAGAA AAAGATACATTGCTGCTTCCAAACAAGATGGCATTTCAAACATAAAAATGACACTGAAA AGTGGTTTTTATACCCAAAACCACTGCCAAAGTTTTGGAGATTTGAAGACGATAAACGAT TCCAAGATCCCTCTGACTCTGACTTAAATGACGATGGAGACAGTACTGGGACCGGAGCCG CTACACCGCACCGCCATGGCTACTATTACCCAAGTTACTTTACCGATCACTACTACTACT ACACAAAATCTGGTTTGAAAGGAAAAGGAAATATAAAAGTACCATACACCGGTGAATATT TCGATTTAGAGGATTACAAAAAACAATACATTTACCATTTAAGTAATCAGGAAAATACGC AAAACCCACTTTCACCTTATTCTAGTAAGGAGGAGTCACTAGAGGAAGAATTTTTAACAG TGTTTCAGTACCTAAACTCTAAGAAAGAAATTTTAGCTAATAAAAATGTTCCCTACAGAG **ATTTTTATAATTCTCGTAAGGTAGATCGAGACTTGTCTTTAAGTGGTTGTATTTCTCAAC** GTCAATTGAGTGAATATATATGGGAGAAAATAAATTTAGAACCTGAAAGGATAGTTTATC AAGACCCGGAAACGTCAAGGAAACTCAGTTTGAGAGACATTTTTCAGTTTGGTTGTTCTT ATAGAAATATTTACCTAATAGATTACCATCTAACTCCTAACAAAGTAGCAAAGTTGGTCG GCAAAGAAATGAGGTTTTACCTATTAGCCAAAGTGTTTCTGGAGTTTGATAATTTCATTG AAGGTGAGTACCTAGCAGAAATTTTCATAAAATACGTTATTCATATCCTCGAAAAATCAA AGTACCAATTGGCCCAAGTATCAGTTAATTTTCAATTCTATTCCAGTGGTGAAGACTGGT ACAAGAAATTTTCTCAATGGTTGCTACGATGGAAGCTAGTATCGTATAATATCCGCTGGA ATATACAAATTGCCAGGATTTTTCCCAAACTATTCAAGGAAAATGTCGTGTCAAATTTCC AGGAGTTTTTGGATCTTATCTTCAATCCTTTATTCACTCTGGAAAAGGAGCAGTTACCAA CTATGGATCTGGTCATTAAAGAGTCGGATGAATATTACTGGAAAGAATTTACTGATATGA ATTGTAAGCCAAAATTTTGGACAGCACAGGGTGACAATCCAACTGTTGCGCATTACATGT ATTATATTTATAAAAGTTTAGCGAAAGTTAATTTTCTGCGGTCACAAAATCTTCAAAATA CAATCACCCTAAGAAATTATTGTTCTCCACTATCCAGCAGAACTTCCCAATTTGGAGTGG ATTTATATTTTACAGATCAAGTTGAATCGTTAGTGTGCAACTTACTGCTTTGTAATGGTG TCTTTCAAATACCCATTTTAGCTGCGCCATTATCATCTGTTTCATTACTGAATTCGCAAA

YJL070C, 888 aa (SEQ ID NO 148) MOAVERRPSLLFDEYONSVTKPNETKNKEARVLSENDGDVSPSVLKQKEISVDDMDMISL PTEFDROMVLGSPMFFDLEDEENKIDPLPSVSHHYGNGESDSFVSSYTPSNLKTGEETKD LFINPFELVSQMRKRYIAASKQDGISNIKNDTEKWFLYPKPLPKFWRFEDDKRFQDPSDS DLNDDGDSTGTGAATPHRHGYYYPSYFTDHYYYYTKSGLKGKGNIKVPYTGEYFDLEDYK KQYIYHLSNQENTQNPLSPYSSKEESLEEEFLTDVPTFQEFRDDFAYIIELIQSHKFNEV SRKRLSYLLDKFELFQYLNSKKEILANKNVPYRDFYNSRKVDRDLSLSGCISQRQLSEYI WEKINLEPERIVYQDPETSRKLSLRDIFQFGCSSNDQPIAIGLKLIDDEFLDWYRNIYLI DYHLTPNKVAKLVGKEMRFYLLAKVFLEFDNFIEGEYLAEIFIKYVIHILEKSKYQLAQV SVNFQFYSSGEDWYKKFSQWLLRWKLVSYNIRWNIQIARIFPKLFKENVVSNFQEFLDLI FNPLFTLEKEQLPIDSSVNTDIIGLQFFLSNVCSMDLVIKESDEYYWKEFTDMNCKPKFW TAQGDNPTVAHYMYYIYKSLAKVNFLRSQNLQNTITLRNYCSPLSSRTSQFGVDLYFTDQ VESLVCNLLLCNGGLLQVEPLWDTATMIQYLFYLFQIPILAAPLSSVSLLNSQKSTFLKN KNVLLEHDYLKDQETAKINPSRDITVGEQRSYETNPFMKMFKMGLKISLSSKSILYNSSY TLEPLIEEYSVAASIYLLNPTDLCELSRTSVLSSGYEGWYKAHWIGVGVKKAPYFEENVG GIDNWYDTAKDTSIKHNVPMIRRRYRKETLDQEWNFVRDHFGVINSIW

YJL078C, 3146 bp, CDS: 501-3146 (SEQ ID NO 149) TTTTTCTTCGCACATGGCTGGTTCTGCTGGAGGCGGCTGGGTGTTTATAGTTACCGCAAT GCAGGTCGCTTCGTTTACTTTTCTCTGCGTGCTCGAGAACTGATAAATACTGGTTTAGGA AGCAACGCTACGCACTAGCTGTGTGTGCTTGCTCTTGTGTTCGTCTTTCGTATATTGC GGGTTCCCGCGGTTAATTCAACAACAAATATGGTATCTAGGCAGGGACCCAGCAACGGAA GGATGTAATTGCTATATAGGGCCGATGAAACAGTTCTCATGTTTCAACTCGGTCGAAGAA TTCTCTAAAACATATTCTATACTTCAAAGTTTTTAGCTTCTTGCTTTTCGGTAGTTGCCA AACCAATATCGGCATAAAATTATAATTGCTGCACCCCTGCAACTCCAAACAACTTAAAAAC AACTTAAAACGAAAACGCTTATGCTGGAGTTTCCAATATCAGTTCTGCTAGGATGCCTAG TAGCCGTCAAGGCACAAACCACGTTTCCAAACTTCGAGAGCGATGTGCTGAACGAGCATA ACAAGTTCAGAGCGCTACATGTTGACACAGCGCCGCTCACCTGGTCCGACACTCTGGCCA CCTATGCGCAGAACTACGCCGACCAATATGATTGTTCGGGTGTCTTAACGCATTCCGATG GCCCATATGGTGAGAACCTTGCCCTTGGTTACACAGACACGGGAGCGGTGGACGCCTGGT ACGGGGAGATAAGCAAGTATAATTATTCAAATCCCGGATTTTCTGAATCCACGGGTCACT TCACACAGGTGGTTTGGAAGTCAACCGCCGAGATTGGATGTGGTTATAAATATTGTGGTA CGACATGGAACAATTATATTGTGTGCTCCTACAACCCTCCTGGAAACTACCTGGGTGAGT TTGCAGAGGAAGTGGAACCACTTATAAGCACTGTTTCCTCGTCCTCATCCTCGTCCTCTT CTACCTCAACTACATCAGACACAGTCTCCACCATCTCATCCAGTATTATGCCCGCTGTAG CGCAAGGGTATACAACAACGGTATCGTCTGCGGCTAGCAGCAGTTCTTTAAAATCGACGA CCATAAACCCTGCCAAGACCGCTACCCTCACTGCGTCCTCTTCTACCGTAATTACTAGTA GCACAGAATCAGTTGGATCCTCCACTGTCTCATCAGCCTCAAGCTCTTCTGTCACTACTT CCTATGCTACCTCCTCGAGTACCGTCGTCTCTAGTGATGCTACTTCATCCACTACCACCA CCTCATCGGTTGCTACATCGTCCAGTACCACTTCTTCCGACCCTACCTCGAGCACTGCTG $\tt CTGCTTCTTCTGATCCTGCCTCAAGTTCCGCTGCCGCTTCCTCCAGCGCGAGTACCG$ AGAACGCCGCTTCTTCTAGCAGCGCCATCTCGAGCTCTTCATCAATGGTTTCTGCTCCTT TGAGTAGTACTCTTACTACTTCCACCGCAAGCTCCAGAAGTGTAACTTCCAATTCAGTTA ATTCTGTTAAGTTTGCAAACACTGTGTTTTCTGCTCAAACAACCTCTTCTGTAAGCG CCTCATTATCATCTGTAGCTGCTGACGATATTCAGGGTAGCACTTCCAAGGAGGCCA CAAGCTCAGTTTCCGAACATACTAGTATAGTAACTAGTGCAACTAATGCTGCCCAATATG CAACGAGACTTGGGTCATCTTCCAGAAGTTCTTCCGGGGCCGTCTCTTCCTCAGCTGTGT CGCAATCTGTTCTGAATTCCGTTATAGCCGTCAACACCGACGTATCTGTAACCTCAGTTA GTAGCACAGCCCATACCACAAAGGACACCGCCACCACTTCAGTAACCGCCTCAGAAAGTA TCACTTCGGAAACTGCTCAGGCTTCAAGTTCAACAGAGAAGAATATTAGTAACAGTGCCG CCACATCGAGTAGCATTTACTCCAACAGTGCTTCTGTGTCAGGACACGGTGTAACATACG CTGCCGAATACGCCATTACATCCGAGCAATCCTCTGCGCTTGCCACATCTGTGCCTGCTA CAAATTGCTCTAGTATCGTGAAGACCACAACTTTAGAAAATTCGAGTACCACAACCATCA CAGCCATTACTAAGAGTACTACAACCTTGGCCACTACTGCTAACAACTCCACAAGGGCAG CTACCGCAGTAACCATAGATCCCACATTGGACCCTACCGACAACTCAGCTAGTCCAACCG ACAATGCTAAACACACCTCTACATATGGATCTTCTTCCACAGGCGCATCTTTAGATAGCT TACGCACAACCACCAGTATTAGTGTCTCAAGCAACACCACAGTTAGTCTCTACCTGCA CTTCCGAGAGCGATTATTCCGATAGTCCTAGCTTCGCCATCTCCACTGCCACCACCACTG **AAAGCAATCTGATCACAAACACCATCACAGCTTCTTGTAGTACGGATAGTAATTTCCCTA** CCTCCGCTGCTTCTTCTACAGATGAGACGCCCTTCACTAGAACAATCTCGACATCTTGTA GCACTTTGAACGGCGCCTCAACCCAAACCAGTGAGCTAACCACATCGCCTATGAAAACCA ACACGGTGGTTCCAGCTTCTTTCCCTTCAACTACAACCACTTGTCTAGAAAATGATG ACACTGCCTTTTCTAGTATCTACACTGAAGTCAACGCCGCAACTATCATTAACCCCGGAG AAACATCTTCTCTCGCTAGCGATTTCGCCACATCTGAAAAGCCAAACGAGCCCACTTCTG TCAAATCCACCTCAAACGAAGGCACCTCTTCCACAACAACAACCTACCAACAGACTGTTG CTACACTGTATGCCAAGCCCTCCAGCACAAGCCTAGGTGCAAGAACAACTACTGGTAGCA ACGGTCGTTCAACTACCAGCCAACAAGACGGGTCTGCCATGCATCAGCCAACTTCCTCGA TCTACACTCAACTAAAAGAAGGCACATCAACCACCGCAAAACTTTCTGCATACGAAGGTG CTGCAACACCTCTTTCCATTTTCCAGTGCAATAGTCTAGCTGGAACGATTGCCGCTTTTG TCGTAGCTGTTCTGTTCGCCTTCTAG

YJL078C, 881 aa (SEQ ID NO 150) MLEFPISVLLGCLVAVKAOTTFPNFESDVLNEHNKFRALHVDTAPLTWSDTLATYAONYA DOYDCSGVLTHSDGPYGENLALGYTDTGAVDAWYGEISKYNYSNPGFSESTGHFTQVVWK STAEIGCGYKYCGTTWNNYIVCSYNPPGNYLGEFAEEVEPLISTVSSSSSSSSSTSTTSD TVSTISSSIMPAVAQGYTTTVSSAASSSSLKSTTINPAKTATLTASSSTVITSSTESVGS STVSSASSSSVTTSYATSSSTVVSSDATSSTTTTSSVATSSSTTSSDPTSSTAAASSSDP **ASSSAAASSSASTENAASSSSAISSSSSMVSAPLSSTLTTSTASSRSVTSNSVNSVKFAN** TTVFSAQTTSSVSASLSSSVAADDIQGSTSKEATSSVSEHTSIVTSATNAAQYATRLGSS SRSSSGAVSSSAVSQSVLNSVIAVNTDVSVTSVSSTAHTTKDTATTSVTASESITSETAQ ASSSTEKNISNSAATSSSIYSNSASVSGHGVTYAAEYAITSEQSSALATSVPATNCSSIV KTTTLENSSTTTITAITKSTTTLATTANNSTRAATAVTIDPTLDPTDNSASPTDNAKHTS TYGSSSTGASLDSLRTTTSISVSSNTTQLVSTCTSESDYSDSPSFAISTATTTESNLITN TITASCSTDSNFPTSAASSTDETAFTRTISTSCSTLNGASTQTSELTTSPMKTNTVVPAS SFPSTTTTCLENDDTAFSSIYTEVNAATIINPGETSSLASDFATSEKPNEPTSVKSTSNE GTSSTTTTYQQTVATLYAKPSSTSLGARTTTGSNGRSTTSQQDGSAMHQPTSSIYTQLKE **GTSTTAKLSAYEGAATPLSIFQCNSLAGTIAAFVVAVLFAF**

YJL179W, 109 aa (SEQ ID NO 152) MSQIAQEMTVSLRNARTQLDMVNQQLAYLDRQEKLAELTKKELESYPTDKVWRSCGKSFI LQDKSKYVNDLSHAETVLLDQRKTLKIKKNYLETTVEKTIDNLKALMKN

YJL180C, 1478 bp, CDS: 501-1478 (SEQ ID NO 153)

AATAGTTCTTTATCTTTAATGTTTTTCTTTGATCCAGAAGAACAGTTTCGGCATGTG ATAAATCATTAACGTATTTGGATTTATCCTGTAAGATAAACGATTTACCGCAAGATCTCC ATACTTTGTCCGTTGGATAAGACTCTAGTTCTTTCTTTGTCAATTCAGCAAGCTTTTCTT GTCTGTCCAAATATGCTAGCTGCTGATTGACCATATCCAATTGTGTCCTGGCGTTTCTTA ATTTAGTAAAGAGCTCTGTAGATAGTTCTTTAATTCCCATCTGCTCATCTGAGAAATTTC AAAAAATTAAGGTAAAGGAAAAGGCTAAATAAGAACAAAACACTTGAAGGCAAACGAAAC ACACGATTGAGAATAACACTCCTACGGAAACAAATAGATTGAGCAAAACTTCACAGAAGT TTTGGGAAAAGGTGTCACTAAATAGGGATGTTGAGAAAGGAAAGATTGCTCTACAATTAG ATGGCAGGACTATAAAAACTCCTCTAGGAAATGGAATTATAGTTGATAATGCAAAGTCTC TCTTAGCATACCTATTAAAACTGGAGTGGTCGTCCCTATCCAGTCTTTCCATCAAAACTC ACTCTTTGCCACTAACTTCATTAGTGGCAAGATGCATAGATTTACAAATGACAAATGAGC CTGGCTGTGACCCTCAATTAGTTGCAAAGATTGGAGGCAACAGTGATGTTATAAAAAATC AAGGAAGATTACGCAATGCGCAAAATGAGTTATATATACCCATCATCAAAGGAATGGAAG AGTTTTTACGCAACTTTTCATCCGAGTCTAATATTCGACTACAAATTTTAGATGCCGACA TCCATGGGTTACGAGGCAATCAGCAGTCGGATATCGTTAAGAATGCAGCAAAAAAATATA TGAGCAGCTTATCACCATGGGATCTTGCAATTCTTGAAAAAACTGTATTAACCACAAAGT CCTTCATTTGCGGCGTGCTATTATTAGAAAATAAAAAAGATACTGCGAACTTAATTCCCG CCTTGAAAACTGATATGGATAATATTGTACGTGCCGCCACCTTAGAAACAATCTTCCAAG TTGAAAAGTGGGGAGAGGTTGAAGATACTCATGACGTTGACAAAAGAGACATCAGAAGAA AAATTCATACTGCTGCGATTGCTGCTTTTAAGCAATAA

YJL180C, 325 aa (SEQ ID NO 154)
MLPSLRKGCFIVNSIRLKLPRFYSLNAQPLGTDNTIENNTPTETNRLSKTSQKFWEKVSL
NRDVEKGKIALQLDGRTIKTPLGNGIIVDNAKSLLAYLLKLEWSSLSSLSIKTHSLPLTS
LVARCIDLQMTNEPGCDPQLVAKIGGNSDVIKNQLLRYLDTDTLLVFSPMNEFEGRLRNA
QNELYIPIIKGMEEFLRNFSSESNIRLQILDADIHGLRGNQQSDIVKNAAKKYMSSLSPW
DLAILEKTVLTTKSFICGVLLLENKKDTANLIPALKTDMDNIVRAATLETIFQVEKWGEV
EDTHDVDKRDIRRKIHTAAIAAFKQ

YJL181W, 2336 bp, CDS: 501-2336 (SEQ ID NO 155) GCAAGTCAGTACGATGCATCCTTGGATCAAGAAGGTGAGTCTGGAAACGGTGCTTCTAAT GGCGATGTTTACCATTATAATGAAGGGGACTTGGCTGCCTCCTTCAAGGGATGTAGATCA AGAGGTACGTGTGCTAGTGAAATAGGTCACATGTACCAGAAAATCAAGAAATCTTAGATG TGTGTAATCTTGCAATTTAGTTTCAAACAAGATCCTTGTATTTATATAAACAAAGATATA ATTTTTAAAAAAAATTAGAAAAAGCAAATATAATTCAGGTCCCACTTGGAATAATGGCA TTCTTGGCTTTTTTTTTTTTCATTTTCGTAAAGGGTCTTAAAAGGATTAAAAAATGCAGTA TTGAAATAAAGAACAATTACGAACGGTGAAGCTGCTATTTTGGTTATTATACCCTTCCAG GACAGTACGCGCAAACTATTATGGAGATATTCAAGGAAGAAGAAGAAGAAGCTTTTTCGG CGATAGAAGGTATAATATATGCCTGTGAGGTGTATGACCCCTGTACCCCGTCATTTACATA **AAAGCAAAACAAAGATCATCAATGCTGCTAAATTAATTATAGAAACGCATCTTTCATATT** ATACAATACTCAATAACATTTCAGATATACAAGCCTATCTTTCTACTTGGCTTAGGGATC TTGGAACGACAGGTCCATACCAAACAATTCTTTCAGAAAGTATTTCTCTCATGTTTGACC GTCTTTATCTCAGATTGAAAAGCTACCAGAAGCTCTTAAACGATGCAGGATTAAAGAATT TTTTTTCAAGCTACGATTATGCTTTCGGGGTTGCATACAACCTTGTAAATTGCTCTGAAT ACAGGTATGACGAAGTTCATTACATATCGAACGGCACTTACTCATTAGTTGCATCGATGA AGATAGATCCTGCTGAAGTCATTAAAAGGGAACATTTTAGGCTTACAATTCCGAAATTTA ACATATCTAATATTAATTGAAATTTTTCATTTGCTCGATGGATTAGCATTTTTTAAGG TGAACCCTGATAGTTTATCTATATCTACAGCTTCAGCAGAAACAATCTTTCGCAGTATCT CCGAAGGTAATCATCAGGTCCTAGAATTGGGGAGAAGTTTAATGTTTCCATTGTTGAGGA CTGGAGATTTTGAAATCTGTCGTATTGACGACGCGGGAGCTGTCATAACATTTACAGAAG CGAAGGATGTAAAACTAGAAATAATCAGTCTGGATGAAGTTTCCTGGGTAATGCAGTGGA AATCTTGTCTTCAAAATTATGAGAGAAGGGCAGCAAATGACAGTTCATTTATCAAAACAC ACCTACAATTTAAGAAGGCCAACAATTTCAATGAAGATAATAATGGGCTAGGACTAATTG

TAGACAGAAATATTCCAACAGATGATTTTACGCTAGCTTCTACAAACCGTCAAAGTCCCC CGCCTTCAAATACTGGTTGTTCATTACACAGGTCTAAACCCTTGCATATCCCTTTATCAT CTGTTATTCGTGAAGACTTTTATGATAGCTCTCTAAATGAGCGTATATCTAAAGACGGAG ATAGCAGTTGTGAATCCTTCAGTGGCGCCGAAAGTATCTTATCAGACTACGATTTTCATG ATAATGAATTTTTTAACAACCAGTCACCTCATTATTTTTCAGAACACATAGACAATAACT CGAGAGAGGTGGTAATAACAGATGAAAATACGATAATATCTTTGGAAAATACCCAAGTAA GTCGGTGGTCAAATTACTCATGGCAAAAAATTTCACCGCATCAATTACAGGTCTCTATTA TCCAACTGCGCATGGGAAACTTCATTGTGGCTTATGATTCTGATTATAACCTTCATCAGT TCAAAATTCGTTTGTGTGACGATATAAAATGTATACAATCCACAGAGCAAGACATACAAA TACGTGTCCCGCTCGGCGCAATAATGTGCAGCGTCACTGGTATCTTGAATATTAGGACGA AGGACGCTGACAAGTTGCTTCGGGTATTAAGCTTTTATACCACTGACCACACGGAAGCTG TATCGCACTCAAACAATCAAGATGCTACTGCAAGTCCACTTTCGTCAGTTTCATCAGCAA TGGATCTCAAGCATTCATTACAGAAATGTTCCTCTACAATAATGCCCCAAGAGTTGACGC AGGACGTCATCGGTTCAAAATCAGACCTAATCAGTAATATTCGTCAAAAAATATAA

YJL181W, 611 aa (SEQ ID NO 156) MEIFKEEEEAFSAIEGIIYACEVYDPVPRHLHKSKTKIINAAKLIIETHLSYYTILNNI SDIQAYLSTWLRDLGTTGPYQTILSESISLMFDRTVSIFRKCTIEGGFPHLIARLYLRLK SYQKLLNDAGLKNFFSSYDYAFGVAYNLVNCSEYRYDEVHYISNGTYSLVASMKIDPAEV IKREHFRLTIPKFNISNILIEIFHLLDGLAFFKVNPDSLSISTASAETIFRSISEGNHQV LELGRSLMFPLLRTGDFEICRIDDAGAVITFTEAKDVKLEIISLDEVSWVMQWKSCLQNY ERRAANDSSFIKTHLOFKKANNFNEDNNGLGLIVDRNIPTDDFTLASTNRQSPPPSNTGC SLHRSKPLHIPLSSVIREDFYDSSLNERISKDGDSSCESFSGAESILSDYDFHDNEFFNN QSPHYFSEHIDNNSREVVITDENTIISLENTQVSRWSNYSWQKISPHQLQVSIIQLRMGN FIVAYDSDYNLHOFKIRLCDDIKCIOSTEODIOIRVPLGAIMCSVTGILNIRTKDADKLL RVLSFYTTDHTEAVSHSNNQDATASPLSSVSSAMDLKHSLQKCSSTIMPQELTQDVIGSK SDLISNIRQKI

YJL187C, 2960 bp, CDS: 501-2960 (SEQ ID NO 157) TCTTGCAACCATCGTCCTCTAAGGAAAGAAATGTGGCACCTTTAAATAGGTTCCACCTCA CAGATGCCAACATGTGGGAGATAGGGGGCTATTCGCAATTTATTAACGTCTCTAGTACTG CGGGTGATAACGACGCGAAAAATATTTTTTCATTTTTCTTTTAACCATCACAATTTGCGA CGCGACGCGAAAAAAATGCAGAGAAGTAAAAGAATGCTGGATAAGAAATCAACAACAG TTGAACATTGGCGTGCCCCTGTGTATTAAGTAAAGGTTGTCCAAGAGGCTCTTTTTTGTA TGTATGCGTGTGTTAACTATCCTGCACATCATCTTGCGCAGTTAGTCCAATAAAAAAGGA TTACTACTGAACAGGTCTTACTATTTTTGATTGCGTAGTGCTGGGGAAAAGTAAACACAC ACAGGCGCACACGAGAACAGATGAGTTCTTTGGACGAGGATGAAGAGGACTTCGAAATGC TGGACACGGAGAACCTCCAGTTTATGGGGAAGAAGATGTTTGGCAAACAGGCCGGCGAAG ACGAGAGTGATGTTTGCTATAGGGGGTAGCACCCCGACCAATAAACTGAAATTTTATC CATATTCGAACAACAAATTGACAAGAAGTACGGGGACCTTGAACCTGTCATTAAGTAATA CAGCTTTGTCAGAGGCTAACTCCAAATTTCTTGGGAAAATTGAAGAAGAGGAAGAAGAGG AGGAAGAAGGCAAGGATGAGGAAAGCGTGGATTCTCGTATTAAAAGGTGGTCTCCGTTCC ATGAAAATGAAAGTGTTACTACTCCTATTACAAAAAGATCTGCGGAAAAAACGAACAGTC CTATTTCTCAAACAATGGAACCAGCGATGGTTTCCGAAAAATGATGCTCGCACTGAAA ATACATCCTCATCCTCTTCATATAGCGTCGCTAAACCTAACCAATCAGCCTTTACGTCTT CGGGCCTCGTATCTAAAATGTCTATGGACACTTCGTTATACCCTGCGAAATTGAGGATAC CAGAAACACCAGTGAAAAAATCACCCTTAGTGGAGGGAAGAGACCATAAGCATGTCCACC TTTCGAGTTCGAAAAATGCATCGTCTTCTCTAAGTGTTTCCCCTTTAAATTTTGTTGAAG ACAATAATTTACAAGAAGACCTTTTATTTTCAGATTCTCCGTCTTCGAAAGCTTTACCTT CCATCCATGTACCAACCATAGACTCATCCCCACTGAGCGAGGCAAAATATCATGCACATG **ATCGTCACAATAACCAGACAAACATCCTGTCTCCCACTAATAGCTTGGTTACCAACAGCT** CTCCACAAACATTGCATTCTAACAAGTTCAAAAAAATCAAAAGAGCAAGGAATTCGGTTA TTTTGAAAAATAGAGAGCTAACAAACAGTTTACAACAATTCAAAGATGATTTATACGGCA CTCAACCTTATCAATTTCGTGGACGCTATGACAATGACACTGACGAAGAGATCTCCACTC CAACAAGACGAAAATCTATTATTGGGGCAACATCTCAAACACATAGAGAAAGCAGACCAT TGTCACTCTCTCTGCCATCGTGACAAACACAACAAGTGCAGAGACGCATTCCATATCTT CCACCGATTCTTCGCCGTTAAATTCCAAAAGGCGTCTAATCTCTTCAAATAAGTTATCAG CAAATCCAGATTCCCATCTTTTCGAAAAATTTACGAATGTGCATTCCATTGGTAAAGGCC

CCATTAAACCAAACAAATATAATTCCTTGAAACGCATATTACTGGAAATTAAAATACTAA TCAGTTCCTGGAAGTTTCAAAATTCATACTATATTATGACAGAATTGTGCGAAAATGGTA ATTTGGATGGATTTTTACAAGAGCAAGTTATCGCAAAGAAAAAAAGGTTGGAAGATTGGA GAATTTGGAAAATCATCGTGGAATTAAGCCTGGCTTTACGATTCATCCATGATTCTTGTC ACATTGTGCATCTGGACTTGAAACCCGCAAACGTCATGATCACATTTGAAGGTAACCTAA AACTAGGTGACTTTGGAATGGCTACTCATTTACCGTTGGAGGATAAAAGTTTTGAAAATG CAGATATTTTTCCCTGGGTCTGATGATTGTTGAAATTGCAGCGAACGTTGTGTTACCTG ACAATGGCAACGCATGGCATAAGTTGAGATCGGGTGATTTATCGGATGCAGGAAGATTAA GTTCCACAGATATTCATTCTGAATCATTATTTTCAGACATTACGAAAGTAGATACAAATG ATTTATTTGATTTTGAAAGAGACAATATCAGTGGTAATAGTAACAACGCTGGCACCTCCA CTGTTCATAACAATAGTAATATCAACAACCCTAATATGAATAATGGCAACGATAATAATA ATGTCAATACTGCCGCTACCAAGAATCGTCTTATTTTGCATAAAAGTTCTAAAATTCCCG TAGAGCCCAATTATGAGAGAAGGCCCACGGCAAATCAAATCTTACAAACTGAGGAATGCC TGTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTTTGGACCTA **AGCCAAAATTTTTTATATGA**

YJL187C, 819 aa (SEQ ID NO 158)

MSSLDEDEEDFEMLDTENLQFMGKKMFGKQAGEDESDDFAIGGSTPTNKLKFYPYSNNKL

TRSTGTLNLSLSNTALSEANSKFLGKIEEEEEEEEGKDEESVDSRIKRWSPFHENESVT

TPITKRSAEKTNSPISLKQWNQRWFPKNDARTENTSSSSYSVAKPNQSAFTSSGLVSKM

SMDTSLYPAKLRIPETPVKKSPLVEGRDHKHVHLSSSKNASSSLSVSPLNFVEDNNLQED

LLFSDSPSSKALPSIHVPTIDSSPLSEAKYHAHDRHNNQTNILSPTNSLVTNSSPQTLHS

NKFKKIKRARNSVILKNRELTNSLQQFKDDLYGTDENFPPPIIISSHHSTRKNPQPYQFR

GRYDNDTDEEISTPTRRKSIIGATSQTHRESRPLSLSSAIVTNTTSAETHSISSTDSSPL

NSKRRLISSNKLSANPDSHLFEKFTNVHSIGKGQFSTVYQVTFAQTNKKYAIKAIKPNKY

NSLKRILLEIKILNEVTNQITMDQEGKEYIIDYISSWKFQNSYYIMTELCENGNLDGFLQ

EQVIAKKKRLEDWRIWKIIVELSLALRFIHDSCHIVHLDLKPANVMITFEGNLKLGDFGM

ATHLPLEDKSFENEGDREYIAPEIISDCTYDYKADIFSLGLMIVEIAANVVLPDNGNAWH

KLRSGDLSDAGRLSSTDIHSESLFSDITKVDTNDLFDFERDNISGNSNNAGTSTVHNNSN

INNPNMNNGNDNNNVNTAATKNRLILHKSSKIPAWVPKFLIDGESLERIVRWMIEPNYER

RPTANQILQTEECLYVEMTRNAGAIIOEDDFGPKPKFFI

YJL188C, 102 aa (SEQ ID NO 160) MTKSLKHKYVLRLDVHLGSSPVSSLSVVTDSVVGSQSDPLWQWSVLLLSLSHFLLDSERL LSLIKRETYRAHTKCTIVKNVSNNVQTHQYDAFTDPRQYHLT

YJL189W, 1042 bp, exon1: 501-506, intron1: 507-892, exon2: 893-1042 (SEQ ID NO 161)
TATTCAAGAATTATTCACATCTTCCAGCGAGTAAACATGCCGCTGGTAATCGCGCGTCC
TCAATATTTGAGTTTTTCAAATAGTGAGGTGTGGATGTATAGAGGAATTACACACTTTTA

TTGATTTCAAAAAACTTATGGGCGTTTTAGGCTCCGGCTCAAACTACCACCACCACGCG GCAGGCCGAGGCAAACAGTACGCCTTGGCGGGGACGCCGAAGCGACTCCTTCTGTTCCAA ATACTTTCTACAATTTTTGGTACATTCATATTATACTGAAAATTCGAAAAAGACAAGCAA ATAAACACAGATAGATCAACATGGCTGTATGTTAGAAAGATATTATAAATCCCAGTTAGA **AATTTGGATTTGAAATAGAAGCAATGTGTAAAATATAGGGAAAGGATTAGGAGTGTTAAC** CATACTAAAATTTTTCTTATCCGAAACAGAAATCTAAAGTCGCCACTACGCAGATTAAAA TATGGTCATAAACTGCTTATTCTGAGAACTTTTGGTGGTCCAGCGTGGTTTATGTCAGGT GGTATTGCCTTGGATCCGTGAATGCATCATATTGATGAGTTTGAACATTGTTACTAACAT TTTTTACAATTGTACACTTCGTATGTGCACGATATGTTTCCCTTTTAATTAGGCTCAAAA GTCTTTCAGAATCAAGCAAAAAATGGCTAAGGCTAAGAAGCAAAACAGACCATTGCCACA ATGGATCAGATTGAGAACCAACACTATCCGTTACAACGCTAAGAGAAGAAACTGGAG AAGAACCAAGATGAACATCTAA

YJL189W, 51 aa (SEQ ID NO 162) MAAQKSFRIKQKMAKAKKONRPLPOWIRLRTNNTIRYNAKRRNWRRTKMNI

YJL190C, 893 bp, CDS: 501-893 (SEQ ID NO 163) TCTCGACAGCCCAAAAGCCGAATTGCGTTAGTTAGCCCACGCGCGAGCGTAAACGCAAGG ACCATTGAGCTTGGAACAGAAGGAGTCGCTTCGGCGTCCCCGCCAAGGCGTACTGTTTGC CTCGGCCTGCCGCGTGGTGGTAGTTTGAGCCGGAGCCTAAAACGCCCATAAGTTTTT TGAAAATCAAGCTAAAAAATGAAAAAAAAAAAAGTTAAATTGGTACTGTGCGCCCATAC ATCACATACTTAAAAGTGTGTAATTCCTCTATACATCCACACCTCACTATTTGAAAAACT CAAATATTGAGGACGCGCGATTACCAGCGGCATGTTTACTCGCTGGAAGATGTGAAATAA TTCTTGAATATGGGTTTGCAGTTAGTCAATTTCAATCTAAATAATCTTAATCGACTATTC AATTCTTAAATTGTAAGGTTTTTTAATGGCCTTTCAGTTCTAGTATTTTTTATAAAACAA GACCAACATACATATCCAAGATGACCAGATCTTCCGTTTTAGCTGATGCTTTGAATGCCA TTAACAACGCTGAAAAGACCGGTAAGCGTCAAGTTTTAATCAGACCATCCTCCAAGGTCA TTATCAAGTTTTTGCAAGTTATGCAAAAGCACGGTTACATTGGTGAATTTGAATACATCG ATGACCACAGATCTGGTAAGATTGTTGTTCAATTGAACGGTAGATTGAACAAGTGTGGTG TTATTTCCCCAAGATTCAACGTTAAGATTGGTGACATTGAAAAATGGACTGCCAACTTGT TGCCAGCCAGACAATTCGGTTACGTCATCTTGACCACCTCTGCTGGTATCATGGACCATG AAGAAGCCAGAAGAAAGCACGTTTCTGGTAAGATTTTGGGTTTCGTTTACTAA

YJL190C, 130 aa (SEQ ID NO 164) MTRSSVLADALNAINNAEKTGKRQVLIRPSSKVIIKFLQVMQKHGYIGEFEYIDDHRSGK IVVQLNGRLNKCGVISPRFNVKIGDIEKWTANLLPARQFGYVILTTSAGIMDHEEARRKH VSGKILGFVY

YJL197W, 4265 bp, CDS: 501-4265 (SEQ ID NO 165) CTTCTTCGGGGTTCCCCAATGTCACTGCCATCTCTÄAAGTAGATAGAAAGGGCGATCGCT ATTTAAGTGTCATGACTTTCTTAACGAGAGGTGTTCCAGCTTCTATTTTGGCTTTCCTAT GTGTCATTACTCTAGGTTATGGTATCATGGCATCTGTTGTCAAGGGTAACGCAACCTCTG TAATCCAACACTTCTGTTGTGTAGTCTAATGTTCGAAAAAAGGTACGCTTCCCTGTTAT AATCAGGTATATTTCGTTATTCTTATAAGCTAAAAGATTAAAAATTTTTCCACTTTCCTT GAAATTTGGTCGGTTCGTGGAAAAATATTATTACGTATTGAAGAAGTGCATGAAGATAAA AGATGGGATTACTGGAAAAATAAAGGGAGGAAAATCCTGCAGAACGTTGTTGTTTCAATC GAAGGTTTCTTCATTCGAAAATGGGTTCTTCAGATGTTTCAAGTCGTGAATGTTCATTGG TTTATAATGAAGATCCCGATTTCACCGATGGCACAACACCATGTGATCGGTTGGGAGTGG **ACTTGATGAATGTTCTAGATGACAAGGATGAAATAAAGCAAGAGTCTGTCCCAGTCTCAG** ATCGTGAAATTGAGGATACGGAATCCGATGCTTCCGCTGTTTCTTCATTTGCTAGCGCTA ATGAGTTAATAGCTGAGCCACACGCTGCAAGTGAAACTAATCTTGGAACTAATGGTCAAG ATGGAAGAAATGTCTTAGAACAACAAGAGACGTGGTTGCTAGACTAATAGAAGAAAACA AGGAAACGCAAAAAGAGGGTGATAAAGTCTGTATTGTCCCCAAGGTTTGGTACGATAAAT TTTTCGACCCCGATGTTACCGATCCTGAAGATATAGGCCCTATTAATACACGCATGATTT GCAGAGACTTTGAAAATTTTGTGCTTGAGGATTACAATAGATGTCCGTATCTGTCTATTG

CAGAGCCTGTTTTCAATTTTCTATCAGAAATTTACGGCATGACAAGTGGCTCTTACCCAG TGGTAACTAATTTGGTTATCAACCAAACCACAGGGGAGTTAGAGACAGAATACAATAAAT GGTTTTTCAGACTACATTACCTGACCGAAAAACAAGACGGGAGGAAAAGGAGGCATGGCC AGGACGATTCAATAATGTACCTCTCGATGTCTGCGTTGAATTTAGTACGTGATTTGGTTG AAAAGAGTATGAATCTGTTTTTTGAGAAAGCTGATCATCTAGACGTGAATGCGGTGGATT TTAAAATTTGGTTTGTCTCAGAGGGATCTGATATTGCCACAGATAGCAATGTTAGTACTT TTTTGAATTCTTCATATGAAATAACTCCGCTTCAATTTCTCGAACTACCGATAAAGAAAC TACTAATACCAGACATGTTTGAAAACCGTTTAGACAAGATAACTTCAAATCCGAGTGACC TTGTCATAGAAATTAAACCTATAGAAGGGAATCACCATTGGCCTTCAAACTATTTTGCTT ATAATAAACTCGAACCAGCATCAGGTACTACTGGTTTGGTCAATTTGGGAAATACATGTT ACATGAATTCTGCGTTGCAATGCCTGGTACACATTCCGCAGTTGCGTGATTATTTCCTTT **ATGATGGTTATGAAGACGAAATCAATGAAGAAAATCCTCTTGGGTACCACGGCTATGTGG** CTAGGGCATTTAGTGACTTGGTTCAGAAGTTGTTTCAAAACAGGATGAGCATAATGCAAA GAAATGCTGCTTTCCCCCCTTCAATGTTCAAATCCACTATCGGGCACTTTAATTCGATGT TTTCTGGTTATATGCAACAGGATTCTCAAGAATTTTTAGCCTTCCTGTTAGACAGTTTAC ATGAAGATTTGAACAGGATAATAAAGAAAGAATACACAGAAAAACCATCATTATCTCCTG GTGATGACGTGAATGATTGGAATGTAGTCAAGAAACTGGCAGACGATACTTGGGAGATGC ATTTAAAGAGAAATTGTTCCGTTATAACGGATTTATTTGTCGGGATGTACAAATCAACGC TATATTGTCCCGAATGTCAAAATGTTTCTATAACGTTTGACCCGTATAATGATGTTACAT TGCCGCTTCCGGTTGATACAGTGTGGGATAAAACTATAAAAATTTTTCCCATGAACTCTC CACCACTTCTTGAAGTTGAGTTAAGCAAATCGTCCACTTATATGGACTTGAAGAATT ATGTTGGTAAAATGTCGGGCCTAGATCCAAATACACTATTTGGCTGTGAGATTTTCAGTA **ATCAAATCTATGTTAACTATGAGTCAACAGAGTCGAATGCTCAATTTTTAACCTTGCAGG** AATTGATCAAACCTGCTGATGACGTTATTTTTTTATGAATTACCAGTAACAAATGACAATG AAGTAATTGTTCCCGTATTGAATACTAGAATTGAAAAAGGCTACAAAAATGCAATGTTAT TTGGAGTCCCTTTCTTTATTACGTTAAAAGAAGATGAATTGAATAATCCAGGTGCAATAA GAATGAAATTGCAAAACAGGTTTGTCCATTTAAGTGGTGGGTATATCCCATTTCCTGAAC CTGTAGGAAATCGAACCGATTTTGCTGATGCTTTTCCATTATTAGTAGAAAAATATCCAG AGGATAAATCCTTTTTTTCCATCAAGATTCTGTCTGTAGAAAAAGAGCAGCAATTTGCTA GTAATAACCGAACAGGGCCTAATTTCTGGACCCCTATCTCCCCAGTTAAACCTTGACAAAG CTACAGATATAGACGATAAACTTGAAGATGTGGTGAAGGATATCTACAATTATTCATCCT TAGTAGATTGTGCTGAAGGGGTCCTTATGCAAGTGGATGATGAGGGAGATACCGAGGGTA GTGAAGCAAAGAATTTTTCCAAGCCCTTCCAATCGGGAGATGATGAAGAAAATAAAGAAA CTGTAACAAATAATGAAAATGTAAATAATACTAATGATCGGGATGAAGATATGGAACTAA CAGATGATGTTGAAGAAGATGCAAGTACAGAGCCAGAATTAACAGATAAGCCAGAGGCGT TTATTGTTGTGAGTGGAGCGAATTGGGTTCAAATGAGGCATTTTCCGATGATAAAATAT ATAACTGGGAAAATCCAGCTACTTTGCCTAACAAGAGTTGGAGAACGCTAAGTTGGAAA GATCTAACGCTAAGGAAAGAACCATAACCTTGGACGATTGTCTCCAATTATTTTCCAAAC CAGAAATACTAGGATTAACCGATTCGTGGTACTGCCCTACATGCAAGGAACATCGTCAGG CTACCAAACAATACAACTTTGGAATACACCAGATATTCTGCTAATTCACCTTAAAAGGT TTGAAAGTCAAAGGTCTTTTAGCGATAAAATTGATGCCACGGTTAATTTCCCCATTACAG ATTTGGATCTGTCGAGGTACGTTGTCTATAAAGATGATCCCAGAGGTTTAATCTATGACC AGAATTTTGCCGACAATAAATGGTACTATTTTGATGATTCTCGAGTAACTGAAACTGCGC CAGAAAATAGTATAGCTGGATCGGCTTATTTGCTATTTTACATTCGCCGTCATAAAGATG GCAATGGATTAGGCAGCTCTAAACTACAGGAAATAATCCAAAAGTCACGCCACGGATATG ATGAGCGTATCAAAAAGATATACGATGAACAGATGAAGTTGTATGAATTTAATAAGACTG ACGAGGAGGAAGATGTTTCTGATGATATGATAGAATGTAATGAAGATGTGCAGGCCCCTG **AATATAGTAATCGTAGTTTGGAGGTTGGGCATATTGAAACTCAGGACTGCAACGACGAAG** ATGACAATGATGATGGTGAGAGGACAAATTCAGGTAGGAGAAAGTTAAGATTGTTGAAAA **AAGTCTACAAGAATAATTCAGGCTTGGGTTCATCGAGTACGTCTGAAATATCTGAGGGAT** GCCCAGAAAACGAAGTCGCTGATTTGAATTTAAAAAATGGTGTGACACTAGAATCGCCAG AATAA

YJL197W, 1254 aa (SEQ ID NO 166) MGSSDVSSRECSLVYNEDPDFTDGTTPCDRLGVDLMNVLDDKDEIKQESVPVSDREIEDT ESDASAVSSFASANELIAEPHAASETNLGTNGQDGRNVLEQQRDVVARLIEENKETQKEG DKVCIVPKVWYDKFFDPDVTDPEDIGPINTRMICRDFENFVLEDYNRCPYLSIAEPVFNF

LSEIYGMTSGSYPVVTNLVINQTTGELETEYNKWFFRLHYLTEKQDGRKRRHGQDDSIMY LSMSALNLVRDLVEKSMNLFFEKADHLDVNAVDFKIWFVSEGSDIATDSNVSTFLNSSYE ITPLOFLELPIKKLLIPDMFENRLDKITSNPSDLVIEIKPIEGNHHWPSNYFAYNKLEPA SGTTGLVNLGNTCYMNSALOCLVHIPOLRDYFLYDGYEDEINEENPLGYHGYVARAFSDL VQKLFQNRMSIMQRNAAFPPSMFKSTIGHFNSMFSGYMQQDSQEFLAFLLDSLHEDLNRI IKKEYTEKPSLSPGDDVNDWNVVKKLADDTWEMHLKRNCSVITDLFVGMYKSTLYCPECQ NVSITFDPYNDVTLPLPVDTVWDKTIKIFPMNSPPLLLEVELSKSSTYMDLKNYVGKMSG LDPNTLFGCEIFSNOIYVNYESTESNAOFLTLOELIKPADDVIFYELPVTNDNEVIVPVL NTRIEKGYKNAMLFGVPFFITLKEDELNNPGAIRMKLQNRFVHLSGGYIPFPEPVGNRTD FADAFPLLVEKYPDVEFEQYKDILQYTSIKVTDKDKSFFSIKILSVEKEQQFASNNRTGP NFWTPISQLNLDKATDIDDKLEDVVKDIYNYSSLVDCAEGVLMQVDDEGDTEGSEAKNFS KPFQSGDDEENKETVTNNENVNNTNDRDEDMELTDDVEEDASTEPELTDKPEALDKIKDS LTSTPFAILSMNDIIVCEWSELGSNEAFSDDKIYNWENPATLPNKELENAKLERSNAKER TITLDDCLQLFSKPEILGLTDSWYCPTCKEHRQATKQIQLWNTPDILLIHLKRFESQRSF SDKIDATVNFPITDLDLSRYVVYKDDPRGLIYDLYAVDNHYGGLGGGHYTAYVKNFADNK WYYFDDSRVTETAPENSIAGSAYLLFYIRRHKDGNGLGSSKLQEIIQKSRHGYDERIKKI YDEOMKLYEFNKTDEEEDVSDDMIECNEDVQAPEYSNRSLEVGHIETQDCNDEDDNDDGE RTNSGRRKLRLLKKVYKNNSGLGSSSTSEISEGCPENEVADLNLKNGVTLESPE

YJL198W, 3149 bp, CDS: 501-3149 (SEQ ID NO 167) TGTCGTATTTCCACTGATTTGGATGTATGTTGCATGGTGCTAGATTGTGAATAAATCATT TCCACTGGTTTCTAGCAGAGGTAAGAAAATCAGTAGTAGCGGCAGCAGCCAAGAAAAATG GCAGCCTGGCAAGCAGCGAAGGCCATCTGTGCTGCATTTCCACACTCCTTGTATGACTGC ATACGCATAAAGAGGTGCCTTGCTGTAGGCGTATATGATCCTAAGCAACAGAGAAACCAC GGTTCTCTTCTTATTTCGTTATTGTCTTCCCTTTTTACTATGGGTAAAGTCGCCC TTTGCGCTGCTTCTCGAAGAATGAATGGCTCACTGAAAAATTTTGATTCATCGATATAAA GAACACTGTTCACTTCGATGTCATCCGGCCAATAAAGTTGTTTTTAGGATAAACGAGTAA GTGGTAGCTGGTACAGGATCATGAGATTTTCACACTTCTTGAAGTACAATGCTGTCCCAG AATGGCAAAACCATTATATGGACTACAGCGAGCTGAAAAATCTTATTTACACGCTACAAA CAGATGAACTTCAGGTTGGTGATAACGAAGAAGGATTTGGCGCAGGAAAGAGCTCTAACA GTATGAACAAAGATGCAGGCATCGTTGAGGAAACCATCGAGTTGCGAGAGTTGCCTACTG CTCAGACGGTCGCTGCCAAACCTTCTCCTTTCAGAAGAATGAAGGAAAAGATATTTTACA AAAGAAGGTCGTCTTCCGCATCGTCCGTCTCCTCCACGGCCAACGAAAATCTGCAATTAG ACACTTATGATACGTTTGTTGGTGATTTAACAGCTGAAAAACAGAAAGTAGATGATTTTT ATAAGAGGACAGAAGCGAAGTTCTACGACAAATTTGACGCGCTGGTGAAGGACCTGAAGA AAATCGGAGTTATAGAATACGATATCGACGATGATACTCTGTTTAACGAACCGATTGCCA GCACAAATGACGAAGTTCCCCCACTAGACTTGGATGATGACGAAGACGACGACGAATTTT ACGATGATCAATCTAATATTGAAGATAATACTGCTTTGCTGCATCATTCGCAGTATAACA TTAAGTCTCAGAAAAAATCGCTGTTGAAGAAGTCGATCGTAAACCTATATATCGATCTTT GCCAGTTGAAGTCGTTCATCGAATTGAACCGCATTGGGTTTGCAAAAATTACAAAGAAAT CAGACAAAGTTCTTCACTTGAATACAAGAACCGAACTGATCGAATCGGAGCAGTTTTTCA AAGACACATATGCATTCCAGGCAGAAACGATCGAATTGCTAAATTCCAAAATTTCCCAGC <u>AGTTGAAATCCTACCTGCATGACCACATTGTTTGGGAAAGAAGTAACACTTGGAAAGACA</u> TGTTGGGACTGCTATCGCAAGCTGACGAGTTGACACCAAAGGAAACAGAATATAATGCAA ATAAGCTGGTAGGCAAGTTAGATTTGGAATACTACAGATGGCCACTACCCAGACCGATAA ACTTAAAATTCACTAGTATAAACAACGTTGCACTACCGAAATTATTTTTCACCAAGAAAG CATACAAGATTTACTTATTATTCTAGTCACTGGACTCTTGTTAGGAATAAAGACCTTCA ACGACGCTGCTCAGCACCGCTGCATGGCCCTTGTCGAGTGTGTCGCCTTTTTTGTGGGCTA GTGAGGCCATCCCATTACACATTACAGCATTCCTTGTACCACTACTTGTAGTCCTTTTCA AAGTCCTAAAAACCTCCGACGGGGCTATAATGAGTGCTGCAAGCGCTTCATCAGAAATTT TGGCCGCCATGTGGTCTTCTACAATTATGATTCTGCTGGCAGGTTTTACTTTGGGTGAAG TACTTGCACAATATAACATCGCCAAAGTTCTTGCCTCGTGGTTGTTGGCCTTCGCTGGTT GTAAACCCAGAAACGTTCTTTTAATGGCAATGTGTGTCGTGTTCTTCCTATCAATGTGGA TTTCCAATGTCGCAGCACCTGTTCTAACATATTCGTTGTTATCTCCCCTATTGGATGCCA TGGATGCAGATAGCCCATTTGCGCAAGCATTGGTGTTAGGTGTAGCGTTGGCTGCAAATA TCGGTGGTATGTCTTCACCAATCTCTTCACCTCAAAACATCATTTCCATGTCGTACTTGA **AACCCTATGGTATTGGCTGGGGCCAATTCTTTGCTGTTGCATTGCCATCTGGTATCCTGG**

YJL198W, 881 aa (SEQ ID NO 168) MRFSHFLKYNAVPEWQNHYMDYSELKNLIYTLQTDELQVGDNEEGFGAGKSSNITDRFKN KFSFKNAKEDTSSGMNKDAGIVEETIELRELPTAQTVAAKPSPFRRMKEKIFYKRRSSSA SSVSSTANENLQLDTYDTFVGDLTAEKQKVDDFYKRTEAKFYDKFDALVKDLKKIGVIEY DIDDDTLFNEPIASTNDEVPPLDLDDDEDDDEFYDDQSNIEDNTALLHHSQYNIKSQKKS LLKKSIVNLYIDLCQLKSFIELNRIGFAKITKKSDKVLHLNTRTELIESEQFFKDTYAFQ **AETIELLNSKISQLVTFYARITDRPHNISHSKQELKSYLHDHIVWERSNTWKDMLGLLSQ** ADELTPKETEYNANKLVGKLDLEYYRWPLPRPINLKFTSINNVALPKLFFTKKAYKIYFI ${\tt ILVTGLLLGIKTFNDAAQHRCMALVECVAFLWASEAIPLHITAFLVPLLVVLFKVLKTSD}$ GAIMSAASASSEILAAMWSSTIMILLAGFTLGEVLAQYNIAKVLASWLLAFAGCKPRNVL LMAMCVVFFLSMWISNVAAPVLTYSLLSPLLDAMDADSPFAQALVLGVALAANIGGMSSP ISSPQNIISMSYLKPYGIGWGQFFAVALPSGILAMLLVWILLFTTFKMNKTKLEKFKPIK TKFTVKQYYIITVTVATILLWCVESQIEGAFGSSGQIAIIPIVLFFGTGLLSTQDLNAFP WSIVILÄMGGIALGKAVSSSGLLSTIAKALQKKIENDGVFAILCIFGILMLVVGTFVSHT VSAIIIIPLVQEVGDKLGNPKAAPILVFGCALLSSCGMGLASSGFPNVTAISKVDRKGDR YLSVMTFLTRGVPASILAFLCVITLGYGIMASVVKGNATSA

YJR049C, 2093 bp, CDS: 501-2093 (SEQ ID NO 169) ACTGCCATCTCTCCATTCTTTGAAAAGATTATTAAGTTCGTCGTTAAGTTCCGCAATCT GCATTTCATTTAAAGACGGATCATATATTCTTGTGCTTTTTTGTTTTATCTCTTTACTTA CTTGTCGCTTCCATTCGTTGGCCTCTTTTATGGATTTTACCTTAGACACGTTCCTGGGCC GTACCAGAACTGAGTTGGCCTTATCTACATTTCTACTCATTTTGAATGCACAGGTATCTG ATTACTGATGTGGTGCGCCTTGCGATATAACGGTGTGTCACTTTTATTTGCTCTTTCATG CATCCTGAAATTATTTCACCGCACTACGCAAAGAGAACGGAGAAAAAGGTATAATAGGGC AAATGATCATTGACATCGTGATCGTAAGCCAAAAAAAAATACAATAGGCTCCCTAAATAA GTAGAGTAAAAGCTCTTGAGATGAAGGAGAATGACATGAATAATGGCGTAGATAAATGGG TAAATGAGGAAGATGGTCGAAATGATCATCATAACAACAATAATAACTTGATGAAGAAGG CCATGATGAACAATGAGCAAATTGATAGAACTCAGGATATCGACAACGCCAAAGAAATGT TGAGGAAAATATCAAGTGAAAGCAGCTCGCGCAGAAGCTCCCTGTTGAATAAAGATTCAT CTCTCGTGAACGCAATGCAAACAGTGGCGGTGGTACGAGCATTAACGGAACAAGAGGAA GTTCTAAGAGTAGTAATACACACTTTCAGTATGCCTCCACGGCGTATGGTGTAAGAATGT TGAGTAAAGATATATCTAATACCAAAGTGGAACTGGATGTGGAAAATTTGATGATTGTTA CGAAACTCAACGATGTCTCACTGTATTTCTTAACAAGAGAGTTGGTAGAATGGGTTTTGG TACATTTTCCACGTGTGACTGTTTATGTGGATTCCGAATTGAAAAACAGCAAAAAATTTG CCGCTGGCGAGTTATGTGAAGATAGTAAATGTAGAGAATCAAGGATCAAGTATTGGACAA AGGATTTCATCAGGGAACATGATGTTTTCTTCGATTTGGTAGTGACTTTGGGTGGCGACG GTACTGTTCTTTTGTAAGTTCCATTTTTCAGAGACATGTACCACCCGTTATGTCGTTTT CATTAGGGTCTCTAGGATTTTTAACAAATTTTAAGTTTGAACATTTCAGGGAGGATTTAC CTCGGATTATGAATCATAAAATCAAGACAAATTTACGGTTGAGGTTGGAGTGCACAATTT ATCGTAGACACCGCCCTGAAGTAGACCCCAAACACGGGGAAGAAAATATGTGTGGTGGAAA TGATTGCTGCTACTCCGACTGGGTCCACGGCCTATTCTTTGAGTGCAGGTGGGTCATTGG TATGCCCAACCGTCAATGCAATCGCTTTAACACCCATTTGTCCACATGCATTGAGTTTCA GACCCATCATCTTACCAGAAAGTATAAATTTAAAAGTGAAAGTCTCGATGAAGTCAAGGG

YJR049C, 530 aa (SEQ ID NO 170)
MKENDMNGVDKWVNEEDGRNDHHNNNNLMKKAMMNNEQIDRTQDIDNAKEMLRKISSE
SSSRSSLLNKDSSLVNGNANSGGGTSINGTRGSSKSSNTHFQYASTAYGVRMLSKDISN
TKVELDVENLMIVTKLNDVSLYFLTRELVEWVLVHFPRVTVYVDSELKNSKKFAAGELCE
DSKCRESRIKYWTKDFIREHDVFFDLVVTLGGDGTVLFVSSIFQRHVPPVMSFSLGSLGF
LTNFKFEHFREDLPRIMNHKIKTNLRLRLECTIYRRHRPEVDPNTGKKICVVEKLSTHHI
LNEVTIDRGPSPFLSMLELYGDGSLMTVAQADGLIAATPTGSTAYSLSAGGSLVCPTVNA
IALTPICPHALSFRPIILPESINLKVKVSMKSRAPAWAAFDGKDRIELQKGDFITICASP
YAFPTVEASPDEFINSISRQLNWNVREQQKSFTHILSQKNQEKYAHEANKVRNQAEPLEV
IRDKYSLEADATKENNNGSDDESDDESVNCEACKLKPSSVPKPSQARFSV

YKR094C, 1255 bp, exon1: 501-508, intron1: 509-876, 877-1255 (SEQ ID NO 171) AGGTTGTGTTCTTCAATGATGGGCAATGCAATTTGGCGTTAAGCGCCTGAGCAATAAGGT AACAGCGAAATTTATGACATATTATTTCGAACCTTTTACAAACTAGTAGATTTAGTGATT TATTACCTATTGGCATTCATTTGTGTTCTATATGTGGATGAGGATAGCCGCCTTTCTTCT CATCGGAGGCCATATCATCTTTCGACAATCCTTTTTAAATACTATTTCCATCCGTGCCTC TTTTCATGTTTTTCAGATTCTGAAGTACCGCAATAGGATATGGCGGATAATCCGCCATAT GATCCGCCTCATACTAGCCATTACCCATCTATCCCAGGCATTATGGGTATGCAACTCATA **ATCTCAAATACACAAATAAGAGCAACCTTATATATCACTTTTTCCCGTTCAGCAAGAGGT** AAAGCCACCAAAGGTTCAAAATGCAAATGTATGTTACGGCGAATACAGAATACTATGTTC GAAATAATATGAGGATTATACGATAGCAAAAAAGCCATAAACGAAAGACATAAATGGAAA **ATGATTGACAAGCTCACAATTTATTAAACAAGTAGCAATTGAGAAAAACTATTACTCGCG** GCAAGCTTCTGAGTTTACATTAAATCTGTAGAGCAAATTGAAAATGTCGCATATGTGCTG AAGGGTTTGTTTGTTCCATCTTATTTTGCATAACATAGTTATATTTACTTGGTCGCATAA TTACTCCATAAATGAACTTATTCCAATTTTGTACAGCTTCGTTAAGACTTTGACTGGTAA GACCATCACTTTGGAAGTTGAATCTTCTGACACCATTGACAATGTCAAGTCCAAGATCCA AGACAAGGAAGGTATCCCACCTGACCAACAAGATTGATCTTTGCTGGTAAGCAATTGGA AGACGGTAGAACTCTATCTGACTACAACATCCAAAAGGAATCCACTTTACATTTGGTCTT GAGATTAAGAGGTGGTATCATTGAACCATCTTTGAAAGCCTTGGCTTCCAAATACAACTG TGACAAATCTGTTTGTCGTAAATGTTACGCCAGATTACCACCAAGAGCTACCAACTGTAG AAAGAGAAAGTGTGGTCACACCAACCAATTGCGTCCAAAGAAGAAGTTGAAATAA

YKR094C, 128 aa (SEQ ID NO 172) MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYN IQKESTLHLVLRLRGGIIEPSLKALASKYNCDKSVCRKCYARLPPRATNCRKRKCGHTNQ LRPKKKLK

YLR040C, 224 aa (SEQ ID NO 174) MIFAPSFSLIKNILLVSFLISHSFAAKTLTSSSNDDTLARSAAADADMAFFMEFLNDFDT AFPQYTSYMMQNHLTLPQPVADYYYHMVDLASTADLQSDIAQSFPFTQFQTFITAFPWYT SLLNKASATTIYLPQHFITGETEATMTNSSYASQKNSVSNSVPFSTANAGQSMISMANEE NSTTALISASNSSSTSRTSQSQNGAHAKSLYFPMALFGIFAVAL

YLR048W. 1618 bp, exon1: 501-590, intron1: 591-949, 950-1618 (SEQ ID NO 175) GCACCCTTTTTCTTTTCAATAACAAAAAAGGCTTGGGCATTACGTTTTCAACACTTTT AATATTTCCCTTTTTACATCCGTACATATAAAATGTAAACCCATGCATTCATGACAATTT TACCTATTCTTAAAGGCCTTTGTCACTTCTTTATGGGAATGGCGCTACTTTAATTTTCC GCCTACTTTGAAAAATTTACCAAGGCGAAATTGAGTGCGCTAGGCGGAAGTTCCAGGGCA GAGGAGCTGGAAAGATGGAATGGAAGGACTGCAACACTCAGTAAGAAGGTTCGTGGTAGG GAACATCACCTTCTCTAGTTCCTGTAAAAATAATATGATCAAGTTTGAATCCTCGTATTG AAAAATCGCGAGTTATTAAGTGTGTAATTTAGAATACCGAAATAGCACAAGAAGAGATAA GATAAGATACTGATAGGATAATGTCTTTACCAGCTACTTTTGATTTGACTCCAGAGGATG CCCAACTTTGTTGGCCGCTAACACCCATTTAGGTGCTAGAAACGTTCAAGTATGTACAC ATATCCCATACGATTATGTTCTATAGATGATAATAGGTCTCGAAAAGAATATGTCCCCGA TTTAATCATATTTGGAGGTCAGAGGACCAAAGGTAATTTCAGAGGAATTTTGAACACGCC GGGTTTAGAAGAGTTAGAATTTCACTTCTTAGTGAGGGTAAGGAGAAGAAACTCAATAAG AATATACATCCTCGACTGTGTCAAAGATTATGAACTCCGATGAAACAGTAAAACGTCAAA **AAATTCCACGGGATATAATTCGGTACTTTATTGGATATGGAAGAAAACATTATATGCA** ACCATACGTTTTCAATGCTAGACCAGATGGTGTTCACGTTATCAATGTTGGTAAGACCTG GGAAAAGTTGGTTTTGGCTGCTAGAATTATTGCTGCCATTCCAAACCCAGAAGATGTTGT TGCCATCTCTCCAGAACCTACGGTCAAAGAGCTGTCTTGAAATTTGCTGCTCACACTGG TGCTACTCCAATCGCCGGTAGATTCACTCCAGGTTCTTTCACTAATTACATCACCCGTTC TTTCAAGGAACCAAGATTGGTTATTGTTACCGACCCAAGATTAGACGCTCAGGCCATTAA GGAAGCTTCTTACGTTAACATTCCAGTCATTGCTTTGACTGATTTGGACTCCCCATCTGA ATTTGTTGATGTCGCCATCCCATGTAACAACAGAGGTAAGCACTCCATCGGTTTAATCTG GTACTTGTTGGCTAGAGAGTTTTGAGACTAAGAGGTGCTTTGGTCGACAGAACTCAACC ATGGTCCATCATGCCAGATTTGTACTTCTACAGAAACCCAGAAGAAGTTGAGCAAGTTGC TGAAGAAGCTGCCGCCGAAGAAGGAGGAAGAAGAAGTTAAGGAAGAAGTCACTGA AGGTCAAGCTGAAGCTACTGAATGGGCTGAAGAAAATGCAGACAACGTTGAATGGTAA

YLR048W, 252 aa (SEQ ID NO 176)
MSLPATFDLTPEDAQLLLAANTHLGARNVQVHQEPYVFNARPDGVHVINVGKTWEKLVLA
ARIIAAIPNPEDVVAISSRTYGQRAVLKFAAHTGATPIAGRFTPGSFTNYITRSFKEPRL
VIVTDPRLDAQAIKEASYVNIPVIALTDLDSPSEFVDVAIPCNNRGKHSIGLIWYLLARE
VLRLRGALVDRTQPWSIMPDLYFYRNPEEVEQVAEEAAAAEEGEEEEVKEEVTEGQAEAT
EWAEENADNVEW

GGAGTTTGGCTTCCCTCTATTTGTATATTGATCGCCATCCCTACGAAGTTATTGGGAACG CGGCTACACTTAGAAAGAAATGACATTTGCTGTCTTATAAAAGGACTTGACAGACCAAAG ACGCGTATAATACACCAAGAATGGCCTTATTGGAGAAGTTGCATCGAAGGATTGTTGATA TGGGGCTTGTCCCGCGTATAATCGCCTTATTACCAGTTATTTCCATGCTATGCGCTCTAT CTGAGAATGCATTGATGCCTTCACAAGCGTATAGTTACTTTAGAGAATCTGAATGGAACA TTTTGAGGGGCTATCGATCTCAAATTAAAGAAATGGTAAACATGACTTCTATGGAAAGAA ACAATTTGATGGGTTCTTGGTTACAAGAATTTGGTACTAAGACTGCTATTTACGAAAATG AACAATATGGAGAAACATTGTACGGTGTAATGCACGCTCCTAGGGGTGATGGAACAGAAG CGATGGTGCTTGCCGTTCCATGGTTTAATTCAGATGATGAATTCAATATTGGCGGCGCAG CTTTGGGTGTATCTTTAGCAAGATTTTTCTCACGTTGGCCAGTATGGTCCAAGAATATAA TTGTTGTCTTCAGCGAAAATCCTCGTGCAGCATTAAGATCATGGGTTGAGGCATACCATA CTTCCTTAGATTTGACTGGTGGTTCCATTGAAGCTGCTGTTGTGTTGGATTATTCGAGTA CGGAAGATTTCTTCGAGTATGTAGAAATCTCATACGACGGTCTGAATGGTGAGCTGCCCA ATTTGGATCTTGTCAACATCGCTATATCCATTACGGAACATGAAGGTATGAAAGTTTCTT TGCACGGTCTACCCAGTGATCAGTTAACTAATAATAATTTCTGGTCAAGATTAAAAATAT TATGCCTGGGAATAAGGGATTGGGCGTTGTCCGGTGTTAAAAAGCCCCATGGTAACGAGG CATTTAGCGGCTGGAGGATTCAATCTGTAACATTGAAAGCACATGGAAACAGTGGTCATG ATATTACTACATTTGGACGTATACCCGAAGCAATGTTTCGCTCTATTAATAACCTTTTGG **AAAAATTTCACCAATCGTTCTTCTTTTATTTGTTATTAGCACCACGTCAGTTCGTATCCA** TTAGTAGTTATTTGCCAAGCGCTGTGGCTTTATCTATAGCATTCGCCATAAGTTCATTAA ATGCATTTATAAACAATGCTTATGCAAATATATCCTTATTTTCCGAGTATAATTTGGTAG CGTTGTTGGTTTGGTTCGTGTCATTGGTGATATCATTTGTTGTTTCACAAGCGTTTCTTC TAATACCTTCATCGGGATTATTGATGACAATTAGCATGGCATCTTGTTTTTTACCTTTGA TACTTTCCAGAAAAATTCACATCTCAGAACCACTATCATACAGGTTGAAAAAATGTTGCTT TTTTATATTTCAGTTTGGTTTCAACATCTTTGCTAATGATAAACTTTGCAATGGCTTTAC TGATCGGCACATTGGCATTTCCTATGACATTTGTGAAGACCATTGTTGAAAGTTCTAGCG AACATGAGGTGACAACTCAATCCTCTAACCCAATAAAAACTGAGCCGAAAGATGAGATAG AGCTCGTCGAGAATCACATGGATACAACGCCAGCAACCCCCCAACAACAGAAACAAAAAC TGGATTTGAAATGTTGGAGTTGGTTTGTACTTTGTATAGGTTGGCTTCCATGTTGGCTAT **GTTAG**

YLR088W, 614 aa (SEQ ID NO 178)
MALLEKLHRRIVDMGLVPRIIALLPVISMLCALFGFISIAILPMDGQYRRTYISENALMP
SQAYSYFRESEWNILRGYRSQIKEMVNMTSMERNNLMGSWLQEFGTKTAIYENEQYGETL
YGVMHAPRGDGTEAMVLAVPWFNSDDEFNIGGAALGVSLARFFSRWPVWSKNIIVVFSEN
PRAALRSWVEAYHTSLDLTGGSIEAAVVLDYSSTEDFFEYVEISYDGLNGELPNLDLVNI
AISITEHEGMKVSLHGLPSDQLTNNNFWSRLKILCLGIRDWALSGVKKPHGNEAFSGWRI
QSVTLKAHGNSGHDITTFGRIPEAMFRSINNLLEKFHQSFFFYLLLAPRQFVSISSYLPS
AVALSIAFAISSLNAFINNAYANISLFSEYNLVALLVWFVSLVISFVVSQAFLLIPSSGL
LMTISMASCFLPLILSRKIHISEPLSYRLKNVAFLYFSLVSTSLLMINFAMALLIGTLAF
PMTFVKTIVESSSEHEVTTQSSNPIKTEPKDEIELVENHMDTTPATPQQQKQKLKNLVLL
ILTNPFISITLFGLFFDDEFHGFDIINKLVSAWLDLKCWSWFVLCIGWLPCWLLILASSF
ESKSVVVRSKEKOS

ATTTCTCTGATCTCTCATTTTCTGTTGTACAGCAGTGGGACAGTAGAGCCATTGAAAAAA CTACAATCATATCTTGTATGCGGCCCGCAAACCAAGAGATTTATCCTTTGAGACATTGTG AGACCCTCCGTTCGCAACCGTGCTCTCTGTTTTCATCACTATATGCACGCTCTTTTCCAAA GCTCCTGCACTTTGCACGTGGCGGAGCCATCGCCCGGCTTCCATATGTACGGCTGCCACA CCTAA

YLR159W, 114 aa (SEQ ID NO 180) MKFQYALAKEQLGSNSRSGVKKLISKHHWLPEYYFSDLSFSVVQQWDSRAIEKTTIISCM RPANQEIYPLRHCETLRSQPCSLFSSLYARSFQSSCTLHVAEPSPGFHMYGCHT

YLR167W, 959 bp, CDS: 501-959 (SEQ ID NO 181) ATCAAAAGAGTGTTTCAAGTAAGTAAAAACATTTGAGCCTCCCCATTTGTTGAAAGGAGA GAAATTAAACTTGGTTGGGGTTAATTATTTGATGGGTATATTAATTTGCAACCGCAAGGT ATCGATAATAATATTCTACAAAACCTTTATCAATAGTGGTGAAGTCTTTAGTGCGATCT ACCTGGGGTTAATGAACGAGAAGTTCTTGAGATATCTTTCCTGTTTACCTCCGTGCATCC GGGCGCACTTTTTCAAGCGGTGGGAACTCATCAAAATGAAAAACTAGATACTTTTAGACT TATTAAATGGTTTAAATATTTTGAGATGTTCGTTATATCAGAAACTTCCTTACTTCTATC AATTTTGCCGACAAGCCAAGATGCAAATTTTCGTCAAGACTTTAACCGGTAAGACTATTA CCCTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCCAAGATCCAAGACAAGG AAGGTATTCCACCTGACCAACAAGATTGATCTTTGCTGGTAAGCAATTGGAAGATGGTA GAACTTTGTCCGACTACAACATCCAAAAGGAATCTACTCTACACTTG&TCTTGAGATTGA GAGGTGGTGGTAAGAAGAAGAAGAAGAAGGTCTACACCACCCCAAAGAAGATCAAGCACA AGCACAAGAAGGTCAAGTTGGCTGTCTTGTCCTACTACAAGGTCGATGCTGAAGGTAAGG TTACCAAATTGAGAAGAGAATGTAGCAACCCAACTTGTGGTGCTGGTGTTTTCTTGGCTA ACCACAAGGACAGATTGTACTGTGGTAAGTGTCATTCCGTCTACAAGGTTAACGCTTAA

YLR167W, 152 aa (SEQ ID NO 182) MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYN IQKESTLHLVLRLRGGGKKRKKKVYTTPKKIKHKHKKVKLAVLSYYKVDAEGKVTKLRRE CSNPTCGAGVFLANHKDRLYCGKCHSVYKVNA

YLR232W, 848 bp, CDS: 501-848 (SEQ ID NO 183) AGCCACCAATTCCACCAGGCCCGGCATTCAAGTACTTGTAAGAACACCAACAGGCAAAGT CAACACCCCAATCATGAAGTTGCAATGGGACGTTCCCTACAGCGTGTGCTAAATCCCATC CAACCAATATGTCGGGGAATTGGTGGGCAAATGAGGTGATTCGGCCAATATCGAAATATT GCCCCGTGTAATACTGAACACCTGACAAACAGACCAGCGCCAATTCATCTTGATTTACCT CTATGGTATCCAGGATATCTTGAGTTCTGATATAAGTCTCTCCCTCGCGTGGCTCGATCT GAATAAAAACATTCTCAGGTTCCGAAATTCCATGAATTTTGCACTGGTTGTAGAAAGCAT AATAGTCTGATGGAAAGGAGCCCTTTTCAAAAAGGATCTTGAATCTTTTCTCAGTAGGTT TATAAAACGTAATTAACAATGAATTCAAATTTGCAGTGAGACTATTCATTACTGCAACTT CATTTTCTTGAGCACCCACGATGGGGGCTAGTAGTGGAAGAATAGGTAAGTCAATGCTGA CCCAAGGCACCTTTCCTCGGCTTCTTCAGGATGTTTGAAATGCGATTCCACAGCACAAT CGCTCCACGCATCTAGCTCAGCATTAATTGAATTCCTAGTTGACTTCGGCATCAAACCTA AAGAATTCCCGCATAAGTACGTCACAGGCTTATCGTCGGACGATAGTCCCATGGATTTAA ATGTAGGGATGTTGAATTCATCCCTCAGAGATTCCGGATATTCTCCGTCTAATTCCAAAG CTTTCTCCATAATTACCAGTTTGTTTCTTTTTTCCACAGAATATTTAGGCTTAATATGTA **CGTATTGA**

YLR232W, 115 aa (SEQ ID NO 184) MGASSGRIGKSMLTQGTFPLASSGCLKCDSTAQSLHASSSALIEFLVDFGIKPKEFPHKY VTGLSSDDSPMDLNVGMLNSSLRDSGYSPSNSKAFSIITSLFLFSTEYLGLICTY

GTGATTTTCGCGTTCACGCCATTATCCAATGTCAAAAAGGATAATGGAAATGTTAACATG CCTGTATGATCCGACCGTTTTTAGCAAACTTATCAGGGGAAAAAGTATATTCCATTAAAT GACACATGCCACCATAGATAATGGATAATGAAGAAGTTAACGAAGAATGTATGAGATTAT TTTTCAAGAACGCTCGTGCGCATCTGGATAAACATCTAACATCAAGGTTGACATGCGATG AAAATGCATATATCACGTTCAGATGCTTCCTGGATGGAATACATCGCAAATCTACTAGGT TTCTCGAAGAGCTACTTTTGAAACAAGAAAATATGTACCATAATAACAATTACGAACGCA TAAATGATTCCGTGATACCATTGGTTCTGAAACTTTTATGGCTTCAAATTCACGAACCTA CACTCCAATGGTTTGAGCACTGGTTCCATGATATCATGCGACTAAGTAACAGAAGAAAGT TCAGAGTTTTTAGAATTTTTCAAAAAAAAAATGATTCAATTTTTCAAAATTACACACAGGT ATTACTATGACATCATCGAACACCTATGCGCAAAGTACGATATGAATTCCGTTATTTCAA ATGCTCTCTCGCGAAGTTGAATTTAATGCAATACACAGATGGACTTTCAACTCATGAGA **AAATTATCTTAAACACGAGTAATCCACTGACGTTTTCCATTGTAATCTCACTACAAAGAT** GCGTGATTAATCTAGGTTCCACACATTTTTATAAAACACTACTAAACAAGCCGTCTAACA AACCCAAGAGTGTGGAAGGTTTTGAGAAGTCTATTAGGTACTTGAATATTGCCTCACTCT **ATCTCCCAGCCGTTGGAGATACTTATTTTCAACGAGCGAAAATTTACTTGATCACTGGGA** AATTCTCACTGTATTTCTTTGAATTAGTAAGAGGAGCATTGGTAAGGATTCCGTCTAAAT GTGCGTTAAACAATTTGAAAGATTTCATTTTGACTCCTGATTTTCCGGAAAGAAGACGTC TGATGAAAAATTGGCAATTCTTGTGTCAAAAGATCTCAAAGGTGAGAAATCATTCTTTG AAGGTCAAATTGTTTTGCAATTTCTATCGATAGTAGAACACACTTTGGTTCCACAGTCAT GGAACGCATCACGTGCTTCTAATTGTTGGTTATTGAAAGAGCATTTACAAATGGCTGCAT TAAAGTATCATTCAGGTAATATTAATGTTATACTTGAAAACTTGGCTGCCACAATGGGAA GTTTCGATCTTATGTTTACAACTCGAAAAAGTAAGGAACAAAAGAACAAACTCAAATATG CAGATTTGAGTGAGCGCCAGGTTTTTTTTTTAGACTTGAGCTTTGATTTTATTGCTAATA TCATAGACGTCGTCATCAAACCCTCCTGGCAAAAAAACATGGAAGACTTTCGATATCTAG CCATTATTCGTTTGCTTATGTGCTGGATTAAGTCATATAGATCTATTTTGCAGTACACTC ACAGACACAGGAAGTTTTGCACTTCATTCGCCTTGTTGCTGAACGACTTGATAAATAGTC CACTGAATTGTTCAGGAAATATATATAGCCACAGGCCGAAAAGAAGCTATCTTTTTAGAG AAGATATTATTTCAGGGAATTTTCTTGCATTAACTTTGCACTAACAGATTTTAATGACG ATTATGTGTATGATTCTCCCGACATGATTAATAATATATTGGATGCCCTACATTGACTA AAGTGCTTTCTCCAAAAGAAGAATGTGTTCTGCGAATTAGATCAATAATATTTTCTGGCA TGAAATTTTTAGAGAAAAATGACACCGGCGTCATATGGAATGCCAGCAAATATAAGTTTG ATTTAATAAGCCCAAATATTAAAATAAAACGCCAAATAGCATTATCGGAAATTTCCTCCA AAATAAATGTAAAAACACAACAGGAAAGAGTAGTCTCTTCGAGAAAAGTTGAGGCCAAAA GAGATGAACAACAGCGCAAAAGAGCCGGGAAAATAGCTGTGACAGAACTGGAAAAAACAAT TTGCAAATGTCCGGAGAACAAAAAATTGTCTCCGCTCCCAGAAAAAGATGGCGTTTCTT CTGAGTTGGTAAAACATGCTGCTTCACGAGGGAGAAAAACTATCACTGGCCCACTATCCT CTGATTTTCTCTCATATCCAGACGAAGCAATTGATGCTGATGAGGACATCACCGTCCAAG TGCCAGATACTCCTACTTGA

YLR233C, 699 aa (SEQ ID NO 186)
MDNEEVNEECMRLFFKNARAHLDKHLTSRLTCDENAYITFRCFLDGIHRKSTRFLEELLL
KQENMYHNNNYERINDSVIPLVLKLLWLQIHEPTLQWFEHWFHDIMRLSNRRKFRVFRIF
QKKMIQFFKITHRYYYDIIEHLCAKYDMNSVISNALFAKLNLMQYTDGLSTHEKIILNTS
NPLTFSIVISLQRCVINLGSTHFYKTLLNKPSNKPKSVEGFEKSIRYLNIASLYLPAVGD
TYFQRAKIYLITGKFSLYFFELVRGALVRIPSKCALNNLKDFILTPDPPERRRLMKKLAI
LVSKDLKGEKSFFEGQIVLQFLSIVEHTLVPQSWNASRASNCWLLKEHLQMAALKYHSGN
INVILENLAATMGSFDLMFTTRKSKEQKNKLKYADLSERQVFFLDLSFDFIANIIDVVIK
PSWQKNMEDFRYLAIIRLLMCWIKSYRSILQYTHRHRKFCTSFALLLNDLINSPLNCSGN
IYSHRPKRSYLFREDIIFREFSCINFALTDFNDDYVYDSPDMINNIIGCPTLTKVLSPKE
ECVLRIRSIIFSGMKFLEKNDTGVIWNASKYKFDLISPNIKIKRQIALSEISSKINVKTQ
QERVVSSRKVEAKRDEQQRKRAGKIAVTELEKQFANVRRTKKLSPLPEKDGVSSELVKHA
ASRGRKTITGPLSSDFLSYPDEAIDADEDITVOVPDTPT

AAAAACGGTCGGATCATACAGGCATGTTAACATTTCCATTATCCTTTTTTGACATTGGATA ATGGCGTGAACGCGAAAATCACATTGATAAAAAAAGCAGTTTGGCGAATTAGTAACTGT AAGGTGTATTATAGACAATAATGAAAGTGCTATGTGTCGCAGAGAAAAATTCTATAGCGA AGGCAGTTTCACAGATCCTAGGAGGAGGCAGATCAACTTCAAGGGATTCCGGCTACATGT **ATGTAAAGAACTATGATTTCATGTTTAGTGGGTTCCCGTTTGCCAGAAATGGGGCTAACT** GCGAAGTTACCATGACTAGTGTTGCAGGGCACCTAACAGGCATTGATTTCAGCCATGATT CGCATGGGTGGGGAAAATGCGCCATCCAAGAGTTATTTGATGCGCCACTGAACGAGATTA TGAATAACAACCAAAAAAAGATAGCAAGCAACATCAAGCGAGAAGCGAGGAATGCAGACT ATCTGATGATATGGACAGATTGCGACCGGGAAGGAGAGTACATCGGTTGGGAGATATGGC AGGAGGCCAAGAGAGGCAACAGGCTCATACAAAATGATCAAGTATACCGGGCAGTCTTTT CGCATCTCGAAAGACAACATATTAAATGCAGCACGAAACCCAAGTCGATTGGATATGA AGAGTGTGCACGCTGTAGGCACGCGGATTGAAATCGATCTTCGAGCAGGTGTTACATTCA CCAGACTCTTAACAGAAACGCTACGAAATAAACTGAGAAACCAAGCCACCATGACCAAGG ATGGTGCAAAACACCGCGGTGGTAACAAGAACGACTCACAAGTCGTATCGTATGGTACAT GCCAGTTTCCAACGCTCGGCTTTGTAGTAGACAGGTTTGAAAGAATACGAAATTTTGTTC CCGAAGAGTTCTGGTATATCCAATTGGTAGTCGAAAACAAAGACAACGGCGGAACAACAA CGTTCCAGTGGGACAGGGGCCACTTGTTCGACCGGCTGAGCGTGTTAACGTTTTACGAGA CATGCATCGAAACCGCCGGCAATGTTGCTCAAGTAGTAGACTTGAAATCAAAGCCAACAA CGAAATACAGACCTTTACCTCTGACCACAGTGGAGCTACAAAAAAACTGCGCCCGGTACC TGCGTCTGAACGCCAAACAATCACTAGACGCAGCAGAAAAGCTATACCAAAAGGGGTTCA TATCGTATCCAAGAACAGAGACTGATACTTTCCCACACGCAATGGACCTAAAATCCTTGG TCGAAAAGCAAGCTCAATTGGACCAACTCGCTGCAGGCGGCAGAACCGCCTGGGCATCGT ACGCGGCATCGCTGCTCCAACCCGAAAACACAAGTAACAATAACAAGTTCAAGTTTCCAC GAAGCGGCTCCCATGACGACAAAGCGCATCCACCAATCCACCCCATCGTAAGTCTGGGGC CTGAAGCAAATGTTTCGCCAGTGGAAAGAAGAGTATACGAGTACGTGGCCAGGCACTTTT TGGCATGCTCAGAGGACGCCAAGGGCCAATCGATGACCCTTGTGTTGGACTGGGCCG TTGAACGTTTCTCAGCTTCAGGTCTCGTAGTCCTAGAGAGAAATTTCCTCGATGTTTACC ACATCGCGAAGGCCGAAATGAAGGCGGGCACTACGGCGCCCCAAGCCGATGACTGAGA GTGAACTCATTCTCCTCATGGATACAAACGGCATTGGCACAGACGCCACCATTGCGGAGC ACATAGACAAGATCCAAGTACGTAATTACGTTAGGAGCGAGAAAGTAGGCAAGGAAACCT ACTTACAACCCACGACCCTGGGTGTCTCACTAGTGCACGGCTTCGAGGCCATCGGCCTCG AAGACTCCTTTGCAAAGCCCTTCCAGCGCAGAGAAATGGAGCAAGACCTCAAGAAAATCT GCGAAGGTCATGCCTCCAAGACTGATGTTGTAAAGGACATAGTCGAGAAGTATAGGAAGT ACTGGCACAAGACGAATGCCTGCAAGAATACTCTCTTGCAAGTTTATGACCGTGTCAAGG CATCCATGTAA

YLR234W, 656 aa (SEQ ID NO 188) MKVLCVAEKNSIAKAVSQILGGGRSTSRDSGYMYVKNYDFMFSGFPFARNGANCEVTMTS VAGHLTGIDFSHDSHGWGKCAIQELFDAPLNEIMNNNQKKIASNIKREARNADYLMIWTD CDREGEYIGWEIWOEAKRGNRLIQNDOVYRAVFSHLEROHILNAARNPSRLDMKSVHAVG TRIEIDLRAGVTFTRLLTETLRNKLRNQATMTKDGAKHRGGNKNDSQVVSYGTCQFPTLG FVVDRFERIRNFVPEEFWYIQLVVENKDNGGTTTFQWDRGHLFDRLSVLTFYETCIETAG NVAQVVDLKSKPTTKYRPLPLTTVELQKNCARYLRLNAKQSLDAAEKLYQKGFISYPRTE TDTF PHAMDLKSLVEKQAQLDQLAAGGRTAWASYAASLLQPENTSNNNKFKFPRSGSHDD KAHPPIHPIVSLGPEANVSPVERRVYEYVARHFLACCSEDAKGOSMTLVLDWAVERFSAS GLVVLERNFLDVYPWARWETTKOLPRLEMNALVDIAKAEMKAGTTAPPKPMTESELILLM DTNGIGTDATIAEHIDKIQVRNYVRSEKVGKETYLQPTTLGVSLVHGFEAIGLEDSFAKP FQRREMEQDLKKICEGHASKTDVVKDIVEKYRKYWHKTNACKNTLLQVYDRVKASM

YLR238W, 1937 bp, CDS: 501-1937 (SEQ ID NO 189) CTTCGTTCACACTTAATATTAAATAACAGCTCTTTCCTAATAATAACATATACACTAGAT TCGTAAAAAAAGAACAATAAACCAATCTTATTGCCAGCGTCTAACTAGTCCTATTATAT TCCAATATATTAAGGGGTAAGGACTACTATTATTCGCCCTGAATTGAAATCTTTTAGAAA GCACCTGTTCTCTCTGGTGTTCTTTTTTTCTCATCTATTATCTAATTTCTTCAACCTT CGTTATTTGTTGTTATTCCGTAATCGTGGTGCTCAACTTTTGAAATTTCACTTGTTTACC ATAACGGAACATAATTAAAAATTTGTTCTTGAAAGTCACAAGCACTACGTGAACACAAAA TTAAGGCAAGAGTGACAAAGTAACCCTCACAAGGAGCCTGTCGTTGGTTATATTGGAAGC

CCAGTTCTCCGGGCAAGAAACAGATAACATATAATAGTATACCCAAGAATGCAAATCTAA TTGATGGATCTACGAATTCATCGAAGAGGCCAATTGAAAAGTATGACAAGAGAATAGCCG ACCCAACAAAAAGCTATTTTCCACATAGCATATCAAGAACACCAAGGAGAAAATATACTT ACATTCTAGTCCTCACATCACTAAATGGAACTTTTGAGAGCAAACATGTGGTGATACCAT TTAAACCAGATGGTTTGAAATTGGGAAGGCCTGTTGCTAATAGTAATAGCAGCTCCAGTT CATCGCTCAGGGGCGGTAAAAGAGTGGATTCACACACTTTTTCCCAAGTAAGGTCCGATA ATGGTAATTTCGATTCAAGAGTACTCTCCAGGAATCATGCATTGTTAAGTTGCGACCCGC TCACGGGTAAGGTATATATACGAGACTTAAAATCCAGTAATGGTACGTTCATTAACGGTC AAAGAATTGGCTCAAATGACGTAGAAATCAAAGTTGGCGATGTGATAGACTTGGGAACAG ATATAGATACGAAAATTGAGCATCGAAAAATAAGTGCCACAGTTGAAGAACTATTTGTAC AACCTTTATTAGAATCACCGATTTTTGAAAATGAAGATAGTGATGATTGCCATACAATTA CAGAAAAAGAGGAGGCTGCTGCCATAACAAGTCACATATATGGTGATTCCAACAACCTAG AATTGGAAGAGTTATCCTGGGCTCTGATACAGAAATACTGAGTGGAATTTTTATTAATA ATTGTATTGGTACGAGCCCGACTTTATCTAATATCATCAAAACCCTGGCAATGGAAATTC CGACACATCTAGAATACACGAACAAACTTTTAGTGGAAAAAAATGATCAGCAACTGGTAA AGCTGCAAAATGGATTAAGAAGGAAACTGTCGGGGAAATACGAAAAGATTATCGAACAAA ACAGAAATCAAGTAAAACAGTTGGAAAGGGACCATATGTTTTTCAAAAAGTCATTTGAAG TGAAGAAAAGAAGAATAATGAAAAGCAAAAAAGCATGGAAAGGGAAATAGAAGACTTGA AAGAACAAGAACTCTCAACTGCATCTAAAAAAAAGACTACCGAACATGACACTAGAGGCG TCCCGGGCATGAATCCTAAGGGTACTGACAAATTTAGCATCAAGAACACGCTATGTAATC ATTTCACACTATTAACATTTGGAACTATTTCCATCGGGATTATAGCTATTGTCTTCAAGA TCCTTTCCCCCAACTAG

YLR238W, 478 aa (SEQ ID NO 190)
MTGPGPEINKEEHPSSPGKKQITYNSIPKNANLIDGSTNSSKRPIEKYDKRIADPTKSYF
PHSISRTPRRKYTYILVLTSLNGTFESKHVVIPFKPDGLKLGRPVANSNSSSSSSLRGGK
RVDSHTFSQVRSDNGNFDSRVLSRNHALLSCDPLTGKVYIRDLKSSNGTFINGQRIGSND
VEIKVGDVIDLGTDIDTKIEHRKISATVEELFVQPLLESPIFENEDSDDCHTITEKEEAA
AITSHIYGDSNNLELEEVILGSDTEILSGIFINNCIGTSPTLSNIIKTLAMEIPFSKCDN
FKLQSMENFLINYTTHLEYTNKLLVEKNDQQLVKLQNGLRRKLSGKYEKIIEQNRNQVKQ
LERDHMFFKKSFEVKKRRNNEKQKSMEREIEDLKTRLEVERYKNSQMMKKNKQKEQELST
ASKKKTTEHDTRGVPGMNPKGTDKFSIKNTLCNHFTLLTFGTISIGIIAIVFKILSPN

YLR241W, 2849 bp, CDS: 501-2849 (SEQ ID NO 191) TTAATTTGAATATGTCCGAAGAAGATGCCACAGTGCATTTTCAGAATCTAATCAATGATA GTGTAAATGCTTTGCTGCCTATCGTGATTGATCATTTACATAATCTGGCACAATACTGGC GGACCTGATTGGTTGATAATTGGTGCTTCAAAATTTAAATTTCGTCACTCTAATTATACT TAACATATAAATGGTACCTTCAATATATCTTCTTAGTAAAAAGTAGCATGATTTTGTGTT AATTTGCACTTTTTTATTTAAAAATAAAAATCACAGTTAATTTTTCATGATCTTGCAAA GACACGCCTCCCCTAATGTGGCATATATAACAATTGTGAATCAGAAAAACTCAACACTT TAACATAATGGCGGCACGAAGGCTAAACAAACAAGATTAGCATTGAATGCCTTTTTTGG GTACAATAGAACAGTACTGAATGACATCATATATCGAAAGGCTCAAGTCGGCAGCATCGT ATCTTGATACAGTTCCAGATGAGCATCATGATTCAGAAAACCCACCGCCAAGGTTGTAA CGACGCAACTGACTATTGCTACTTCACTAGGTATTTTTTGCTTTGCTTTCGTTCTCAATTC TACTAAAAAAGTGGCCTAGATTATACGCAAGCAGACGATATAAAGATGACGGGAACCTTC GCTTACCGTCCTGGAATCAGTCAAGTTTATTCGGCTGGTTAACAGTGTTGTATAAGATAC GGGACGAACAGATTCTGGAATATGCAGGTTTAGATGCGTATGTGTTTTTTGAGTTTTTTCA TAAGATATCATTTTACTGGAAAAATTGATGACGGCAACGATGATGATGACAGTGAAAGTT CTTTAATACATCTGGTAAAAAGAATTGTGGAGGGAAGTGGCGATGGTGACAATCATTCAG CTCCCGAACGTACAAATGTGTACCTCTGGATGTATGTTCTTCACATATTTCTTCACCT TCATAGCAATTAAAATGGCAGTTGCGGAAACAAAGCACGTCGTAAGTACTAGGCAAGCTT ATCTTGGGAAGCAAAATACGATTACTGATAGAACGATAAGGCTCTCAGGCATCCCGATAG AGCTTCGTGATTCGGAAGCCTTAAAGACCAGAATTGAACAATTAAAAATCGGCACCGTTT CATCAATCACTATTTGTCGAGAGTGGGGTCCTTTGAACAAGCTATTTCATTGTCGGAAGA AAATACTCAAAAACCTGGAATTAAAATATTCAGAATGTCCAAGGGAGCTCCGTACTCGAC

AACCATATTCGGAGAACTATCATTTATTGGGAAACGAGCAATCAGGCGCAGTTACACATG GAGAAAATGTTCCATCAAGCAATAATAATGACGAGGATACTATACTATATTCTCAAATTT ATGCCATAGAGTACCTGGAGCAGCAATTAAAATTTATTGATGCTGAAATTATTGAAGCGA GGAAACAACTACTCCGCAACACCTACGGCATTCGTTACGATGGATTCTGTTGCTAATG CGCAAATGGCAGCTCAGGCGGTATTAGATCCTAGAGTACATTACTTCATAACCAGATTGG CTCCTGCACCTCACGATATCAAGTGGGATCATGTTTGTCTTTCTAGAAAGGACCGGTTAA TATCATACTTAGCCACATTGCTAAATTTGAAAACACTTTCGAAATTCTGGCCAAGCGTAG GGCAGCTACTAAAAGATCACCAGTGGGCCGCTAACATTGTAACGGGGCTATTACCAACCT ATCTCTTCACATTGCTTAACTTTGGAATCCCCTATTTTTACGAGTATTTGACTTCTTATC AAGGATTGGTATCATACAGCGAAGAGGAAATCTCACTTGTTTCAAAAAATTTCTTTTATA TTTTTGTCAACCTTTTCTTAGTTTTCACATTGGCAGGTACAGCATCTAATTACTGGGCGT ACCTCAGCGATACCACCAAAATTGCTTATCAACTTGCTACATCTGTGAAGGAGTTCTCCT TATTCTATGTCGATTTGATTATATTGCAAGGTATTGGTATGTTCCCGTTTAAGTTGTTAT TAGTTGGTAGTTTGATCGGCTTTCCTCTAGTGAAAATCAAGGCTAAGACACCTAGGCAAC GGAATGAACTTTACAATCCACCGATATTTAACTTTGGACTACAATTACCACAGCCAATTC TGATTTTGATTATAACGTTGATCTACAGTGTAATGAGCACGAAAATTTTGACTTCAGGGC TGGCGTACTTTATTATTGGGTTTTACGTCTATAAATATCAATTGATTTTTGCCACAGATC ATTTGCCCCATTCTACAGGAAAAGTATGGCCATTAATTTTTAGAAGAATCATCGTTGGAT TGCTATTGTTTCAATTAACAATGACAGGAACACTGGCAGGATTCGAAGGAGGATGGGTTT TGTCATCTTGCCTTTTCCCGCTTCCAGTAGTGACATTATGTTTCCTATATGATTTCGAGA AGAACTATTTGCCGTTGTCAAAATATATCGCATTGAGTTCAATTCGCGAGTACGAAAGAG ACAATTCTACGGTGAATTCTGCCAATGAGGAAGAGTCGTATGCATACCCTTACGCTGTGA GTGAATTAGAGGGTCCGATGTTGGATTGA

YLR241W, 782 aa (SEQ ID NO 192)

MTSYIERLKSAASYLDTVPDEHHDFRKPTAKVVTTQLTIATSLGIFALLSFSILLKKWPR
LYASRRYKDDGNLRLPSWNQSSLFGWLTVLYKIRDEQILEYAGLDAYVFLSFFKMCIKLL
SIFCFFSVCVISPVRYHFTGKIDDGNDDDDSESSLIHLVKRIVEGSGDGDNHSAPERTNV
YLWMYVLFTYFFTFIAIKMAVAETKHVVSTRQAYLGKQNTITDRTIRLSGIPIELRDSEA
LKTRIEQLKIGTVSSITICREWGPLNKLFHCRKKILKNLELKYSECPRELRTRQPYSENY
HLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPKMKIGYRGIFGKEVDAIEYLE
QQLKFIDAEIIEARKQHYSATPTAFVTMDSVANAQMAAQAVLDPRVHYFITRLAPAPHDI
KWDHVCLSRKDRLTKVYSTTVFIGLSSLFLVIPVSYLATLLNLKTLSKFWPSVGQLLKDH
QWAANIVTGLLPTYLFTLLNFGIPYFYEYLTSYQGLVSYSEEEISLVSKNFFYIFVNLFL
VFTLAGTASNYWAYLSDTTKIAYQLATSVKEFSLFYVDLIILQGIGMFPFKLLLVGSLIG
FPLVKIKAKTPRQRNELYNPPIFNFGLQLPQPILILIITLIYSVMSTKILTSGLAYFIIG
FYVYKYQLIFATDHLPHSTGKVWPLIFRRIIVGLLLFQLTMTGTLAGFEGGWVLSSCLFP
LPVVTLCFLYDFEKNYLPLSKYIALSSIREYERDNSTVNSANEEESYAYPYAVSELEGPM

YLR321C, 1781 bp, CDS: 501-1781 (SEO ID NO 193) TTCAAGTGCACTCTTTGTAAGGAAGATTACAAGTCTCCAGTGGTCACAAACTGTGGCCAT TATTTTTGTGGATCGTGTTTTGCCAAAGATATGAAAAAGGGCACCAAATGCTTTATATGC AGGAAAAGTTGATGGAGAATGCCATATCACCCCAAAAATTACACGCACCCGATGCTAATG TACAGGAATTATAGAGCACATGACCCATAGATTTATCGAGCATTGTTGCAATTTCGAAAG AAGGCACATAGCAGCACAATGTCGCACCAAAACCAGCTTATTCCACAAGCTTATATTT CTAACTTTCATAACAGATTGACAAACGAAGATGATGGTATCCCCATCTTTACAATGGCTC AACAAACAAGGCAGCATAAAAGGGCTAAAGTGGTCAACTATGCGGAATATGACAACGATC TCTTTGATGAATTCAATATGAACGGTTCTAATTTCAACAATGCTGATACACACTATAAAG ATAATGCAGTGTCTCATGAAAATACTCCGGCACTTACAAATGGTGTTACCATGGACGGTT CCGAATACAATGTCCTAGAGAACATGAATGGAGCTGATAGTATTATCTCTAACAACAAAT ACGATGCGGGTTCAAACATGGTTGTGGAATCTTTATCCGGTTTGAATAGCAATAACAACG CCAGCAATGGTCCGAGCAACAAGCGCAGGCACAGGATATTGGAAACGCCGTTCTACCGG ATCTGCAAGACCAACACCCCTTCAACATATTGAGATACCCTAAAATAAGAGATA

YLR321C, 426 aa (SEQ ID NO 194)
MSHQNQLIPQAYISNFHNRLTNEDDGIPIFTMAQQTRQHKRAKVVNYAEYDNDLFDEFNM
NGSNFNNADTHYKDNAVSHENTPALTNGVTMDGSEYNVLENMNGADSIISNNKYDAGSNM
VVESLSGLNSNNNASNGPSNKAQAQDIGNAVLPDLQDQHHNPFNILRYPKIRDTFINGKV
VSPYRLNTDQETKANANSGEAIMIPITLDIEHMGHTIKDQFLWNYNDDSISPEEFASIYC
KDLDMTSATLQTQIANIIKEQLKDLENIAATEIMSDLHVIINLTCNLQDRFFEDNFQWNL
NDKSLTPERFATSIVQDLGLTREFIPLISQSLHETILKIKKDWVDGHLIQDHVPNDAAFG
YLSGIRLDIDELGSNWCPRVEILTKEEIQKREIEKERNLRRLKRETDRLSRRGRRRLDDL

YLR322W, 815 bp, CDS: 501-815 (SEQ ID NO 195)
GTCATATCAAGATCTTTACAGTATATAGAGGCAAATTCCTCCGGAGATATGGAGTCGTCA
TTGTAGTTCCAGAGAAACTGGTCTTTTATGGTATGACCCATATGTTCTATATCCAAAGTA
ATTGGTATCATGATTGCCTCCAGAATTGGCGTTTGCCTTCGTTTCTTGATCAGTGTTG
AGTCTATATGGAGACACCACTTTTCCGTTAATGAAAGTATCTCTTATTTTAGGGTATCTC
AATATGTTGAAGGGGTTGTGGTCTTGGTCTTGCAGATCCGGTAGAACGGCGTTTCCAATA
TCCTGTGCCTGCGCTTTGTTGCTCGGACCATTGCTGGCGTTGTTATTGCTATTCAAACCG
GATAAAGATTCCACAACCATGTTTGAACCCGCATCGTATTTGTTAGAGATAATACTA
TCAGCTCCATTCATGTTCTCTAGGACATTGTATTCGGAACCGTCCATGGTAACACCATTT
GTAAGTGCCGGAGTATTTTCATGAGACACTGCATTATCTTTATAGTGTGTATCAGCATTG
TTGAAATTAGAACCGTTCATATTGAATTCATCAAAGAGATCGTTGTCATATTCCGCATAG
TTGACCACTTTAGCCCTTTTATGCTGCCTTTTTTTTTAGAGCCATTGTAAAGATGGGGATA
CCATCATCTTCGTTTGTCAATCTGTTATGAAAGTTAGAAATATAAGCTTGTGGAATAAGC
TGGTTTTGGTGCGACATTGTTGTCGTATTTTCTAA

YLR322W, 104 aa (SEQ ID NO 196) MRHCIIFIVCISIVEIRTVHIEFIKEIVVIFRIVDHFSPFMLPCLLSHCKDGDTIIFVCQ SVMKVRNISLWNKLVLVRHCVLLCAFLLSFFNVLHSIISICRIF

YLR325C, 737 bp, CDS: 501-737 (SEQ ID NO 197)
CCACATGTCACAACTACTTTGTGAAGTTGCAATGCGTGATTAGTATTATAAAACATCATA
GCCTTGCCAAATAAACTCGCTTCCCAGAAAAGACGCCAAATTAACTGCCGCTGTTATGTG
ACAAAACAGGGCATCTCACATATTCGCGTACTGGTGTTCTTTTAGCTCATTCCGATATTA
TTCCAAGACGGAATTTTCATCTAGAGAAAATGCATCCGTGCATTTTCATAAAACCCACACA
ATTAAAATGCCTTGCGAAAAGGAGGACTCGTCCGTGCAACTGTTGAAAAAAATAGACGGA
GCATCATACGTTCGAGTGGAAAATTATGGAGAGTTTTCCAAGCTCTATGGCATGTAGAGT
CGTGATTGCTGCTGTACGCTTTTGCACAATATTGAATCTTCAATCTAAAGAATTAAATTT
TCTAATTTCAATGTAGAAAATATTTCAACTGTTAGTTTTTTATTTCAGGTTGAATATAGTA
CGACAAAATATCAAGGAAAAATGGCTAGAGAAAATCACCGACATCAAACAATTTTTGGAAT
TGACCAGAAGAGCTGACGTTAAGACCGCCACTGTTAAGATTAACAAAAAATTGAACAAGG
CCGGTAAGCCATTCAGACAAACCAAGTTCAAGGTTAGAGGCTCTTCTTCTTTTGTACACTT
TGGTTATCAACGATGCTGGTAAGGCTAAGAAATTGATCCAATCTTTGCCACCAACTTTGA
AGGTTAACAGATTATAA

YLR325C, 78 aa (SEQ ID NO 198)

MAREITDIKQFLELTRRADVKTATVKINKKLNKAGKPFRQTKFKVRGSSSLYTLVINDAG KAKKLIQSLPPTLKVNRL

YLR344W, 1331 bp, exon1: 501-519, intron1: 520-966, exon2: 967-1331 (SEQ ID NO 199) TAAGGGCTGTCAATTTTCATTTCCCTCAAAGTTAATGCGCAAGAGTTAGGATGATCTTG ATTATTAGTTATTTGTTTGTTCCATCAATTATGCCGACGTCCATGAATGCTATTGAAGTA TCGATTACTTATGCTATTCTATTGTATTTGAGCCGGCGGCTAGTAAACAAGACAGCATAC CTTTCCAACATCCGTACATATTGATTATTGTATCTATGATTTTCATGTAATGTATGGGTT AACTAATCCTTTCTCTTTTTTTTTTTTTTCTGAAAATCAGTAGCTAGAGGAACCTGTTC GTGAAAGATATGGAATATTCCGTCTAGGGAAGAGCCGAGAGCTGAGAGCAGTATCCATCG GATGGAATCTTGCCTGGATGCGTAACGACGACAGCTTGTCTAGAAGGCGAAGTACAAGAT ACTAAGAAGACTATAACAACAGAAGACAATTTTGTAGTGCGATTCTATATTATTGACGTA ACCAACAAAAAGTATCAGAATGGCTAAACAATCATTAGGTATGTGCACAAATGCTAAAT CACTGAAACCCTGTAGAGCTGGAATTGAAAATATAGTTTGTACCTTTTGCCTGAGGGCAG AATGACTCAATGTTATCTTAATTCGATTAGAAAAAGAAGGTGCGTTATCCAAGGTTGAAA CTTGTAAACTATTTAGGTGATGTCTCATAACTGCAACCACTGGAAAATGACGCAAATATC AAAATAATAGGGAGATAAAGTCTCACGACATGAAAAAATCATAGAATTATTGTTCAATTT ATCTAGCCGTATCTTACCTTATGGAAAAAGTGTGAATATGTTTTTCTAAATCGAGCTTCC CGGAAATTACACTATATTATGCATCCGTGATACATCTGAAATTCAATACTTTCTCCAAGG TCCTGCTTACTAAGAGGGTAAGATTTGTTGAAACTCGAAATACTAACATTATTTCATTA TTTTAGACGTTTCCTCCGACAGAAGAAAGGCTAGAAAGGCTTATTTCACCGCCCCATCCT CCCAACGTCGTGTTTTGCTATCTGCTCCATTATCTAAGGAGTTGAGAGCTCAATACGGTA TCAAGGCCTTGCCAATCAGAAGAGATGATGAAGTTTTGGTTGTTCGTGGTTCCAAGAAGG GTCAAGAAGGTAAGATTTCATCTGTTTACAGATTGAAATTTGCCGTTCAAGTTGACAAGG TTACCAAGGAAAAGGTCAACGGTGCTTCCGTTCCAATTAACTTGCACCCATCCAAGCTTG AGTTGGAATAA

YLR344W, 127 aa (SEQ ID NO 200) MAKQSLDVSSDRRKARKAYFTAPSSQRRVLLSAPLSKELRAQYGIKALPIRRDDEVLVVR GSKKGQEGKISSVYRLKFAVQVDKVTKEKVNGASVPINLHPSKLVITKLHLDKDRKALIQ RKGGKLE

1376 bp, exon1: 501-633 intron1: 634-1116, exon2: YLR367W, 1117-1376 (SEQ ID NO 201) ACTTTTTGTCTGCTGCTGGTCGTTTGTCTTTTCGTTTTAAAATTGCGCTAGACAAGTAAAC AGGGATTGCTTAAGAATCAAAGTAGCTTAACTCTAAAGTATTATTTCCTCAGTTGTGGG CCCATGTGTTGGAGGAAGGAATATATTGAAATGTAAATGTTCTTAAGTTCGGTTGAACT TGGATATTGTTACAAGAGTTCTAGTCTTTGATACCATTTTTACGCAATTACAACCGCATT ATTTACCTTTTCATCTTCAGTTTTACGGTTCAGTTTATTCTGTTACGAAAGAACTATGGT GATTCAAAGGCGAAGTGCGTAGGATTGTAACTCCTATATCTTTAGGATACTTACAATTTT GTACTGTTTTCAAGACCACTGTAACCGATAATAAACCGGAGGACACATTTTAACCCACTA TTTTTTCAGAAGATCAGATGCGAGAGCTCGAAGCATAAGTATAATACTAACGTTTCAAA ACATAGTAATTAGGTAAAAAATGACTCGCTCTTCCGTTTTAGCTGATGCTTTGAATGCCA TTAATAACGCCGAAAAGACCGGTAAACGTCAGGTTCTATTGAGACCTTCTTCCAAGGTTA TCATCAAGTTTTTACAAGTTATGCAAAAGCATGGTATGTTCCAACTATTTTTCAATATTT TCACATGTGTTTCAATTTCTGCTTATTTTTAAATGTTACCACGAGGTTTGTCCAAGTTCA ATGTTGCGCAACTCTAACGAAGAAATAATTATTGCCATTGTTTTTTACTCCGGGCTGATA ACTAGATGGTGTGATCGGGCAGTATACTAATTTATACTGGACAAAGACTCGTAAAAGATG TTCTTTGTGCTTAGTCCCATACTGTTTTTTAAGTGTCCGGGATATTTAATCCCATGTGGA AATGCTTCTTACACGGTTATGGATTACACCTCATGTGTAGCTACTATATCCATTACCGTT TACTTTTCCTCAAAATCTCACTCTTAAAATTTTCAATGGCAAAATTCTTCCGCACAACTT AGACAACATTTTCTTGTTTTTTATGAAGTAAGCAAAAATTTCGAATCAACAACGCTCCAT GAGATTCTTCAATACTAACATTTACTCCTTATTTAGGTTACATTGGCGAATTCGAATACA TTGACGACCACAGATCTGGTAAGATTGTCGTCCAACTGAACGGTAGATTGAACAAATGTG GTGTTATTTCCCCAAGATTTAACGTTAAGATTGGTGACATTGAAAAATGGACCGCCAACT TATTGCCAGCCAGACAATTCGGTTACGTTATTTTGACTACTTCTGCGGGTATTATGGACC ATGAGGAAGCTAGAAGAAAGCACGTTTCCGGTAAAATCTTGGGTTTTGTCTATTAA

YLR367W, 130 aa (SEQ ID NO 202) MTRSSVLADALNAINNAEKTGKRQVLLRPSSKVIIKFLQVMQKHGYIGEFEYIDDHRSGK IVVQLNGRLNKCGVISPRFNVKIGDIEKWTANLLPARQFGYVILTTSAGIMDHEEARRKH VSGKILGFVY

YLR393W, 1340 bp, CDS: 501-1340 (SEQ ID NO 203) CCCTCAACCCGCATTTTGCTGAGAATTTTCACCAAGGCCCTAGGTGATATTAGATTCCAC CTGACTAATTGCATTACAGCCGACCCAAGGCAATATCAGTTTAATAAAATATCATGTATC TCACCCTCTTCTTGGTATTAGTAAAGAGACGCCTGATCTTGTAACAGTGGTGAAGATTGT **ACTAGAGCAGAATCAAGAATTTAAAAAGTGTAAAGGCAAGGCAGAGGCGATGTACATAAA** ACTTCGAAGTAAGAAATATTTAATAGTTCTCGCCACATCACTATGCAGCTATATAAAAAC TACTATAAACGTTTGTTTTGTTCCTTACGCACAATATCCTTGCCTAGAAATCGTTTTTGA **AATTTAAATTTTTATTACCATTTATTTGATTCGCCTTCAGAAAAATATGGAAGAGTGCAT** ATTTAAAAAGGACTATTTCAGCATATAGTAAAAGTCAGGTTATTTGTTTATTTGCGATAT CAGAGTAACTTAAACTATGCAGGGCACTTTTAAAAGGTTTTACCATCCCACGCTTA CGCGGATGTCCTTCTTGGATAAATTCCTCAAGCCTATGATGGCAACGGCTTCCCCAAAGG **AATACCAGATCAAACAACTGGTCAAGCCAATAGGCTTAACACAAGCACCAAGGAAAAGCA** CCAAATACTCCCAGGGGAACTCTTTGAGGGATATGTTTGATTCGGAAAAGACAAACCACA GAGTTAAAGAGTTGGCCGTTGAATTCAGCAAATCTGGACTTTATGACGTGCAAGTCTTCC AAAAGACAAAGGGGAAATTGTTTATAGCTCCAGTTTCATATTGGAAAGAAGATAAAGCTT TGTTTTTTCCTCATTTGATAGGAACGGCAATGGATGGTACGAAACAACAGAATATCGAGG ATATGTTAAGGGGTAAAACCAGTATAGTGAGGTTATTTAGTACAGCATCTGGCGATAAGT TGAGTAGTTCATACTTCCAAGGAATCGTAGACGATAACAAAAAAACTGACTACTTGACTG AAGCTGATGCGCGTTTAAGTTTAAATGACAGTAACGTCCAAATCATCGAGGTCAATCTTG TAGAAAACGCTGTGAAAAGTGCTCTAGTGAAAACGCTTGCTCGTTGGGCCAATCGCGTTC CATCCTGGCGCCAGCCATTTTATTTCGAATGTTCTAGAGGCCAATGGCCATTTTCCGTCA TAAAAATTAGGTGGGCAGCTTGCGGGGAGGCTACTCCATCTGAAAAGGAAGCATTGTGGA **AGTTTGCCAAACGTCTGTGA**

YLR393W, 279 aa (SEQ ID NO 204)
MQGTFKRFYHPTLTRMSFLDKFLKPMMATASPKEYQIKQLVKPIGLTQAPRKSTKYSQGN
SLRDMFDSEKTNHRVKELAVEFSKSGLYDVQVFQKTKGKLFIAPVSYWKEDKALFFPHLI
GTAMDGTKQQNIEDMLRGKTSIVRLFSTASGDKLSSSYFQGIVDDNKKTDYLTEADARLS
LNDSNVQIIEVNLVENAVKSALVKTLARWANRVPSWRQPFYFECSRGQWPFSVREELFCN
NVFSGYVFLVDQQLKIRWAACGEATPSEKEALWKFAKRL

YLR423C, 1754 bp, CDS: 501-1754 (SEQ ID NO 205) TTCTATTGGTGTAGTTATACCAGAACCATCCTTCCCAAGGCCTTTTCCCGCAACATATCC CATACTCGAAAGTAACTTCGCACCAATACCATATGTCTTCGTTAATTTTGAGATCGTTGG GGCATTGCCGCTACTAGTTTTCAAGGCATCATTAGTGTATGTCATGTCACTATTCATGCT TGAATTATTATCTTCCTCATCGCTATAATTATAGGAATCGATTCTTCTTTTTTTGAAAAA GAACTTTTTATCTGTGTTGGAGTCCGAATCCTCCATGTTTTGGCGTACTGAAGGCTTAAG TTCTTCGACCTCTCTCGGTTGTACTATTTCGAAATTTTTGGATTTTTGTTATTGTTTTGAC ATAATGTAAATACTAGATGCGCGCTCTAAGGCCTCAGTATTAAAAATTGCAAGATATCCC TAACTTGATAATTATTTGAAAGTCGCATAACGTACGATAAATTCGATACTGCGAGGATAT TATCAACGTATTTAACACCTATGAACGAAGCAGATGTTACAAAATTTGTTAATAATGCCA GGAAAACGCTGACCGATGCTCAACTTTTATGTTCAAGTGCTAATTTAAGGATTGTAGATA TTAAGAAAAATTGTCATCTTGGCAGTTGAGTATTTCAAAACTCAATTTTCTAATAGTTG TAATCCAGAAACAATGGAATCAAGCTGTCTTAGTGGTCTTAGTTGATGAGATGAAGTACT GGCAATATGAAATCACTTCTAAAGTACAAAGGTTGGATGGTATAGTAAATGAATTGAGCA TATCAGAAAAAGATGATACCGATCCCTCTAAACTAGGAGATTACATCTCGAGAGACAACG TTAACTTATTGAATGACAAACTGAAAGAAGTGCCAGTAATTGAGCGTCAAATTGAAAACA TGACGGACGTAACTCAAAAATTCCAAAGTAAATTTGGTATAGATAACCTGATGGAAACAA ATGTTGCAGAGCAGTTTAGCAGGGAACTAACGGACCTTGAAAAAGATTTAGCAGAGATAA TGAATTCATTGACACAGCACTTTGATAAGACATTGCTGTTACAAGATAAAAAATTGATA ACGATGAACGTGAGGAGCTGTTTAAGGTGGTACAAGGCGACGACAAAGAACTATACAACA TTTTCAAAACTCTGCATGAGGTAATTGATGACGTGGACAAAACAATTCTTAACTTGGGTC

AATTTTTGCAGGCAAAAATAAAGGAAAAGACAGAACTACACAGCGAAGTTTCTGAAATAA
TAAACGATTTCAATAGAAATTTGGAATATCTTTAATCTTTTAAAGATATTTCCAATCTGA
TTGATAGCTTCAAAAAATTCCTGTACACAAGATATTCAAACAACTAAGGAACTTTGTGAAT
TTTATGATAATTTTGAAGAAAGCTACGGTAACTTAGTTCTAGAAGCAAAGAGGAGAAAGG
ATGTGGCAAACAGAATGAAAACTATATTGAAAGATTTTGTGAAAAGCAGTTGCAGAATTTAG
ATGCTCAGGACCAGGAAGAACGTCAGAATTTTATAGCGGAAAATGGAACTTATCTTCCTG
AGACAATCTGGCCCGGTAAAATTGACGATTTTTCTTCCTGTACACTTTAAATTACAACG
TGAAGAATCCTTAG

YLR423C, 417 aa (SEQ ID NO 206)
MNEADVTKFVNNARKTLTDAQLLCSSANLRIVDIKKKLSSWQLSISKLNFLIVGLRQQGK
FLYTILKEGIGTKLIQKQWNQAVLVVLVDEMKYWQYEITSKVQRLDGIVNELSISEKDDT
DPSKLGDYISRDNVNLLNDKLKEVPVIERQIENIKLQYENMVRKVNKELIDTKLTDVTQK
FQSKFGIDNLMETNVAEQFSRELTDLEKDLAEIMNSLTQHFDKTLLLQDKKIDNDEREEL
FKVVQGDDKELYNIFKTLHEVIDDVDKTILNLGQFLQAKIKEKTELHSEVSEIINDFNRN
LEYLLIFKDISNLIDSFKNSCTQDIQTTKELCEFYDNFEESYGNLVLEAKRRKDVANRMK
TILKDCEKQLQNLDAQDQEERQNFIAENGTYLPETIWPGKIDDFSSLYTLNYNVKNP

1342 bp, exon1: 501-547, intron1: 548-948, exon2: 949-1342 (SEQ ID NO 207) ATCTGTAAATAATAAGCCCATGAAATATCAATCTCACAATGAAAGAATTGTATAATTCAG AATGATTTGACGTAAAAGCAAGTCTCATTCAAGAAACTGTAAAATCCGTACACACTACTG AATTTTACATCCATACATTTTTTTGAAATTTCATGTTTTTTTGAAAAATTGGAAAAGGGC TAAATTATCCGTCGGGGTGTCCTCCTAGCTCGGCTCAACCTAGGCAAATGCGTTTACTGG GGCCATCCAAGCTCATCCTTCCAGAGATTCGCCTTTCAGAGGCAAAGAACTCGTCTCCGC AGGCCTCTTGTTCCGGGAGGAGGAGAATTCTTGCGCGGAAACTGGTTGATGCCTGGGCTA TGGTAATTCTGACACCTTTGCTATCCTAACTGGAAAAGGTCCTTAGTAATAACAATATCA GGTACTTTAACATTGTTAAAGATATACTATTAGTGAAAAACCGATCTTACGAAAAGCCAA TTTTACGGTATGTTTTACGAGTACAGTGCAGATATGTTGAGAGAGTTTCACATTACATGG GATAATAGCTTAATATTGCGATTGAAAATATGTGAGTGCACTCCGATGGAATAATAAACG TCACGGGTTACCAAATACGAGGCCGAATTAACTCTACGCTACTATAAAAATTATCACTAG ATTTTAAAGTAATACACAGTTTATTGGAAAATACAATATGACTCAATGCGAATTTAAA **AATTTCAGTCAATACAGCTTGACAAATTCATATTTATCGTCCCTCCATGTTCGTACGCCA** TTCCAAAATGATGCGCCATGTTGAAAATTTCTCGAAGAACCTAGCAGTGGTGTGAAATAA ATTACTAACAATAAGATGTACAATTTTTTGTGCGCCCATTACAATCAGTTTGTTGAACAC CAATGTCGATGGTAACATTAAAATTGTTTACGCTTTTGACCACTATTAAGGGTGTTGGTCG TCGTTACTCCAACTTGGTCTGTAAGAAGGCTGATGTTGATTTGCACAAGAGAGCTGGTGA ATTGACCCAAGAAGAATTGGAAAGAATTGTCCAAATCATGCAAAACCCAACTCATTACAA GATCCCAGCCTGGTTCTTAAACCGTCAAAACGACATTACTGATGGTAAGGACTACCACAC TTTGGCTAACAACGTCGAATCCAAGTTGAGAGATGACTTGGAAAGATTAAAGAAGATCAG AGCCCACCGTGGTATTAGACACTTCTGGGGTTTACGTGTTAGAGGTCAACACCAAGAC CACTGGTAGAAGAAGAGCTTAA

YML026C, 146 aa (SEQ ID NO 208) MSLVVQEQGSFQHILRLLNTNVDGNIKIVYALTTIKGVGRRYSNLVCKKADVDLHKRAGE LTQEELERIVQIMQNPTHYKIPAWFLNRQNDITDGKDYHTLANNVESKLRDDLERLKKIR AHRGIRHFWGLRVRGQHTKTTGRRRA

YML063W, 255 aa (SEQ ID NO 210)
MAVGKNKRLSRGKKGLKKKVVDPFTRKEWFDIKAPSTFENRNVGKTLVNKSTGLKNASDA
LKGRVVEVCLADLQGSEDHSFRKVKLRVDEVQGKNLLTNFHGMDFTTDKLRSMVRKWQTL
IEANVTVKTSDDYVLRIFAIAFTRKQANQVKRHSYAQSSHIRAIRKVISEILTREVQNST
LAQLTSKLIPEVINKEIENATKDIFPLQNIHVRKVKLLKQPKFDVGALMALHGEGSGEEK
GKKVSGFKDEVLETV

YML128C, 2042 bp, CDS: 501-2042 (SEQ ID NO 211) TTAATAGGGTTAGCCACCATTGTCTCGAACATGTTCACAGGCTCGGAGCTTGTGGCGGGT GCCTCGCTTACTGGAGTACCATTTAGCGGTGTGTTTGAAGCTAACGAGTTCATCTTCAAT CTTTATTTCCACTTCTTTACAAGCTTTCTGCCTTTCTCTATGACGTCTTTCCCAAAACAC TACCTCTTGACACGACTTGTTTTTCGTTTTTCTCTAAGAATATCACTATTTTCACTTT TTTCACCTTTTCCACCATTACGTCGGTAAGCAACAGCATTACGCCGGCCTCACCTTAGAG GGGAAGAATAAGGGATCTTTGGAACTGAAGGAAAATAAGGGAGGAGGGAAACAAGGAG GCGGTGAAAGGGGATCGACAGGGTATTTAAAGCCACTCATGGAGTCGTATTCCTAGCATG ATTAGATTACCGGAGTTTAGAAGAGGATCTGCAATAGAAGAGGAGACAACTACAAAAGAA CTGTTAATTAAGAGAAGAAGATGAAGCAATTCAAGTTGGTTAATGCGGTTTCCGCATCAT TTGTGCTTATTGGCTTAGTGTTGGCCAATTCAGATTCAGTGTTCGACAAGTGGACGCAGG AAGACCTGGCCGATTATTTACGTGATAATAAGAAGAGCTTGGAAAAGTACGCTACAGACT CCATTGAGGACTTGAAAACGGAGGCATCGCAGGTATGGGACAAACACGCGCAGCCCAAAC CATGGTGGCAGGTGTGGTCTAGTGACAGCAGTAGCGTGAGCAACAGTAACCCCGGATGGT TTGGTTATACTGGTTCTTCGGATCACCCAGTTTCTGACTGGCTCTTTGACACCTGGTCCA CAGACAGTCTACGTAACTTCTTGAAGAAAAACGGCGTGGATGTTGACGACGCTAAGGCTT CCAAGGACTCGCTGGTGAAGACTGCTAAGGAGACTTCAACAAGATTTCCAAATCTTTGA AGTCGTCGGGATACTATCCTTCTAGCTCTTACTTTGATAGCTGGTCAACCAAAGATTTGC AAAACTGGTTGAATGACAATGGTATCGACTACGACAAGGCAGTTCAAAGCAAGGACGAGC TAGTTCAGAAAGTCAAGGAAAACATCTACCGAACTTCAGAAAAGGCAGAACAGCAGCGTC TGGGTTTGCTAGAAAGCTTGGATTTGGCTCACCAACAATATTAGACACATCGGGACAAA ACAAGGTCAATATTGACAAGAACATGGCCAAGAAACACGACTATTTGGTTAGAATGGCCA AAGAAAATTCTGCCAATTTGAAAGATGATATCTACTGGTACCTGGACTATATGAAAAGAG AGTCTTCTCCATTTTTGACCAAGACCCCAGAATACGTTGGTTCCGTTTGGGACTCTTCTA AAAATTTCCTCACAAATTTGTACTCCAAGTTCAGAGGTAAGACTGACAATGTGATCAATG ATACTTTTTTGGTTGGCCTAGACTCTTGGCCAAAGGACAAATTGAAAATGTTTTTAGATG CTCGTGGTATTAAGTACTCAATGCTGTCTACTGAACATCAATTGAGAGAATTAGTCAAAA AATCCAGAAACGAAAAACTCAAGATCCTGCCAAAAGACTACCAAAAATACTTTGACAACA GTAACTGGTCTTTGGATGACATAAAGGGTTGGTTTGCTGACAAAAAGGACGACTTCCAAG ATTCTCAGACTTACTCCACAATTATGCAGGATTTTGACAAGGTTTCCAAAAACACAAATG ATGCTAAGGACCAAATCGCTAAGACCTGGTCAAATACCTTTCAGAGCTGGTCTCAAGAAG ACCTATTGCAGTACCTAAAATCATTCGGTGTTCCGGTTAAACAGACTTCTACGAAGGACG ACTTAATCAACTTGGCCAAGCAGAATACGCAATGGTTGTTCGGCACTGTTAAGGAGCCTG CTTACAAGAGGTACCTACATAACGTTAAAAACTGGTCGAAAAGCATATTAGGGTTCAACT

YML128C, 513 aa (SEQ ID NO 212) MKQFKLVNAVSASFVLIGLVLANSDSVFDKWTQEDLADYLRDNKKSLEKYATDSIEDLKT EASQVWDKHAQPKPWWQVWSSDSSSVSNSNPGWFGYTGSSDHPVSDWLFDTWSTDSLRNF LKKNGVDVDDAKASKDSLVKTAKENFNKISKSLKSSGYYPSSSYFDSWSTKDLQNWLNDN GIDYDKAVQSKDELVQKVKENIYRTSEKAEQQRLGLLESLDLAHQQILDTSGQIKDTVFD KWSSDQLTNWLESHKVNIDKNMAKKHDYLVRMAKENSANLKDDIYWYLDYMKRESSPFLT KTPEYVGSVWDSSKNFLTNLYSKFRGKTDNVINDTFLVGLDSWPKDKLKMFLDARGIKYS MLSTEHQLRELVKKSRNEKLKILPKDYQKYFDNSNWSLDDIKGWFADKKDDFQDSQTYST IMQDFDKVSKNTNDAKDQIAKTWSNTFQSWSQEDLLQYLKSFGVPVKQTSTKDDLINLAK QNTQWLFGTVKEPAYKRYLHNVKNWSKSILGFN

YML130C, 2192 bp, CDS: 501-2192 (SEQ ID NO 213) ACGAGATCATTTTCTTATCTATCTATTGAGTAATGCTTACTTTTCATATTTTCAATGAAC AATAGGATATGTAGGAGAATTGATATATTCACTGCGTATCAGAGAAAAGGTCTACTGACA TTTTATGGCAAATGTATTCTACACAAATCGAGAATACCACAGACAATGGTACAAGACATA CACAAAGAGAAGACTGTTCTAATTAAACAAATAATATTGAGCTACCTGCTAAGTATGTCC TTTTCCCTTTGTCCTTTGGTTTCTCTTATAGAAGACCCTGGAAATTTTTCGCATTTTTCC GGCTTTGGGCGTTAGTAAGAACAAAAAGAAAGAAGAAGAACAAAAAAGAAACGATACGGA GTACGTGTCATAAAAACTTGTTCAATCATCCTTGAAGCTAAGTATAAAGAGCTTGAAAAG GTTTACCACTTAAACTGGTTATACTATTTCAAGAGTGTAAACATTTTATTGCATATACCA CAGTAACGTGCAGGTAAAACATGAGATTAAGAACCGCCATTGCCACACTGTGCCTCACGG CTTTTACATCTGCAACTTCAAACAATAGCTACATCGCCACCGACCAAACACAAAATGCCT TTAATGACACTCACTTTTGTAAGGTCGACAGGAATGATCACGTTAGTCCCAGTTGTAACG TAACATTCAATGAATTAAATGCCATAAATGAAAACATTAGAGATGATCTTTCGGCGTTAT TAAAATCTGATTTCTTCAAATACTTTCGGCTGGATTTATACAAGCAATGTTCATTTTGGG ACGCCAACGATGGTCTGTGCTTAAACCGCGCTTGCTCTGTTGATGTCGTAGAGGACTGGG ATACACTGCCTGAGTACTGGCAGCCTGAGATCTTGGGTAGTTTCAATAATGATACAATGA AGGAAGCGGATGATGACGAATGTAAGTTCTTAGATCAACTATGTCAAACCAGTA AAAAACCTGTAGATATCGAAGACACCATCAACTACTGTGATGTAAATGACTTTAACGGTA AAAACGCCGTTCTGATTGATTTAACAGCAAATCCGGAACGATTTACAGGTTATGGTGGTA AGCAAGCTGGTCAAATTTGGTCTACTATCTACCAAGACAACTGTTTTACAATTGGCGAAA CTGGTGAATCATTGGCCAAAGATGCATTTTATAGACTTGTATCCGGTTTCCATGCCTCTA TCGGTACTCACTTATCAAAGGAATATTTGAACACGAAAACTGGTAAATGGGAGCCCAATC TGGATTTGTTTATGGCAAGAATCGGGAACTTTCCTGATAGAGTGACAAACATGTATTTCA ATTATGCTGTTGTAGCTAAGGCTCTCTGGAAAATTCAACCATATTTACCAGAATTTTCAT TCTGTGATCTAGTCAATAAAGAAATCAAAAACAAAATGGATAACGTTATTTCCCAGCTGG ACACAAAAATTTTTAACGAAGACTTAGTTTTTGCCAACGACCTAAGTTTGACTTTGAAGG ACGAATTCAGATCTCGCTTCAAGAATGTCACGAAGATTATGGATTGTGTGCAATGTGATA GATGTAGATTGTGGGGCAAAATTCAAACTACCGGTTACGCAACTGCCTTGAAAATTTTGT TTGAAATCAACGACGCTGATGAATTCACCAAACAACATATTGTTGGTAAGTTAACCAAAT ATGAGTTGATTGCACTATTACAGACTTTCGGTAGATTATCTGAATCTATTGAATCTGTTA ACATGTTCGAAAAAATGTACGGGAAAAGGTTAAACGGTTCTGAAAACAGGTTAAGCTCAT TAGAGAACATCAATTCCACTAAAGAAGGAAAGAAAAAGACTAACAATTCTCAATCACATG TATTTGATGATTAAAAATGCCCAAAGCAGAAATAGTTCCAAGGCCCTCTAACGGTACAG TAAATAAATGGAAGAAAGCTTGGAATACTGAAGTTAACAACGTTTTAGAAGCATTCAGAT TTATTTATAGAAGCTATTTGGATTTACCCAGGAACATCTGGGAATTATCTTTGATGAAGG TATACAAATTTTGGAATAAATTCATCGGTGTTGCTGATTACGTTAGTGAGGAGACACGAG AGCCTATTTCCTATAAGCTAGATATACAATAA

YML130C, 563 aa (SEQ ID NO 214)
MRLRTAIATLCLTAFTSATSNNSYIATDQTQNAFNDTHFCKVDRNDHVSPSCNVTFNELN
AINENIRDDLSALLKSDFFKYFRLDLYKQCSFWDANDGLCLNRACSVDVVEDWDTLPEYW
QPEILGSFNNDTMKEADDSDDECKFLDQLCQTSKKPVDIEDTINYCDVNDFNGKNAVLID
LTANPERFTGYGGKQAGQIWSTIYQDNCFTIGETGESLAKDAFYRLVSGFHASIGTHLSK
EYLNTKTGKWEPNLDLFMARIGNFPDRVTNMYFNYAVVAKALWKIQPYLPEFSFCDLVNK
EIKNKMDNVISQLDTKIFNEDLVFANDLSLTLKDEFRSRFKNVTKIMDCVQCDRCRLWGK
IQTTGYATALKILFEINDADEFTKQHIVGKLTKYELIALLQTFGRLSESIESVNMFEKMY
GKRLNGSENRLSSFFQNNFFNILKEAGKSIRYTIENINSTKEGKKKTNNSQSHVFDDLKM
PKAEIVPRPSNGTVNKWKKAWNTEVNNVLEAFRFIYRSYLDLPRNIWELSLMKVYKFWNK
FIGVADYVSEETREPISYKLDIQ

YMR022W, 998 bp, CDS: 501-998 (SEQ ID NO 215)

AACAGTATTGGCTGTTGATTCATTGCGCTGCAGCAGTCACCTTCAATTTGTGCACCATTT TCGTATTCTGTACTTTGCGATGTAGAGTCTACTAAAATAGCGTCTCTGATAGCCATGGGT GAAGGTCTTCCTCTAGTTCTCACCTTAATTAGCATTCGGTGAGAATGCCTGCATGTTGAA GAGCGATGCCCTCTGATGCACGATGCACCGCATATTTGTTCCCATTAAATATTATCATC TCTGATAGAGCTTGAAGAACTTACCAGACTGTTTCAAGTTTAAAACAAGGCGCCTCATCG CATCTACCTCACGAAGATGCAGCAGCTTATTGTCTCGAGATCCTTCTTATAACTCCTTTT CGCCATTACCCGAAAACGAGATTACAGCCTCTAAACCAAGAGCTCGAAAAGCGCCAAAGT AAACTCTGGCGTTTAGCGTACGAAGGAGATTATCCTAAAAGGAACTTCCCTAGTAATAGT GTAATTTGGAAGGGCATAGCATGTCGAAAACCGCTCAGAAACGTCTCCTCAAGGAGCTTC **AACAGTTAATTAAAGATTCTCCACCTGGTATAGTGGCTGGTCCCAAATCGGAGAATAACA** TATTCATTTGGGACTGCCTAATTCAAGGGCCTCCAGATACGCCATACGCTGATGGTGTTT CACCCAGCATACTACATCCAAATATTTATCCAAATGGGGAAGTGTGCATATCCATTCTAC ACTCCCTGGTGATGATCCTAACATGTACGAATTAGCGGAAGAAGATGGTCGCCAGTGC GTGGTGCCAACATTGATGCTTGCATCTTGTGGAGAGATAATAGACCTGAATTTGAGAGAC AGGTAAAGTTATCCATTTTGAAATCATTAGGATTCTGA

YMR022W, 165 aa (SEQ ID NO 216) MSKTAQKRLLKELQQLIKDSPPGIVAGPKSENNIFIWDCLIQGPPDTPYADGVFNAKLEF PKDYPLSPPKLTFTPSILHPNIYPNGEVCISILHSPGDDPNMYELAEERWSPVQSVEKIL LSVMSMLSEPNIESGANIDACILWRDNRPEFEROVKLSILKSLGF

YMR118C, 1091 bp, CDS: 501-1091 (SEQ ID NO 217) GTCCTTCCGCTTTATATGTTTCGTTATCCTATCACATTATCAAATGACTTTGTGCCACTG TGTTTTGACAAAATTACTGTAATATAATCAATAGTATTTACATGTTTGTACCAGAAGTAC TTGCATCGCATCCAGTTCTCATGCAATATAGTTGTATACCATGTCGTTGAAAGGAACCAG AGTAAACACTTCTACCAGTATTTCTTTACGGTTCGGATCAAAACCATCACTCATTCGGTC ATTCTTACCGTACGATAAACCAAATTACAAGGAAAAGTATCCCTAATTAGAGATCACTGC ATCCGTAATAGTTTTTTTTCTATTTTGGACTTTTGTAAAAAAGGGATTAGGGATACGTTG CTCATAAAAAATTGACGAAGATTTTAGATAATGGCAAATAAAAATGAAATAGTATCAAT ATACCGAAAAATTAATCACACTCAATGCGACTGTGATAGCTGATAAGTGGAGCTCAGAAA TATTCAGAAGCGTAAGAATAATGAAAGCAACCATTCAAAGAGTAACATCTGTATTTGGAG TCTCTAATGGCAGAATGGACCTTTTTTCCAAAGAATTCCACAATGGCCGCGTATCCAAAT CTGATCTTTGGTCAAGCAACAAGGAAGAGGAGCTCTTAGTATCTCAAAGGAAAAAAAGAC CGATCTCTCCTCATTTAACTGTTTACGAACCTGAAATGAGCTGGTATCTTTCCTCTTTAC ATCGTATATCTGGCGTTTTACTGGCTCTTGGATTCTATGCTTTCACAATTACTTTGGGTG TGACGACAATAATGGGAATGGATACGACTTTTCAGGATCTAAACAAGTGGTATCACGAAA AGATGCCTAAGTGGTCCCAATGGGTGGCCAAAGGCTCTGCAGCATATCTGTTTGCATTCC ATTTTGGTAACGGTATAAGGCATCTCATCTGGGATATGGGCTACGAATTGACCAACCGTG GGGTTATAAAAACCGGATCAATCGTTTTAGCCGGCACACTCGTCTTAGGAACGTATTTAC TGGCTCAGTAA

YMR118C, 196 aa (SEQ ID NO 218) MKATIQRVTSVFGVPRASVFVPRISTPFILHNYISNGRMDLFSKEFHNGRVSKSDLWSSN KEEELLVSQRKKRPISPHLTVYEPEMSWYLSSLHRISGVLLALGFYAFTITLGVTTIMGM DTTFQDLNKWYHEKMPKWSQWVAKGSAAYLFAFHFGNGIRHLIWDMGYELTNRGVIKTGS IVLAGTLVLGTYLLAQ

TATCATATTCCTAAACAAAAATGTACAGCGAATATAAAGCCAGCGTCAGTGTCTTCCTGG
AAGGTTGCGCAACTAAAGAAGTTGAAATTAAAATGGCAAGCGCTACATTTTCATCCATTT
TCACTCATCAGATGTCCAAGATTTTCGAAAAATAAATATTCTCATTTTTCTCTCAATGAA
ATAATTGTTACTAACATTGAATTTCCTCGTAACTAATTGCATTACTTCTTTAGACTTTTG
GTAAGAAGAAATCAGCTACTGCTGTTGCCCATGTCAAGGCCGGTAAGGGTTTGATCAAGG
TTAATGGTTCTCCAATCACTTTGGTTGAACCAGAAATCTTAAGATTCAAGGTTTACGAAC
CATTATTGTTAGTTGGTTTGGACAAATTCTCCAACATCGATATTAGAGTTAGAGTTACTTG
GTGGTGGTCATGTTTCCCAAGTTTACGCCATCAGACAAGCTATTGCTAAAGGTTTAGTTG
CTTACCATCAAAAATATGTCGATGAACAATCCAAGAACCAGAACCAAAGAAATTCGGTG
GTAAGGGTGCTCGTTCCAGATTCCAAAAATCTTACCGTTAA

YMR143W, 143 aa (SEQ ID NO 220) MYSEYKASTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF SNIDIRVRVTGGGHVSQVYAIRQAIAKGLVAYHQKYVDEQSKNELKKAFTSYDRTLLIAD SRRPEPKKFGGKGARSRFQKSYR

YMR174C, 707 bp, CDS: 501-707 (SEQ ID NO 221)
GTCCCATCATTCTTACACCTCGTACTGTATTCATGATCATCTATCCATTTTACATACCG
CTCCCTTTAAGATACGTTTATTCGTAACTCCCATTTACCAATCACTATGAGCCGTCCACG
TTTCCAAAAAAACCTAAACATATGATGCAAACCTCCAATGAGACTCAACGTAACATGCAA
GTAAATACAGAAGGTTAAGAGATAGTTGTCTTAAAGGGGTACCGAAAGCATTTAGGGGAG
GCTTAAGGGAGGGTGCCGATCCTATGAAGTATTAATACGTAATGCCAAAAGGAATTGTTG
AACATCTGAAGTGGATAGATTAATCGTACAGTAATCGTACAGTACTATGTCTTACTGATG
TCGGGAATCTCAGGGGGGACCGCCCCCGGCTAGAATTATCTATATAACGGTAAAAAGAAT
AAAACTCTATTCTAGTTCTCGCCATTTACCTTGACTTTAATGAACCAATAAAAGAAATTT
CTACAACCAAGACATCCAGAATGAATACAGACCAACAAAAAGTGAGCGAAATATTTCAGA
GCTCAAAGGAAAAATTGCAGGGCGATGCAAAAGGTAGTGACGCTTTTAAGAAAATTG
CTAGTCAAGACAAGGACGGCAAGACTACCGATGCTGATGAAAAGTGAAAAACACAACTATC
AAGAGCAATACAACAAGCTCAAAGGGGCGGGCATAAGAAGGAGTAG

YMR174C, 68 aa (SEQ ID NO 222) MNTDQQKVSEIFQSSKEKLQGDAKVVSDAFKKMASQDKDGKTTDADESEKHNYQEQYNKL KGAGHKKE

YMR191W, 1877 bp, CDS: 501-1877 (SEQ ID NO 223) GGTTCGATACAACACTTGTGCTGGCTGGTATATCAACCATGGGTACGTCAGCATATTGAT TCGATGTGGCAGTGTACGAGAGCCATTCTGTATCGTTCGACAAAGTTTGCATGACTTCAT GTTGTTTCGTAGCAGTATTCGTTGGTCCAGATGCAGGAATGCTGGTTATAAAGTTTGTTG TTCCTGGTCCACATTCATCTTTGGATGGCGTTGTTGGTGGCGAATTTGTCTTAGGCCTTT TGTTCGCGATGTGCTTTTGGATAGCCTGGAATACGAAATCTTTGTCTTCCTGTAAAGTCG CCGTTTCCTTTAACCATTTGTGCTCCCTTCTTAAGTTATGTGACGGCTTCGTCACCATTA CCGCCTTGTGTGTACGTGTATGATTTTTTAAATATATACAACAATAATCTGTATTTTTTC AAATCCGAAATGTATCACCAATGATCACCCAGCCTGCTAAGTGCCCTCTATTGATCCGTA TATCAGCTTTTAGATCAGGCTCGAGTTTCTTGTTATATGTGCATTGCAAAAGCATAAACA AATCCTGGCAGCCGAAGCCGGCAATCCACTTCGAAACGCACGGCTGAACTATATAAATA TAAAGGACATGTGGAGAGAAGCTTCTCTTCCTTCACATTTCGCATTTCATGATCTAAAGT GGTTCTTTCACAATAGAAGAGCACCAACACGAAATATGGCTGTCGGTGGTAATAACTGGA GCATGTGGCTGCGAATGTCACGGGTCCACCTCAGGCAGATCACGAAGTCTCTGGACCGAA CGCTGATCAGTTTGAGCCATGGGAATTTTTCCCACCAATATAATCGCAATATTTTTGTCA CTTGGTGGAAGAGCCTATTTGAGGCTTCTACAGCTTTTAGGAGGGCAAGTGGTTTAACGG TATCTCCTCTCACGAGGAGGAATCGCAAGGTTTGACCATTTCAGACCTGTTCCCAATG TCAGTAAATTTGCTTCTTTTCCCAGAGTGCCCAAAGGAGCCCCAAGGGGCCTTTTTACCA ACTGGAATATGACTACATCAAAGAGATTATTAGGGCAGAGAGCTTATTCGACTTCCAGTA TCAAATTTACCCAAGAAGCCGTGAATAACATGACTATATCTTTGAGGTGTTTTTTCAACT CACTAGGCGGATTAAATCAGTGCTCCCACTCTAATTCCTGCAAAGCTTATCAGAATGCGT CTAATGTTACCTCTAAACAGGATCACGTCCAACCAGTTGCCCTTAAGAAGTTATCTCAAA AGGATATCAATTTCATTCGTAATTTAGAACTATTTAAGATAATGAAGACCCAGAATGAAG TCGTTGATGAAACAAGCGCATATTACATGGAAAAACCAGGTTCCTATATTGAATTTACCA TTTCAGAATTTAACGTTAATGGGACATTCTCCGCACCTTTGTCATTTTTAGATCCTTCTT
TGTTAGCGGATTTGGATGAAATGATTAGAAATTACAAATACGAATTAAAATCAATATACA
GTAGTGTTGACATGATCTTGCAGAATTATGGATCATTGCCGATAACTTTTCATCGAAATA
AGATTCGAATACATTTTCCAAACTCAACTGTGGTGGAAACAGAAAAACTAATTGCAGGTC
TGAATATTGCTACGGGTGTTATTTACGCAGATACGTCTCCCGATATCAGTCTAGAAGGTA
CAAATTTGAATGCTCTGGTTAATGTTGACAATTCAGGAAGCGTATGGTCTTTTGTTAAGG
AGCCCTCGTTTCCCTCTAGGAGCGCTTTTTCACCTATTTTATCAGATGCATCCTATGATA
CTTATGAATTGGTCTAG

YMR191W, 458 aa (SEQ ID NO 224)
MITQPAKCPLLIRISAFRSGSSFLLYVHCKSINKSWQPKPGNPLRNARLNYINIKDMWRE
ASLPSHFAFHDLKWFFHNRRAPTRNMAVGGNNWSMWLRMSRVHLRQITKSLDRTLISLSH
GNFSHQYNRNIFVTWWKSLFEASTAFRRASGLTVSPLTRRGIARFDHFRPVPNVSKFASF
PRVPKGAPRGLFTNWNMTTSKRLLGQRAYSTSSIKFTQEAVNNMTISLRCFFNSLGGLNQ
CSHSNSCKAYQNASNVTSKQDHVQPVALKKLSQKDINFIRNLELFKIMKTQNEVVDETSA
YYMEKPGSYIEFTISEFNVNGTFSAPLSFLDPSLLADLDEMIRNYKYELKSIYSSVDMIL
QNYGSLPITFHRNKIRIHFPNSTVVETEKLIAGLNIATGVIYADTSPDISLEGTNLNALV
NVDNSGSVWSFVKEPSFPSRSAFSPILSDASYDTYELV

YMR230W, 1228 bp, exon1: 501-552, intron1: 553-962, exon2: 963-1228 (SEQ ID NO 225) **ATCAAATATTGATCGAGTTCATATAAAGCTAAAGAGTAGGAAATATACCATCAATGGTGA** TATAATTTGGCTACGTTGTCTTCCGGTGTTTTTCAATTGATTTAAGTTACAACACTCAAA TCTGGGTAATTTGATCTTTTTTAATAATTATTTTAGTGACATATAGTTCTTAGAGTTCGC AGATTTATTTTGTCATTTTTTGGATCGGCGTCTTATAAAATCAAGACATAATACATCCGC ACATCGCGCATGTGTGGGTGTATATGCCCTTTTCACGATTTTTAAGTTGCGTCTCAAAAT AGTTTCCGAGTTGGAAGCCTGAGTTTTTCAAAACAATATAGGAATTAAAGGTATACGTCT TTGGATACATGTTATTTGAAATGGGGTAGAACTAGCACAACTGAAACCAAGAAAACACAG ACTTGTTTCAAGGTATGTTTGCATTTTTTAGGTGAAATATGCAGTGATATGCTCCGAAAT GGATAGCAAAGATGATAAATGAAAATACAATTAAATTGAACTTGAATATCATTAAAAGTG GTAGAAAACCGATTGTTTCAAAAAGATCTTTGTGGACAAGTACGGCAGTGCATGAATCCG AAAGAAAAGTGCAACCTAAGCAGAATTCCATTATTTCACGCGTCCATTTTTATAATGTTT GAACTTTTGAGTCCTTATAGAAATGCTAATATTATGATCAAAGCGATTATATCATTTACT ATCGTAAGAATATTATTACTAACAAGGAAGATCATTGAATTACGATCGCATATCGAAAT AGAAGGTGTTGTCGTCGCTAAGAAGGATTTCAACCAAGCTAAGCACGAAGAAATTGATAC CAAGAACTTGTATGTTATCAAGGCTTTGCAATCCTTGACTTCTAAGGGTTACGTTAAGAC TCAATTCTCATGGCAATACTACTATTACACTTTGACTGAAGAAGGTGTTGAATACTTGAG AGAATACTTGAACTTGCCTGAACACATTGTCCCAGGTACCTACATTCAAGAAAAGAAACCC ATCCCAAAGACCTCAAAGAAGATACTAA

YMR230W, 105 aa (SEQ ID NO 226) MLMPKQERNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS WQYYYYTLTEEGVEYLREYLNLPEHIVPGTYIQERNPSQRPQRRY

YNL054W, 3998 bp, CDS: 501-3998 (SEQ ID NO 227)
CCCTTCGCTAAATCATTAAGAGGTCATTCATGAAGTTAATTCAGCACCAAAGTTGGACTG
TTAGACACGAGATACACATTGCAGTCCAAATGTGCAGATTTTTCAGATAATTGTCGTCGC
ACAAGACTGCCCCTCCCGTCCTCAGACAGACACAAAATTAGATTTTACGTTTACATAAAG
ATGTACATAACTTGAAAAAACGTTAATCCCTCTTAAATTTAGACCTTGTAAGTCTTCCTG
GCCACTCTTTGTGATATATTGTAGTGCAATATATTGATTCGTTCTTCTTATTTCTTTGTT
CTTAGGCATTTCCGCTTTAGAAAATTCGTTGGGTGGTTTCTGCGACGGGTATCCCCTTCG
ATTTTGCATAATGATCTTCAATTCTACAACTAAAATCAAGTAGATACAGGAAAATATTCC
ATAAATTATAGTGTAAAATCGCCCTGTATACACCTTATCGTTTCATCTCAGGCAAGTTAAA
GCATTTGGGAAACGTGCTAGATGACAGAAGAAGAATAAACAGTAATGTAGAGACAGAAA
CAGTTGAGGCACCCGTGGCAAATAATCTTTTATTGTCGAATAACAGTAATGTAGTAGCAC
CTAATCCTTCTATTCCCTCTGCCTCCACATCTACCTCTCCGCTACACAGGGAAATAGTTG
ATGATTCTGTCGCTACTGCTAACACCACCAGCAACGTTGTACAGCATAATTTTGCCCACCA

TAGATAACAATTTAATGGATTCCGATGCCACGTCACATAATCAAGATCATTGGCATTCAG ACATAAACAGGGCAGGAACATCAATGTCAACGAGTGATATCCCAACAGATTTACATTTAG AACATATCGGCTCTGTTTCATCAACTAATAATAATAGTAACAATGCCCTAATCAACCACA ACCCTCTGTCATCTCTCCAATCCGTCATCTTCATTACGAAACAAGAAGAGCTCTT TGTTGGTAGCTTCTAACCCTGCGTTTGCTTCAGATGTTGAACTCTCGAAGAAGAAACCTG CCGTCATCTCCAATAATATGCCTACAAGTAACATTGCCCTTTATCAAACAGCGAGATCGG CGAATATTCATGGTCCATCATCAACTTCCGCATCTAAAGCGTTCAGAAAGGCTTCGGCCT TCTCCAATAACACGGCACCCAGCACTAGTAATAACATCGGCTCGAATACACCTCCAGCTC CTCTTTTACCTCTACCTTCACTATCACAACAAAATAAGCCAAAAATAATAGAGAGGCCCA CAATGCACGTCACTAATTCAAGAGAAATACTTTTAGGTGAAAACCTGTTAGATGATACAA AGGCGAAGAATGCTCCCGCGAATTCAACCACACGCATAATGGTCCAGTAGCAAATGATG GGCTGCGTATACCGAATCACTCGAACGCAGATGATAATGAAAATAACAACAAAATGAAGA AGAATAAAAACATTAATAGTGGGAAAAATGAACGTAATGATGACACCAGCAAAATATGCA CTACATCTACAAAACAGCGCCTTCAACCGCACCTTTGGGCAGTACAGACAATACTCAGG CTCTCACTGCTAGTGTCTCCAGCAGTAATGCTGACAATCACAATAATAACAAGAAGAAAA CCAGCAGCAACAACGGCAATAACAGTAATAGTGCATCCAATAAAACCAATGCCGATA TCAAGAATTCTAACGCCGACTTGAGCGCTTCTACCTTAACAATAATGCAATAAATGACG ACTCACATGAGAGTAATTCAGAAAAACCAACAAAGGCGGATTTTTTCGCTGCAAGGCTGG CTACAGCTGTAGGTGAAAATGAAATTAGTGATTCTGAGGAAACATTTGTTTATGAATCGG AACAGCAACCTCCAAAACAACAGCAACAGCAACAAAATCATGGAATAACCTCAAAGATAA GCGCCCCATTGCTAAACAATAACAAAAAATTATTAAGCCGACTGAAAAATTCAAGACATA TTAGCACTGGTGCCATATTGAATAACACAATCGCGACTATAAGCACAAATCCGAACTTGA ATTCTAATGTGATGCAGAACAATAACAATCTGATGTCGGGACACAATCACCTGGACGAGT TGAGCAGTATAAAACAGGAGCCACCGCATCAATTGCAGCAGCAGCAACCACCAATGGATG TACAATCGGTAGATTCGTATACCTCTGACAACCCAGACAGCAATGTTATTGCCAAGTCGC CTGATAAGAGGTCAAGCTTAGTATCCCTATCTAAAGTTTCTCCACATTTACTTTCATCCA CATCAAGCAACGGTAACACAATATCGTGTCCCAATGTTGCCACAAATTCGCAGGAATTGG AACCAAACAATGATATTTCAACGAAGAAATCTCTTTCCAATTCTACTTTGAGACATTCCT CTGCTAATAGAAATTCTAATTATGGTGACAACAAAAGGCCTCTTAGAACAACAGTGTCAA AGATATTTGATTCAAACCCTAATGGAGCTCCTTTACGGAGATACTCTGGGGTACCGGATC ACGTTAATCTAGAAGATTACATCGAACAGCCGCATAATTATCCAACAATGCAAAATAGTG TGAAAAAGGATGAATTTTATAACAGCAGGAACAATAAGTTTCCCCATGGTTTAAACTTTT ATGGTGATAACAATGTTATTGAAGAGGAAAATAATGGTGACTCGTCTAATGTAAATCGAC CGCAACACACTAACCTTCAGCATGAGTTTATTCCAGAAGATAACGAAAGTGATGAAAACG ATATTCACTCCATGTTTTATTATAATCATAAGAACGATTTAGAAACAAAACCGCTAATAT CCGATTATGGTGAAGATGAAGACGTAGATGATTATGATCGCCCAAATGCTACTTTCAACA GTTACTATGGCTCAGCATCCAACACGCACGAACTTCCATTACATGGAAGGATGCCTTCAA GATCAAATAATGATTACTACGATTTTATGGTTGGCAACAATACTGGCAATAACAACCAAT ATAGCATAATGAATGGTAGCATCCATATGAATGGTAACGATGACGTTACCCATTCCAATA TCAATAATAACGATATTGTTGGTTACTCACCGCACAACTTTTACTCAAGGAAGTCCCCAT TTGTGAAAGTAAAGAATTTTCTTTATCTTGCATTTGTTATATCATCACTATTGATGACAG GATTCATTCTGGGATTTTTATTGGCCACTAATAAAGAACTACAAGATGTAGACGTGGTAG TGATGGATAATGTGATTTCAAGTTCGGACGAGTTGATCTTCGACATCACAGTAAGTGCTT TTAATCCAGGATTCTTCAGTATAAGCGTTTCCCAAGTCGATTTGGACATTTTTGCAAAAA GTTCTTACCTGAAGTGCGATTCTAATGGTGACTGTACAGTAATGGAACAGGAACGGAAAA TTTTACAAATAACGACAAATCTTTCGTTAGTTGAAGAGAGTGCTAATAATGATATTAGTG GTGGGAACATAGAGACGGTATTACTAGGAACCGCTAAAAAACTAGAGACACCATTAAAGT TCCAGGGCGCGCATTTAATAGGAACTACGATGTGTCAGTCTCGAGTGTCAAGCTTTTAA GTCCTGGGTCTCGTGAAGCCAAGCACGAAAACGACGATGATGACGATGATGATGGCGACG ATGGTGACGATGAAAACAATACTAATGAAAGACAATACAAAAGCAAACCAAATGCTAGAG ATGACAAAGAAGATGATACTAAAAAATGGAAGCTACTAATCAAGCATGATTACGAATTGA TAGTCCGTGGAAGCATGAAGTATGAGGTGCCCTTTTTCAATACGCAAAAATCTACGGCTA TTCAAAAGGATTCCATGGTCCATCCTGGTAAGAAGTGA

YNL054W, 1165 aa (SEQ ID NO 228) MTEEDRKLTVETETVEAPVANNLLLSNNSNVVAPNPSIPSASTSTSPLHREIVDDSVATA NTTSNVVQHNLPTIDNNLMDSDATSHNQDHWHSDINRAGTSMSTSDIPTDLHLEHIGSVS STNNNSNNALINHNPLSSHLSNPSSSLRNKKSSLLVASNPAFASDVELSKKKPAVISNNM PTSNIALYQTARSANIHGPSSTSASKAFRKASAFSNNTAPSTSNNIGSNTPPAPLLPLPS LSQQNKPKIIERPTMHVTNSREILLGENLLDDTKAKNAPANSTTHDNGPVANDGLRIPNH SNADDNENNNKMKKNKNINSGKNERNDDTSKICTTSTKTAPSTAPLGSTDNTQALTASVS SSNADNHNNNKKKTSSNNNGNNSNSASNKTNADIKNSNADLSASTSNNNAINDDSHESNS EKPTKADFFAARLATAVGENEISDSEETFVYESAANSTKNLIFPDSSSQQQQQQQQPPKQ QQQQONHGITSKISAPLLNNNKKLLSRLKNSRHISTGAILNNTIATISTNPNLNSNVMON NNNLMSGHNHLDELSSIKQEPPHQLQQQQPPMDVQSVDSYTSDNPDSNVIAKSPDKRSSL **VSLSKVSPHLLSSTSSNGNTISCPNVATNSQELEPNNDISTKKSLSNSTLRHSSANRNSN** YGDNKRPLRTTVSKIFDSNPNGAPLRRYSGVPDHVNLEDYIEQPHNYPTMQNSVKKDEFY NSRNNKFPHGLNFYGDNNVIEEENNGDSSNVNRPOHTNLOHEFIPEDNESDENDIHSMFY YNHKNDLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGRMPSRSNNDYY DFMVGNNTGNNNQLNEYTPLRMKRGQRHLSRTNNSIMNGSIHMNGNDDVTHSNINNNDIV GYSPHNFYSRKSPFVKVKNFLYLAFVISSLLMTGFILGFLLATNKELQDVDVVVMDNVIS SSDELIFDITVSAFNPGFFSISVSQVDLDIFAKSSYLKCDSNGDCTVMEQERKILQITTN LSLVEESANNDISGGNIETVLLGTAKKLETPLKFQGGAFNRNYDVSVSSVKLLSPGSREA KHENDDDDDDDGDDGDDENNTNEROYKSKPNARDDKEDDTKKWKLLIKHDYELIVRGSMK YEVPFFNTQKSTAIQKDSMVHPGKK

YNL067W, 1076 bp, CDS: 501-1076 (SEQ ID NO 229) GACGACTATTGATGCCAGGCAAATTTTGGATTTACTGCTCCTCTTTTAAGAAGACAAGTG TATTTTCATGTTTAGCATTGCCATTTCTTCTGTGTCACACGTTGTGCTTGCCAGGAACTA TAGGAGAGACGTATACAAGCATCAATGTTACGAATGTACGATCCCGTTTGCATCTGATGT GTAAACTCATGTGGTGCACTGGTGTTTTCCAAGACTGCACTATTAACTGGGAATTTTT TTTTTTCTTCTAGTGAATTTTTTTTAAAGCGACGCACAGGAAAAGTGAAAATTATTTAA ACGGACGCAAACATGAAAAAAAAATTACCAACCATATTTCTATTTCCTTTTCCCTTTAC CTATTCTCTTTTTGAAATAGTTCATTTTCTCTCTCTGAAACGACAATAAACCAAACTCTA GCCTCCAATAGTCACTAAAGATGAAGTACATTCAAACCGAACAACTAAATTGAAATCCCAG AAGGTGTTACTGTCAGCATTAAGTCCAGAATCGTCAAGGTTGTCGGTCCAAGAGGTACTT. TGACCAAGAACTTGAAGCATATTGATGTTACCTTCACCAAGGTCAACAACCAATTGATCA AGGTTGCTGTTCACAACGGTGACAGAAAGCACGTTGCCGCTTTGAGAACCGTTAAATCTT TGGTTGACAACATGATCACTGGTGTCACCAAGGGTTACAAGTACAAGATGAGATACGTCT ACGCGCATTTCCCAATCAACGTCAACATTGTTGAAAAGGATGGTGCTAAATTCATTGAAG TCAGAAACTTTTTGGGTGACAAGAAGATCAGAAACGTCCCAGTTAGAGATGGTGTTACTA TCGAATTCTCTACTAACGTAAAGGACGAAATCGTCTTATCTGGTAACTCTGTTGAAGACG TTTCCCAAAATGCCGCTGACTTGCAACAAATCTGTCGTGTTAGAAACAAGGATATCCGTA AGTTTTTGGATGGTATCTACGTTTCCCACAAGGGTTTCATTGTCGAAGACATGTAA

YNL067W, 191 aa (SEQ ID NO 230) MKYIQTEQQIEIPEGVTVSIKSRIVKVVGPRGTLTKNLKHIDVTFTKVNNQLIKVAVHNG DRKHVAALRTVKSLVDNMITGVTKGYKYKMRYVYAHFPINVNIVEKDGAKFIEVRNFLGD KKIRNVPVRDGVTIEFSTNVKDEIVLSGNSVEDVSQNAADLQQICRVRNKDIRKFLDGIY VSHKGFIVEDM

YNL075W, 1373 bp, CDS: 501-1373 (SEQ ID NO 231) TCGATGGATATCCCATCCAAGAACAGGAATACTGGGTTTTTGAAGACCAGAATGGAGATC TCTGAGGAAGAAAAGATGGTACGTACAATATCACGGCTTGACAATACGAGTATTGCAAAC AGTAATGGAAATGGTAATGATGACACCTCTAATCAGAGAACGGAAGCACTGGGGCGTAAG TTCTTTCAAAAAAAGATAATGTCATATATTTTACTATCTACGCAGTGAAAGAGTTCCTTC TAATGACACACTATTCACTTCGGGTAACGGATATTGTGTACTGAAAAATATAAAAATTT GTTGGACTTGAAAGGGCATATATACTCGGTTTTATCATTGATTCAAGTGTTCCCATAAAT **AATAAAACAGTTAAATCGAAATGCTAAGAAGACAAGCCCGTGAAAGGAGAGAATATCTAT** ACAGAAAAGCGCAAGAATTACAAGATTCTCAACTGCAACAAAAACGTCAAATAATTAAAC AAGCGCTAGCTCAGGGGAAGCCATTGCCAAAGGAACTAGCAGAAGATGAGAGTTTACAAA AGGATTTCAGATATGACCAAAGTTTAAAGGAGAGCGAAGAAGCAGATGATCTACAGGTTG ATGATGAATATGCTGCCACAAGTGGTATAATGGATCCAAGAATCATCGTCACAACATCTC GTGACCCAAGCACTCGTCTCTCGCAATTTGCCAAAGAAATTAAACTGCTATTTCCAAATG CTGTCAGGCTGAACAGAGGTAATTATGTGATGCCAAATCTAGTGGATGCTTGTAAAAAAT

CCGGTACTACAGATTTGGTGGTATTACATGAACATAGAGGTGTTCCAACTTCTTTGACCA
TATCACATTTTCCACATGGACCCACTGCACAGTTTAGTTTACACAATGTTGTTATGAGAC
ATGATATTATAAATGCTGGTAACCAAAGCGAAGTGAATCCACATCTAATATTTGATAACT
TTACTACCGCTTTAGGGAAAAGAGTAGTCTGTATTTTAAAGCACTTGTTCAATGCGGGGC
CCAAAAAAGAGTTCCGAAAGAGTAATCACTTTTGCGAATAGGGGTGATTTCATTAGCGTTA
GACAGCATGTATATGTGAGAACAAGAGAGGGGAGTAGAGATTGCCGAAGTTGGTCCTAGAT
TTGAGATGAGGTTGTTTGAACTGAGGTTGGGAACTTTAGAAAATAAGGACGCTGATGTTG
AGTGGCAGTTGAGAAGATTCATAAGGACTGCCAATAAAAAAAGACTATTTGTGA

YNL075W, 290 aa (SEQ ID NO 232)
MLRRQARERREYLYRKAQELQDSQLQQKRQIIKQALAQGKPLPKELAEDESLQKDFRYDQ
SLKESEEADDLQVDDEYAATSGIMDPRIIVTTSRDPSTRLSQFAKEIKLLFPNAVRLNRG
NYVMPNLVDACKKSGTTDLVVLHEHRGVPTSLTISHFPHGPTAQFSLHNVVMRHDIINAG
NQSEVNPHLIFDNFTTALGKRVVCILKHLFNAGPKKDSERVITFANRGDFISVRQHVYVR
TREGVEIAEVGPRFEMRLFELRLGTLENKDADVEWOLRRFIRTANKKDYL

YNL096C, 1418 bp, exon1: 501-644, intron1: 645-989, exon2: 990-1418 (SEQ ID NO 233) AAACACCTACTTATAGACACGACCAAACTTTCCACAACCTTTCATCAGAGAGAAATGTTG ATCAAGTTGAATGCGTGAAAGTAGCAATTCGAAACAACAACTACCTGTCATTCTGCATAG CTCCATCCGTACCTCTTTAAATCCGTACATTATTGTTTTGCTTAATTTCAATATTTCGGA AAAAGCGAGCGCCCTGGTAAAATGTGGTTCAAGCCTGCGAGCCTTTGCTTGGTAACTCAC CAAATGCAATTCAGTCACGTTCCACACAGTTTGGGTTTCCAGCCTGGCTTTAGGGAAGAA TGGGCTCACTAGGCGTTCATAATACGCGGAGGGGGAAATACCAAATGCTATTGATTATGG TTAAAATATGTGTTATTTGACTTTGTATATACAAACAGAAGAGAAACCAACACACTAAAG ACTAGACACATAACTGACCAATGTCCTCTGTCCAATCCAAGATCTTATCCCAAGCTCCAA GTGAGTTGGAATTACAAGTCGCCAAGACCTTCATCGATCTAGAAAGCTCCTCTCCAGAAC TAAAGGCTGACTTGAGACCATTGCAAATCAAATCTATCAGAGAAGTATGTTAAAAGTTAT ATAATTTGGAAGCAGCAACATTGTGATTTCTTCTAAAGGGGTTCTTTGCAGTAATTTTTT CAAAAAAGAGTGATTTTGAGCAGTATCTGTATGAAATTTTCATGTGTTCGAGAAAAATAG TAATTCCGAGAGCTGTCAATACCATGAACGTTGCGATGAGCCTTTGAACTATAAAGGCCT CCTTGGTCAGTACCAATATCGATGAATAAAATAGAAGCACGCGAAAAAGACCTTACCCCA AGGAGAAGAATCACAAACCCTTTTTTGTTATGAATGAACCAATTCAGTTACTAACTTTAT TTCAACGCTGCTTGATTCTTATTGTTTAGATTGATGTCACCGGTGGTAAGAAAGCACTAG TCCTTTTTGTCCCAGTTCCAGCTTTGTCTGCATACCATAAGGTCCAAACCAAATTGACCC GTGAATTGGAAAAGAAATTCCCTGACCGTCATGTTATTTTCTTGGCTGAAAGAAGAATCT TGCCAAAACCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAACTTTGA CTGCTGTTCACGACAAGGTTTTGGAAGACATGGTTTTCCCAACTGAAATTGTCGGTAAAA GAGTTAGATATTTGGTTGGTGGTAACAAGATCCAAAAGGTTTTGTTAGACTCCAAGGATG TTCAACAAATCGACTACAAGTTGGAATCTTTCCAAGCTGTCTACAACAAGTTGACTGGCA AACAAATTGTTTTTGAAATTCCAAGCCAGACCAACTAA

YNL096C, 190 aa (SEQ ID NO 234) MSSVQSKILSQAPSELELQVAKTFIDLESSSPELKADLRPLQIKSIREIDVTGGKKALVL FVPVPALSAYHKVQTKLTRELEKKFPDRHVIFLAERRILPKPSRTSRQVQKRPRSRTLTA VHDKVLEDMVFPTEIVGKRVRYLVGGNKIQKVLLDSKDVQQIDYKLESFQAVYNKLTGKQ IVFEIPSOTN

YNL162W, 116 aa (SEQ ID NO 236) MVRCLIYFFYLVNVPKTRKTYCKGKTCRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGF GGQTKPVFHKKAKTTKKVVLRLECVKCKTRAQLTLKRCKHFELGGEKKQKGQALQF

YNL178W, 1223 bp, CDS: 501-1223 (SEQ ID NO 237) GGTCCACGTCACACACAATAACATTTACGTAGTGTTCACGCGAAGCAGTTACATCT CAACTAACATAATTGCTGGTGAGCCTACAACACTGCATGCGTAAACGTCAACGGGATTAC CATGTTCCTTTGGAATAATCTAATTCCTCATGATTAAATGAGACTGTTTTTTGTTTCCGT AACATTTCTTTTCTTGAGATGAGGCGCCGCGAGCCTTTCTCCCATGGGCAGTGGTAAAT TTTCCAAATCAATGCAGCTCTTTGAAATACAACAGCATTTTTCATACATTTTAAGCAATT TCTAGTTTGTAGATATTGTTAGATTAGTTTTTGAACATTGTTTTGATAACTGAAAATAAA ACGGTGTCTTCTACGCTGAATTGAACGAATTCTTCACCAGAGAATTAGCTGAAGAAGGTT ACTCCGGTGTTGAAGTCCGTGTCACTCCAACCAAGACCGAAGTTATCATCAGAGCTACCA GAACTCAAGATGTTTTGGGTGAAAACGGTAGAAGAATCAACGAATTAACTTTGTTGGTTC AAAAGAGATTCAAGTACGCTCCAGGTACTATTGTCTTATATGCTGAAAGAGTTCAAGACC GTGGTTTGTCCGCTGTCGCTCAAGCTGAATCTATGAAATTCAAATTGTTGAACGGTTTGG CTATCAGAAGAGCTGCTTACGGTGTCGTCAGATACGTTATGGAATCTGGTGCTAAGGGTT GTGAAGTTGTTTCCGGTAAACTAAGAGCTGCCAGAGCTAAGGCTATGAAATTTGCTG ACGGTTTCTTGATTCACTCTGGTCAACCAGTCAACGACTTCATTGACACTGCTACTAGAC ACGTCTTGATGAGACAAGGTGTTTTGGGTATCAAGGTTAAGATTATGAGAGACCCAGCTA AGAGCAGAACTGGTCCAAAGGCTTTGCCAGATGCTGTCACCATCATTGAACCAAAAGAAG AAGAACCAATTCTTGCTCCATCTGTCAAGGACTACAGACCAGCTGAAGAAACTGAAGCTC **AAGCTGAACCAGTTGAAGCTTAG**

YNL178W, 240 aa (SEQ ID NO 238)
MVALISKKRKLVADGVFYAELNEFFTRELAEEGYSGVEVRVTPTKTEVIIRATRTQDVLG
ENGRRINELTLLVQKRFKYAPGTIVLYAERVQDRGLSAVAQAESMKFKLLNGLAIRRAAY
GVVRYVMESGAKGCEVVVSGKLRAARAKAMKFADGFLIHSGQPVNDFIDTATRHVLMRQG
VLGIKVKIMRDPAKSRTGPKALPDAVTIIEPKEEEPILAPSVKDYRPAEETEAQAEPVEA

TAATCAATGTCTACAATCTGTCAGGTTCTTTCAAAAGAGAATCTGTTGAACAGCGCTTAC CATTACCTGAAATCCTAAAATGTCTGGAAGTAGTTGAAAATGATGGTGTGCAGTATGATA GAATTCAAGGTGTCAATCATAATTTACCAGACTTCAATCTTCCGTACCTTTTACTTGGCT CCACCGAATCGGGTAAATTGTACATATGGGAGTTAAATTCAGGGATTTTATTGAACGTGA AGCCTATGGCTCATTACCAAAGTATCACCAAGATTAAGTCCATTTTAAACGGCAAGTATA TTATTACTTCTGGTAACGATTCGAGAGTTATTATATGGCAAACTGTTGACTTGGTATCAG CGTCCAATGATGATCCTAAGCCTTTATGTATCCTTCACGATCATACTCTACCCGTGACAG ATTTCCAAGTTTCTTCTAGTCAAGGAAAATTTTTATCATGTACTGATACGAAACTCTTCA CAGTATCTCAAGATGCTACCATTAGATGCTATGATTTGAGTTTAATAGGCAGCAAAAAGA TTACAACTCCTTATTCTATCAAATCCATTGTACTGGATCCTGCTGACAGAGCATGCTATA TCGTTAATCTGCTACAGTCCGCCGGAGTAAACACAGTTCAAAAAGGTAGGGTTTTTTCCC TAGTGCAACGTAACTCACTAACTGGCGGCGAAAATGAAGATTTGGATGCACTATATGCAA TGGGCCAACTTGTCTGAGAATGTCCTAAATTCAAATGTGTCATGCCTAGAAATATCAA TGGATGGTACATTATTATTGATCGGTGATACGGAGGGGAAAGTTTCTATTGCGGAAATTT **ACTCAAAACAAATCATTAGAACTATCCAAACTTTAACTACATCAGGATTCAGTTGGAG** AAGTGACCAATCTCTTAACCAACCCTTACAGACTCGAACGTGGAAATTTACTTTTTGAAG GAGAATCCAAAGGCAAACAACCTAGTAATAATAATGGTCACAATTTTATGAAGATACCAA ACTTACAAAGAGTTATCTTTGATGGTAAAAACAAAGGCCATTTACACGATATTTGGTATC AGATAGGAGAACCAGAAGCAGACAGATCCTAACCTCGCATTACCACTTAACGACTTTA ATGCCTATTTGGAGCAGGTCAAAACGCAAGAATCGATATTTTCACATATCGGTAAGGTGT CAAGCAATGTAAAAGTGATTGACAATAAAATCGACGCCACTTCATCTTTAGACAGCAATG CCGCTAAAGATGAGGAAATTACAGAACTTAAGACCAACATAGAAGCATTAACTCATGCCT ACAAGGAGTTACGTGACATGCACGAAAAGCTGTACGAGGAACACCAACAGATGCTTGACA **AGCAATAA**

YNL182C, 555 aa (SEQ ID NO 240)
MDEQVIFTTNTSGTIASVHSFEQINLRQCSTQSRNSCVQVGNKYLFIAQAQKALINVYNL
SGSFKRESVEQRLPLPEILKCLEVVENDGVQYDRIQGVNHNLPDFNLPYLLLGSTESGKL
YIWELNSGILLNVKPMAHYQSITKIKSILNGKYIITSGNDSRVIIWQTVDLVSASNDDPK
PLCILHDHTLPVTDFQVSSSQGKFLSCTDTKLFTVSQDATIRCYDLSLIGSKKKQKANEN
DVSIGKTPVLLATFTTPYSIKSIVLDPADRACYIGTAEGCFSLNLFYKLKGNAIVNLLQS
AGVNTVQKGRVFSLVQRNSLTGGENEDLDALYAMGQLVCENVLNSNVSCLEISMDGTLLL
IGDTEGKVSIAEIYSKQIIRTIQTLTTSQDSVGEVTNLLTNPYRLERGNLLFEGESKGKQ
PSNNNGHNFMKIPNLQRVIFDGKNKGHLHDIWYQIGEPEAETDPNLALPLNDFNAYLEQV
KTQESIFSHIGKVSSNVKVIDNKIDATSSLDSNAAKDEEITELKTNIEALTHAYKELRDM
HEKLYEEHQQMLDKQ

YNL190W, 1115 bp, CDS: 501-1115 (SEQ ID NO 241) AATGCGCTCCCGTACGTCAGTGGCTGTTGCTGAAACGAGACAATTTCTCAATTCGTTTGT TTGTGTACTGTATTTGTTATCTTTACTATATATATGTTGTTAAGTTTCTTTTACCAATTA GTGCTCACTTCTCCTCTTTTATTAGGTGTGTGTGTTGTGCGTAATTTTCGTTTCGCTG ATTACTTTATATAGTGTAGTTTGTTCTTGAATGTAATAAAGACTTCTGTTTTATTTTGTT TTGTTATTTAGAAACAGTCTATCTGGTTTAACTTAAACGAGTGAGCTTAAGATAATCTGA CTTCTAACTCACACTTTTGGAAGAACATTTATTTTTTCGACCTTCTTTCCCAAATACC CAGCGCTTTATAATTGAAATATGAAGTTCTCTTCTGTTACTGCTATTACTCTAGCCACCG TTGCCACCGTTGCCACTGCTAAGAAGGGTGAACATGATTTCACTACCACTTTAACTTTGT CATCGGACGGTAGTTTAACTACTACCACCTCTACTCATACCACTCACAAGTATGGTAAGT TCAACAAGACTTCCAAGTCCAAGACCCCAAACCACACTGGTACTCACAAGTACGGTAAGT TCAACAAGACCTCCAAGTCTAAGACCCCAAACCATACCGGTACTCACAAGTATGGTAAGT TCAACAAGACTTCCAAGTCCAAGACTCCAAACCATACCGGTACTCACAAGTACGGTAAGT TCAACAAGACCTCCAAATCCAAGACTCCAAACCACACTGGTACTCACAAGTACGGTAAGT TCAACAAGACCTCCAAGTCTAAGACCCCAAACCATACCGGTACTCACAAGTATGGTAAGT TCAACAAAACCAAACATGACACTACCACTTATGGTCCTGGTGAAAAGGCCCGTAAGAACA ATGCCGCCCTGGTCCATCTAATTTCAACTCCATAAAATTGTTTGGTGTTACCGCTGGTA GTGCTGCCGTAGCCGGTGCCTTATTACTATTATAA

YNL190W, 204 aa (SEQ ID NO 242) MKFSSVTAITLATVATVATAKKGEHDFTTTLTLSSDGSLTTTTSTHTTHKYGKFNKTSKS KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKS KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTKHDTTTYGPGEKARKNNAAPGPS NFNSIKLFGVTAGSAAVAGALLLL

YNL208W, 1115 bp, CDS: 501-1115 (SEQ ID NO 243) GGTTATACACATATATATTTTTCATTTTTAATGTCTTAGCTTTTGTATCTTAGATGAA GTTTTAGTTCTGTATATCACGATCAAGATATCATACAATCATAAATTCAATTATTCTTCT GTTTCCCCTCTTGAGGCATCAAACGAGTGTTTGACTGATACACCCAACATACTAAGGCA ACTTTTCTGGCTGCCCAAAGCTGTGGCACGTATGAAACTGCTTTTCGGCTGCATAAAACA ACCATGTGGAGTTTTTACTGTATTCGCATTTCGCCCCGCTAGCATTCTTCGTTCATGCTA AAAATGAGGCGTGGGCTAATATTCAGTATTAATAATTCCGGCACCCGCACAGCCCATACC GGAAAAGGGGCTGGCTGTTGGCCTTGGCAAAAAACTCAATCTGAGCAGTCATTTATAAAG AAAGACTTTAATTTGTCTTGCTAAACACTTGTAAGCCTTCCAAATATAGATCACTTAAGA CAATCTAACAAGTGTCCAAAATGTCTGCAAACGAATTCTACTCAAGTGGCCAACAAGGTC AATATAACCAGCAAAACAACCAAGAAAGAACTGGTGCTCCAAACAACGGTCAATATGGTG CCGACAATGGTAACCCCAACGGTGAACGTGGTTATTTTCCACTATTGTAGGTGGCAGTG CCGGTGCGTACGCTGGATCTAAGGTGTCGAACAACCATTCTAAGTTGAGTGGTGTGCTGG GCGCCATAGGTGGTGCATTCCTTGCCAACAAGATATCTGATGAGCGTAAAGAGCATAAGC AACAAGAGCAATACGGCAACTCAAACTTCGGAGGTGCTCCTCAAGGTGGACACAACAACC **ATCACCGTCAGACAATAACAACAATAACGGTGGATTTGGCGGTCCAGGCGGCCCTGGCGG** TCAAGGTTTCGGAAGACAAGGCCCACAAGGATTTGGAGGTCCTGGTCCACAAGAGTTTGG TGGTCCAGGTGGCCAAGGATTCGGTGGTCCAAATCCTCAAGAATTCGGCGGCCAGGTGGC CAAGGATTCGGTGGTCCAAACCCTCAGGAATTCGGGGGCCAAGGTCGTCAAGGATTCAAT GGCGGTTCACGTTGGTGAATGGCTCAACAGAGTGA

YNL208W, 204 aa (SEQ ID NO 244) MSANEFYSSGQQGQYNQQNNQERTGAPNNGQYGADNGNPNGERGLFSTIVGGSAGAYAGS KVSNNHSKLSGVLGAIGGAFLANKISDERKEHKQQEQYGNSNFGGAPQGGHNNHHRQTIT TITVDLAVQAALAVKVSEDKAHKDLEVLVHKSLVVQVAKDSVVQILKNSAARWPRIRWSK PSGIRGPRSSRIOWRFTLVNGSTE

YNL210W, 1313 bp, CDS: 501-1313 (SEQ ID NO 245) TCATAACGGGTTCTTTTCAAAAAACCGTAAAAATTTGAGGTCACACCAACTAAATACAAA TTGTTTCATCACGGTGACTATATCAAGAACTTCGTAAGGAAACATTTAGAAAACTCAATA TAGTAAAGTTTCATCAGCAATCTTATCTGAGTAATATTATCTACGATCTAAATATAGGAT GATCTGCCGATTTAGGAATCGTACTGTAGATTGCTCTTGGCGACAGATATAGTGAAATAC CTTTTACAAAGTGGATACAGGTTGCCTATCACTACCGCCATTTCACTAGCAAGTAGAGTA CTATCCGCTAAACGGGACGATCGCATTTTAGCCGCCGACAGTGTTAATATAAGTAATGAA CTTGGGTTAATTTGATTACGCGTCACAGCTACTAATAAAATAAGACCGAGAGTTTTAATC CCAAATTGGTGAAACTATTAGAAGAGCTCCAGGAGGGAAAGCAATTCAACAATAAAAACA ATTTACTAGAGTTTTGCGTCCACCTTGACAAGATAAAAGGAGTCATTAGACCAAACTATG ACACTATATATTTTGTGCCTGTTGGAGGTGGATCTCCTCAATCTGGTATTTACCGACA ATATATTGGAAATATGTTTGCCCAGGTTTGTTTCAAGGGAGGACTTGAGGGTTTTTAATA ATACTTTTTACACATATCACGATAACCGCCTACGTATTCTCCAAGAAGACTTTTCTCAAT TGTTCAAAAAATCAAAACTAAGGCTTCTGTACTATGTTTTACAGTTGAGGAAATTTTTC TGACAAACCAAGAAATTTTACCTCAAAACTCAACAGTGGCAGAACTGCAAAAGAGCACTA ATAAAGTACAGACAAATGGGCCGCAACGGCACGATTTCATAGTCACTCTAGAAATAAAAC TGAACAAAACACAAATCACTTTCCTCATTGGAGCTAAAGGAACGAGAATTGAAAGCTTGA GGGAAAAATCAGGCGCCAGCATAAAAATAATACCTATTAGTGATAAAATGACTGCACATG AAAGGAACCACCCTGAATCTGTTCAACAAACAATACTAATTTCGGGTGACTTATACTCAA TTGCATTAGCCGTCACCAGTATAGAGTCTGCATTAATTACTTTGGATTTATAG

YNL210W, 270 aa (SEQ ID NO 246) MSNQHSPQPFCLDTKLVKLLEELQEGKQFNNKNIFPEKALYLKLALDYSFFRKNLLEFCV HLDKIKGVIRPNYDTIYILCLLEVDLLNLVFTDNILEICLPRFVSREDLRVFNNTFYTYH DNRLRILQEDFSQLFKKIKTKASVLCFTVEEIFLTNQEILPQNSTVAELQKSTNKVQTNG PQRHDFIVTLEIKLNKTQITFLIGAKGTRIESLREKSGASIKIIPISDKMTAHERNHPES VQQTILISGDLYSIALAVTSIESALITLDL

YOL031C, 1766 bp, CDS: 501-1766 (SEQ ID NO 247) AGTTTTTTTTCTCGAGAAATTGTGAACAAAAGAAAGCAAAGACACAGAAGATGATAAGAG AGAGAAACAACGAAGAAAGAACAATGTTGGGGTTCACCCGAGAGATATTGACATACT GACCTTAGAAAAGGCATTACTGAGGCTACTGACTAAAGCGCGTTACATAAATGCATAGTA TATTTCTTGTTGTATACGCAGCGGCCAACTAGTGGCAGCAAGAATGTAATGAACGATTCA TCTGCAGGTTTGGAGGCCGCAACTAGATCAAAACGTAAATAGCGGGTGAAGTGTTCTGGA CGTTAGAAGTAACGTCCGCAGATCGAAGCTAAACACGAGATTAGATTTCGGGTAACGGAA TTGTGATAATTAAGAAAGACCAGACTATGTGAAAAGGCCACGTAAATGATAGAGCACACA TTAGCAACTATAATAGACTAGTTTTCGCATCGCTGGAAGTTCTCGATATTGAATATCACT TCCAAGAACGCAAACTTAGAATGGTCCGGATTCTTCCCATAATTTTGAGCGCCCTATCTT CGAAATTAGTGGCGAGTACAATATTGCATTCATCCATACACTCAGTGCCATCTGGAGGCG AAATCATATCTGCAGAAGATCTTAAAGAACTTGAAATTTCAGGGAATTCGATCTGCGTTG ATAATCGTTGCTATCCTAAGATATTTGAACCAAGACACGATTGGCAGCCCATACTGCCAG GTCAAGAACTCCCCGGTGGTTTGGACATTAGAATAAACATGGACACAGGTTTAAAAGAGG CAAAACTAAATGATGAGAAGAATGTCGGTGATAATGGTAGCCATGAGTTAATTGTATCTT CAGAAGACATGAAAGCATCGCCTGGTGACTATGAATTTTCCAGTGATTTCAAAGAAATGA GAAACATCATAGATTCTAACCCGACTTTATCTTCACAGGACATTGCCAGATTGGAGGATA GTTTTGATAGAATAATGGAATTTGCGCATGATTACAAGCACGGCTACAAAATTATTACCC ATGAATTCGCCCTCTTGGCCAACCTTAGTCTCAATGAAAATTTGCCGTTAACATTGAGAG AGCTCAGTACTAGAGTCATTACCAGCTGCTTGAGAAACAATCCTCCTGTAGTCGAGTTCA TTAATGAAAGTTTTCCAAATTTTAAAAGCAAAATCATGGCCGCTCTGTCAAATTTGAATG ATTCTAACCACAGATCCTCTAATATCCTAATAAAAAGATACTTGTCCATTTTAAACGAAT TACCTGTCACATCCGAAGATCTTCCTATATACTCTACGGTTGTTTTACAAAATGTATATG AAAGAAACAACAAGGACAAACAGTTACAAATAAAAGTCCTGGAGTTGATCAGCAAAATTT TGAAGGCCGACATGTACGAAAATGACGATACAAATCTAATTTTGTTCAAAAGAAATGCTG AGAATTGGTCGTCAAATCTGCAAGAGTGGGCAAACGAGTTCCAAGAGATGGTCCAGAACA AAAGTATAGATGAACTACATACAAGAACGTTTTTTGACACCCTTTACAACTTGAAGAAAA TTTTCAAAAGTGACATCACGATCAACAAAGGGTTTTTGAATTGGTTAGCGCAACAATGTA TTGATAAGAAACTTATCGACAGCAGACACTTGATCTTTGGCAACCCCATGGCTCATAGAA TAAAAATTTCAGAGATGAACTCTGA

YOL031C, 421 aa (SEQ ID NO 248)
MVRILPIILSALSSKLVASTILHSSIHSVPSGGEIISAEDLKELEISGNSICVDNRCYPK
IFEPRHDWQPILPGQELPGGLDIRINMDTGLKEAKLNDEKNVGDNGSHELIVSSEDMKAS
PGDYEFSSDFKEMRNIIDSNPTLSSQDIARLEDSFDRIMEFAHDYKHGYKIITHEFALLA
NLSLNENLPLTLRELSTRVITSCLRNNPPVVEFINESFPNFKSKIMAALSNLNDSNHRSS
NILIKRYLSILNELPVTSEDLPIYSTVVLQNVYERNNKDKQLQIKVLELISKILKADMYE
NDDTNLILFKRNAENWSSNLQEWANEFQEMVQNKSIDELHTRTFFDTLYNLKKIFKSDIT
INKGFLNWLAQQCKARQSNLDNGLQERDTEQDSFDKKLIDSRHLIFGNPMAHRIKNFRDE
L

PCT/BE00/00077 WO 01/02550 83/161

GGTGTACTTCGCTACTAAAGGGTGAAAGAAGAAGAAGAATGA

YOL048C, 106 aa (SEQ ID NO 250) MFFKVSNFTSLTLLSLIPIVGPILANQLMAPKRTFTYLQRYFLLKGFSKKQAKDFQYEHY ASFICFGMSAGLLELIPFFTIVTISSNTVGAAKWCTSLLKGERKKE

YOR010C, 1256 bp, CDS: 501-1256 (SEQ ID NO 251) ACATTTCCCAAAAAAGACATTTCTGTCCAAAAGTAGAAGGCAAGAAAACCCTGGAGGAAT CATAGGCAAAGAAAGAAGAAGAAGATCATCTTTAAAACTACCTTTCAAGCCTTTATTC GTTCCTCGTAAAGGACACACGAAAAAAATAAACAGTACCTTGCAGAAGGAGTGCAGAGTT AGGTCGCAGGGAATCCTTGAAAGCCAAGAGTTTTTTTTCCGTAATGATCTCCCAAAGCAA CCATCAACATTGTGGTGCAAAGTTTAGTGTAAGATGTTCTACTGAACTATCTTAATAGCT GAGCATCATGTGAGTAAACGAGTAAGCAAGAAAACAACAAAGTAATGTTCAACTTTCGTA ACTACGGAAAATAATATATAGTAGTTAACGAAATTCGAACAATGAGAGCTCTCACATAT CATCTTCTTTTCCAGTTTAGCCATTATCAGCACAATAATACAAAACACACTCGTACACTC GCTTCAACTATAACAAAAAAATGGCTTACATCAAGATCGCTTTATTAGCTGCTATCGCTG CTTTGGCTTCTGCCCAAACTCAGGAAGAAATTGACGAATTGAACGTTATTTTGAATGACG TTAAGTCCAACTTGCAAGAATATATTAGTTTGGCTGAAGATTCTTCATCTGGATTTTCCT TAAGCAGTCTGCCATCTGGTGTTTTAGACATCGGTTTAGCTTTGGCTTCCGCCACTGATG ACTCCTACACTACTTTGTACTCTGAGGTTGACTTTGCTGCTGTTAGCAAGATGTTGACCA TGGTTCCATGGTATTCTTCCAGGCTTCTACCAGAATTGGAATCCTTGTTAGGAACTTCTA CCACCGCTGCCTCTTCTACTGAAGCTTCTTCTGCTGCTACTTCTTCCGCTGTTGCTTCCT CCAGTGAAACTACTTCTTCTGCCGTCGCTTCCTCCAGTGAAGCTACTTCTTCTGCCGTCG CTTCTTCCAGTGAAGCTTCTTCTTCTGCTGCTACTTCTTCTGCTGTCGCTTCTTCCAGTG AGGCTACCTCTTCCACCGTCGCTTCCTCTACCAAGGCTGCCTCTTCCACTAAGGCTTCTT CCTCTGCTGTTTCTTCAGCTGTTGCTTCTTCCACCAAAGCCTCCGCCATTTCTCAAATCA GTGATGGTCAAGTTCAAGCCACTAGCACTGTTTCCGAACAAACTGAAAACGGTGCTGCCA AGGCTGTCATCGGTATGGGTGCTGTCATGGCCGCTGCCGCCATGTTATTATAA

YOR010C, 251 aa (SEQ ID NO 252) MAYIKIALLAAIAALASAQTQEEIDELNVILNDVKSNLQEYISLAEDSSSGFSLSSLPSG VLDIGLALASATDDSYTTLYSEVDFAAVSKMLTMVPWYSSRLLPELESLLGTSTTAASST EASSAATSSAVASSSETTSSAVASSSEATSSAVASSSEASSSAATSSAVASSSEATSSTV ASSTKAASSTKASSSAVSSAVASSTKASAISQISDGQVQATSTVSEQTENGAAKAVIGMG **AGVMAAAAMLL**

YOR019W, 2693 bp, CDS: 501-2693 (SEQ ID NO 253) CATTGATCTCGAGCACAGCTGCTCTTTTCTCTCAATGAATTACGTTATATGTTAATCACA CAAGCATCAGTTTTTCATCGCAAAAGAAAATATTTAGAGTTCTTGCAATTCAGATGTACC TCAATTAATAACTCAATCACCTCCTATGTTCTTGCTGGTAGTACTGCTTTTTGTCTTAATT ACTGCTGAATCAGCCTTCTAGAAGACCGTTCTGTTTCAGCCGCTCGCCCCTTTTCAAAGC TTGCGCGGCTGAGTTTTATGAGGGGCGGCTTTTTTGTGAATGGCAATCTACCATTATTAG TAGCAATATGATTTGCAGATAGATACATATATATCCTTCTGGGTTCATGTCTCGTTACCA TCCACACTAATGCATAGGACCAGAAAGAAAGGACATCGAATCCAACACGTATTAAAATAA GGACTCCTCATTAAAAAGGCTTTTAATATTCAACTTGCTATAGATCACGCACCCTTTTGG CAAGTCAACCTTAAATTATTATGATTTCTGTTTGCCCACAAAATGACTTGCAAAAATGCT ACAGAAGCCTCACATTCGATGTTCCAGGACAACAATTCGAAGAGAGAAATGAACAAAACC TTAAAAAACGGCCCAAAAAGAAAGGCAGTTTCCAACCATCTGTTGCCTTTGACACAGTGC CTTCCACCGCTGGTTATTCTTCTATAGACGACAGCAGGGAAGGATTCAAAGGTGTACCTG TTCCCAACTATTACACGATGGAAGAGTGCTATGACGATGAAACAGACTCTTTTTCGCCAA ATTTGCAATATTATTTGAGAGATACATTCCAATCATCACCTTTTCTGAATACTAGAAAAG AGAACAAATCTGAATCCAGTAGTTTTCCAATGAGATCCTCAAAGTTGTTGGAAAAGAATT CTGACATCAAAAAATATTTCTTGGTATCCAAGAATGGAAAAATAGTGAGGAGAGACTATC CAAGCACGCCAGTAATTGTCAACGAAACGTTGATGATAAACAGGTTTGAAAAGAACTGGA GGTTTACTTACCCAGAACTTATCTTCTCTGAAGAGCGTATTAAACCGTTATATAGAGGAG ATGATAGTGCACCATGTACAAAAGAACAAAAAGAAAGCATAAAATACTTCAACAAAAGG TCGGATATCCCAATAACCCTAAGACAATAGTTTGTCACATTAACGGAAAAAAACATACGT GGGTTGCCCTAGACTGGACAGTCTACAAGTTTGCACGAAATCTTGATCACATTGTTGTCA TAACTACACTGCCAAAAATGATTTCTAACAGGAAAAAACTGCAAAAGATGATACAGAAT

GGGCACCGGGATATCAAAAAGAAGTAATAGATCAAAAATTAAACGACATTTTTGATTATA TTTTACAGCTAGTAAAAGTGGTCAAAATATCCGTCAAAATTACTTTAGAAATAATTGTAG GCAAAATTAAAAAAGTCTGGTAGATGTCATTAATGTCCATACTCCAGATTTCTTAGTTC TTGCTACTTTAAAGCACGAGCGAAATGAGAATCTTATTACATATAAATCCAAAAAGCTGA CAGATGTCTTTCCTGTTAGTTATCCGATTCCCACATTTGTTGTTCCCTCGAAACGAATGT ATTCGTTCGAACTGAATCTACAAAGAGAAGTAAATGAACATTATGTCTCAAAAAAATCATA TATCAGATATTTCTTCACATATTTCCGTAGATTCGTACGCCGAAGATTTCAAAAGGCAAG GCTACATCAAAAAGCAGTTCAACACCTCTAATGATTCCATTCCAAGAAAATTGACCGGTC TCGCCCAGCATTCAAGAAGGAAGATCACGGGTGATATAGAAAAATTACAAGACGATGAGA AAGATAGAGAATGTACTAAGGAAAAACTTTTGTTGAAGAAAATTGATATCATAATTAGAG AGTCATTGAAGTCTTCTTTAGCGATAGAGACGTTGCCTGGTAAAAATGTATCGCAGTCCA GTCACGGTGACCAAATTTCCAGCTTTAAGAATGCTTTGATAGGCAATGGGTCGAAAAACA CAAAGTTTAGAAAATCTTTAATACCATATTCTTCCTCAGAGGAACAAAATACCACAACAA CTATTAAACTCAGTAGCTCGCCTACGTCCCAAATCAAGTTTGCAACCTCTGTAAAACACA AAGATGGAAGAGCCGCCCTTGGCAAAGCCAGAAATCTGCCTGATATAAGGCACAGTATTT CCTTCGACAAAGAAAATTCCTTTGATCCATCTGATAAAAGCAGTAGTGTTGATAATAGCA TTCCTTTGAGGAAAGTTAAAAGTGCCGGTGCGTTAAGAAAAGTCAAAACTAATGACTCCT CAAGTAGTGCAGGGTCAAAGAAAAGCTCGTCTAGTTTTAGTACTGTGAACACCTTCACTG CCAGTAGAAGGAATAGTAGCAGTGGCGATGTTTTTGAAAGTGATGATCGTAACGACAAGA AAAAGAAGAAAAAAAAAAAAAAGAAGAAATCATTGTTCTTATTCGGCAAAATATGA

YOR019W, 730 aa (SEQ ID NO 254)
MISVCPQNDLQKCYRSLTFDVPGQQFEERNEQNLKKRAKKKGSFQPSVAFDTVPSTAGYS
SIDDSREGFKGVPVPNYYTMEECYDDETDSFSPNLQYYLRDTFQSSPFLNTRKENKSESS
SFPMRSSKLLEKNSDIKKYFLVSKNGKIVRRDYPSTPVIVNETLMINRFEKNWIKLWRQR
KLQINERLNDKKKWFTYPELIFSEERIKPLYRGDDSAPCTKEQKRKHKILQQKVGYPNNP
KTIVCHINGKKHTWVALDWTVYKFARNLDHIVVITTLPKMISNRKKTAKDDTEWAPGYQK
EVIDQKLNDIFDYILQLVKVVKISVKITLEIIVGKIKKSLVDVINVHTPDFLVLATLKHE
RNENLITYKSKKLTDVFPVSYPIPTFVVPSKRMYSFELNLQREVNEHYVSKNHMKHEHTD
VESMSSSMFKKNTISDISSHISVDSYAEDFKRQGYIKKQFNTSNDSIPRKLTGLAQHSRR
KITGDIEKLQDDEKDRECTKEKLLLKKIDIIIRESLKSSLAIETLPGKNVSQSSHGDQIS
SFKNALIGNGSKNTKFRKSLIPYSSSEEQNTTTTIKLSSSPTSQIKFATSVKHKDGRAAL
GKARNLPDIRHSISFDKENSFDPSDKSSSVDNSIPLRKVKSAGALRKVKTNDSSSSAGSK
KSSSSFSTVNTFTGGGVGIFKVFKSGSSSGNKSSSRRNSSSGDVFESDDRNDKKKKKKKK

YOR027W, 2270 bp, CDS: 501-2270 (SEQ ID NO 255) **AATTTTCCCCCCGTCATAAGTTCCTATACACGGCTGGCTCTGATGGCATAATTTCATGCT** GGAACCTACAAACCCGCAAGAAAATAAAAAATTTCGCCAAATTTAACGAAGACAGCGTGG TTAAAATTGCTTGTTCGGACAATATTCTATGTCTGGCAACTTCTGATGATACTTTCAAGA CAAACGCCGCAATTGACCAAACTATTGAACTAAACGCAAGTTCAATATACATAATATTTG **ACTATGAGAACTGATATCTTCGTGAAGATTCGTGTAGTATGATAGAACATTCCAGAAAAA AAATTCAGATTCATCGCTCTCTCTTCGCTTCTCCTCCTTTAAGGAATAAAGAAAAATCA** TTAAGGTATCTTGTTTAAGCCCAAAAGTCTGCTCCCAAATTCCTCACTGTAGCTACTAAA CTGCATTTACCGCTAAGGATTACGATAAAGCGATAGAGCTCTTCACTAAAGCTATTGAAG TTTCTGAAACTCCAAACCATGTTTTATATTCTAACAGGTCCGCCTGTTATACTTCTTTAA CTAAGGGTTATAATAGACTCGGTGCCGCCCACTTAGGTCTTGGCGATCTCGACGAAGCTG **AAAGCAACTACAAAAAAGCCTTGGAGTTGGATGCCAGTAACAAGGCCGCCAAAGAAGGAT** TGGATCAGGTTCATCGTACCCAACAGGCAAGACAGGCACAGCCTGATTTAGGGTTGACAC AGTTGTTTGCTGACCCAAATTTAATTGAAAATTTAAAGAAGAACCCAAAAACTAGCGAAA TTGGCCAAGATCTGTTTACTGATCCAAGATTAATGACCATCATGGCTACATTGATGGGGG TTGATTTAAACATGGATGATATAAACCAATCAAACTCCATGCCAAAGGAACCGGAAACCA GTAAAAGCACTGAACAAAAGAAAGATGCTGAACCACAAAGCGATTCCACTACGAGCAAGG AAAATTCCTCTAAAGCACCACAGAAAGAAGAAGTAAGGAATCCGAGCCAATGGAAGTTG

WO 01/02550 85/161

ATGAAGATGACTCTAAAATTGAGGCCGACAAGGAAAAGGCCGAAGGTAACAAGTTTTACA AGGCACGTCAATTCGATGAAGCTATAGAGCACTACAACAAGGCGTGGGAACTGCATAAAG ATATTACCTATTTAAACAACCGTGCTGCTGCTGAATACGAAAAAGGCGAATACGAGACAG CTATTTCTACCTTGAATGATGCTGTTGAGCAAGGTAGAGAAATGAGAGCGGATTACAAGG TCATTTCCAAATCATTTGCGCGTATTGGTAATGCCTATCACAAATTGGGTGACTTGAAGA **AAACTATAGAATACTACCAAAAATCATTGACCGAACATCGTACTGCTGACATTTTGACCA** AGTTAAGGAATGCTGAAAAAGAATTGAAGAAAGCTGAGGCGGAGGCGTATGTTAACCCTG AAAAGGCGGAGGAAGCCCGTCTTGAAGGTAAGGAATATTTTACCAAGAGTGATTGGCCGA ATGCTGTTAAGGCTTACACTGAAATGATCAAAAGGGCACCTGAAGATGCTAGAGGATATT CTAATAGAGCTGCTGCACTAGCGAAGTTAATGTCTTTCCCTGAAGCTATCGCAGATTGTA ACAAAGCCATTGAAAAAGATCCAAATTTCGTGAGAGCTTATATCAGAAAGGCCACCGCAC AAATTGCTGTTAAAGAATATGCTTCCGCTTTGGAAACACTAGATGCGGCCAGAACCAAAG ATGCTGAAGTGAATAATGGTTCTAGTGCAAGGGAAATTGATCAACTGTACTACAAGGCAA GCCAACAAAGATTCCAACCTGGTACCAGTAACGAAACCCCAGAAGAAACCTATCAAAGGG CCATGAAAGATCCTGAAGTGGCTGCGATCATGCAAGATCCTGTTATGCAAAGTATTTTGC AGCAGGCCCAACAGAATCCCGCTGCTTTACAAGAACACATGAAAAATCCAGAAGTATTCA AAAAGATTCAGACGTTGATCGCTGCTGGTATCATCCGGACTGGCCGCTAA

YOR027W, 589 aa (SEQ ID NO 256) MSLTADEYKQQGNAAFTAKDYDKAIELFTKAIEVSETPNHVLYSNRSACYTSLKKFSDAL NDANECVKINPSWSKGYNRLGAAHLGLGDLDEAESNYKKALELDASNKAAKEGLDQVHRT QQARQAQPDLGLTQLFADPNLIENLKKNPKTSEMMKDPQLVAKLIGYKQNPQAIGQDLFT DPRLMTIMATLMGVDLNMDDINQSNSMPKEPETSKSTEQKKDAEPQSDSTTSKENSSKAP QKEESKESEPMEVDEDDSK1EADKEKAEGNKFYKARQFDEAIEHYNKAWELHKDITYLNN RAAAEYEKGEYETAISTLNDAVEOGREMRADYKVISKSFARIGNAYHKLGDLKKTIEYYO KSLTEHRTADILTKLRNAEKELKKAEAEAYVNPEKAEEARLEGKEYFTKSDWPNAVKAYT **EMIKRAPEDARGYSNRAAALAKLMSFPEAIADCNKAIEKDPNFVRAYIRKATAQIAVKEY** ASALETLDAARTKDAEVNNGSSAREIDQLYYKASQQRFQPGTSNETPEETYQRAMKDPEV AAIMQDPVMQSILQQAQQNPAALQEHMKNPEVFKKIQTLIAAGIIRTGR

YOR031W, 710 bp, CDS: 501-710 (SEQ ID NO 257) CTGCAGAAGTACAGCTGCCTTTATTTCTTGTGGTCATTTATTGCTTTTATTTTCAAGTCA GATATACAAGAAAATCAAATCCCATCGTCAACGTCACGTATAAACGATTAATTTACAGTA ATACCATACTACCAACATTATTTTAGTCCGACGTTCAGTCCTGTAGGTGTTCCAAATC CTTCTGGCATTGACTTCTGTGCAGAAACCCTTCAAAATGAGTTCCACTTTACGTCAGATC GCATAACAACCGGTCATATATTTTTTTTTTTTTGCTAAACCCCCTACTGCAAGCACTTTTA AGAAAAGAACAATAAATGCGTCTTTATTGCTGTGTGGAAGTGATTTTTTGTCTTTCGGAC AAAAAAAGGATAGGGATGCGAGAGGGCTGTGAAGTAGTGATCAAGCGGGGCCTATATAAG AAGGGCGCACATCGTCCCCCCTAAGAATAGCGAAGCGATATTACACTGAACACTACAATG TCAAATAGTACTCAATAAATATGACTGTAAAAATATGTGACTGTGAAGGCGAATGTTGTA AGGACTCTTGTCATTGTGGGAGCACCTGCCTTCCAAGCTGTTCTGGCGGTGAAAAGTGCA AATGTGATCACAGCACCGGAAGCCCTCAATGTAAGAGTTGTGGTGAAAAATGCAAATGCG AAACCACGTGCACTTGTGAAAAGAGTAAATGCAATTGTGAAAAATGTTAG

YOR031W, 69 aa (SEQ ID NO 258) MTVKICDCEGECCKDSCHCGSTCLPSCSGGEKCKCDHSTGSPQCKSCGEKCKCETTCTCE KSKCNCEKC

YOR096W, 1474 bp, exon1: 501-644, intron1: 645-1045, exon2: 1046-1474 (SEQ ID NO 259) **AAACCCATACACAATGAACCTTATCACACCCAAACATATGATATGGTATTAAAAAATGAA**

AAAAATTCATTATTCTTTAGCGTAATTATTGAAGAAAAAACAGTGCGCGCGGTAATTTTT TGTCACTCAGTAACTAGAGAGAGCCGAATGTACTCCCCCGGCTAGCTGGAGACCATGGC TCTGCCTAGGATTTCTCTTATGCTTTCCTTTCACCAATCACTTTGTTCCGGCGAGGCCCG CGAAGCTCGCTTTCTTCAGCCTAGCAATCATGTTCTTGCCAGCGTCGTAGACTACTGTA TGGCAGTTGCTGCACTTGCCATGAATATCCTAGTGAAGCCTCTATGCAATAATCCAGTTA CTGCGTTAGAATCCTGGTAAAATGTCTAATCTTATTACATTACAGCAACGTATTAGATTT TGATTGAAAATTAGTCCTTGCGACTTGGTATATATCTTATTTTAAGAAAGCTGAAAGGAA GAAAGATCATCACGAACAACATGTCTGCTCCACAAGCCAAGATTTTGTCTCAAGCTCCAA CTGAATTGGAATTACAAGTTGCTCAAGCTTTCGTTGAATTGGAAAATTCTTCTCCAGAAT

YOR096W, 190 aa (SEQ ID NO 260) MSAPQAKILSQAPTELELQVAQAFVELENSSPELKAELRPLQFKSIREIDVAGGKKALAI FVPVPSLAGFHKVQTKLTRELEKKFQDRHVIFLAERRILPKPSRTSRQVQKRPRSRTLTA VHDKILEDLVFPTEIVGKRVRYLVGGNKIQKVLLDSKDVQQIDYKLESFQAVYNKLTGKQ IVFEIPSETH

YOR248W, 100 aa (SEQ ID NO 262) MTPLLCLHHLLQQVSVTKIQTTKMQRSSPLNRLQLPMVASQSQSLSLSPMSPLPSTLQSP QIRLHNTLLSPVHLLLPLQVTYNGTTPLRLLIRPVGEL

YOR293W, 1255 bp, exon1: 501-552, intron1: 553-989, exon2: 990-1255 (SEQ ID NO 263)

AACTTTCGAAATATATACTCTGAGTTCTTGCTCCCCGTTTTGTACGATGTTCCTAATGCA
AACACCGTCCTTTAAAGATCCCCTGATAGGTTTCATTAAAGGCAACTTCCATACACGTT
GAAGTGCCAATTTTTTCCCTACATCCAAGCATTCTGGGTTTGTATGGGTGTTACACCGGT
TTTTCTTTTTTATTTCCAGAGAAGTACAATTTTAGGCGGGTTTCAAATTTCCCCTGTGTG
CGAGAAACGCTCCGGTACGCCTAGGCTCACTCCGGTCCTTCTCCCCATTTCTATCAGCGC
GATAGGCATACTGTGGGAGAGCGGCACTAGGGAGACCGGTGGGAAGCACCGTATCTAGTA
ACGCACGCTCTTTTGCAAAAATATCCATTAATTGCATGTAACTTAGATTAACACTGGTAT
TAAGATTTCGCAATTTTTGGGCTGGATTATTAAGGTCGAGTAGCAAAGTTTAGCAAGAACA
GTACGAACTAAGTAGCCAAGATGTTGATGCCAAAGGAAGCAGAAACAAGATCCACCAAT
ACTTATTCCAAGGTATGTTTTAGAATAACTTTCAGAAAGCATGAAGATACACGGAAAGTC
AAGCGAGGGAAGTTATGCGTATACACAGTAGCGGTAGTGCATTCACATACACGATGTT
TCAAACACACACAGATGGATACCATGCATATGAGGTTAAAGGATTTCTTATGAATATATTAG
TGGATTACATAGAAGAAATTACAAGGAACCGTGTGACGACATTTTCGAAAGGACAGCACA
AGGCCATCGACCTTGGAGACGTATGAAATATGGTTATACTTTGGGCAAGAAAA

YOR293W, 105 aa (SEQ ID NO 264) MLMPKEDRNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS WQYYYYTLTEEGVEYLREYLNLPEHIVPGTYIQERNPTORPORRY

YOR312C, 1432 bp, exon1: 501-507, intron1: 508-914, exon2: 915-1432 (SEQ ID NO 265) TATTTACAAGCTAGATAAAAAAAAATCAAATAGCAAGCTATTCTGTCATATCTTAAGGT CGGGACTGTTCACCCGTACATTTTACGTTTCCGACGCGCGATGCTATCTTTGAATTTTT ATCTCTTTCAGGTAACCCCATGACCAGTAGGGCGGCTTACTACCGAAGAGAAAAATGTCC GCGGCCTAGACAGTTACTTCCCAGGCCAGGCCAGGCCACACGGACAGAGGCAGATTCCA AGTTGTTCCGCATAGTCTGTCTAGCTCTTTCTCAATTTTCCGCCAGATTCTGTCTAATTT TTTGAGGGCATTATTTTTGCAGAAGATAATAGAAGAGAACCGTAACAAAGGAATCAAGCA TTTATATGGTGAGCTCAAATTGAATGAACATATCGTGGAAATTTAAAATACTGAAGAATA CCCAATAAGTCAATGCAACCTGTGAATGTTTTTCCTGAAATACGCCGAATACTGAATACG ATTATTACCATAAATTGCTTCTAGAAGGAAGGCGGTGTACCATTTAATACTGATGATATG GTTAATATCATTTGAGAAGTCTTCACATGAGGACTATAGAACTACCATCCAGGAATTATA AATAAAGCAATATTTTTGAAATATGCAAGTTTACTAACAAGAATAAATTCTTTTTTGATT TTTATCTTTAACAGTGGCTCATTTCAAAGAATACCAAGTCATTGGTCGTCGTTTACCAAC TGAATCCGTTCCAGAACCAAAGTTGTTCAGAATGAGAATTTTTTGCTTCAAATGAAGTCAT CGCCAAGTCTCGTTACTGGTATTTCTTGCAAAAATTGCACAAGGTTAAGAAGGCTTCTGG TGTTTGGGTTAGATACGATTCCAGATCTGGTACTCACAACATGTACAAGGAAATCAGAGA CGTATCCAGAGTTGCTGCCGTCGAAACCTTATACCAAGACATGGCTGCTAGACACAGAGC TAGATTTAGATCTATTCACATCTTGAAGGTTGCTGAAATTGAAAAGACTGCTGATGTCAA GAGACAATACGTCAAGCAATTCTTGACCAAGGATTTAAAATTCCCATTACCTCACAGAGT CCAAAAATCTACCAAGACTTTCTCTTACAAGAGACCATCAACCTTCTACTAA

YOR312C, 174 aa (SEQ ID NO 266) MYLAHFKEYQVIGRRLPTESVPEPKLFRMRIFASNEVIAKSRYWYFLQKLHKVKKASGEI VSINQINEAHPTKVKNFGVWVRYDSRSGTHNMYKEIRDVSRVAAVETLYQDMAARHRARF RSIHILKVAEIEKTADVKRQYVKQFLTKDLKFPLPHRVOKSTKTFSYKRPSTFY

YOR369C, 932 bp, CDS: 501-932 (SEQ ID NO 267) CGCACCTCGTTATTGAGGTATTGCGAATGTAGCAGTTGAATAAGCAAAGACGAGGTTTGT ACATCTTGGCATATTAAATGGTTATTTCGGGGTTTGTTTCGGCTCAACGGTGATATAAAA AGAAATCCAGTACTGTTTACCATTGTGCATCCGTACATTTGATTTGTTTACAACATCTTC CAAGCAAACTTACAATTTGCAAAATTTCATCGAATTCTCCGCAGGACATATTATAAAAGT TATGTCATCTCTTATCACAACAGGTCTATAAGTGTTCCTTGTTCAATTGTTTTTCCCAAT TCAAAACTCTTCACGGAGCAGTTTAATTATCTTACTGTCGAAGAAGTCAAAAACTAGACT ATATATTATTGAGAAGAAAAATGTCTGACGTTGAAGAAGTCGTTGAAGTTCAAGAAGAAA CTGTTGTTGAACAAACTGCCGAAGTTACTATCGAAGATGCTTTGAAGGTTGTTTTGAGAA CCGCTTTGGTTCACGATGGTCTAGCTAGAGGTTTGAGAGAATCTACCAAGGCTTTAACCA GAGGTGAAGCTTTATTGGTTGTTTTGGTCAGCTCTGTTACTGAAGCTAACATTATCAAGT TGGTTGAAGGTTTGGCTAACGACCCAGAAAACAAGGTTCCATTGATCAAGGTTGCTGATG CTAAGCAATTAGGTGAATGGGCTGGTTTGGGTAAGATCGACCGTGAAGGTAACGCCAGAA AGGTTGTCGGTGCCTCCGTTGTTGTCAAGAACTGGGGTGCTGAAACTGATGAATTGT

CCATGATCATGGAACACTTCTCCCAACAATAA

YOR369C, 143 aa (SEQ ID NO 268) MSDVEEVVEVQEETVVEQTAEVTIEDALKVVLRTALVHDGLARGLRESTKALTRGEALLV VLVSSVTEANIIKLVEGLANDPENKVPLIKVADAKQLGEWAGLGKIDREGNARKVVGASV VVVKNWGAETDELSMIMEHFSQQ

YPL047W, 99 aa (SEQ ID NO 270) MTEETITIDSISNGILNNLLTTLIQDIVARETTQQQLLKTRYPDLRSYYFDPNGSLDING LQKQQESSQYIHCENCGRDVSANRLAAHLORCLSRGARR

YPL090C, 1605 bp, exon1: 501-506, intron1: 507-900, exon2: 901-1605 (SEQ ID NO 271) GTAAGCAGAAGCCGGAAGAAGACAAGAGGTTCATTCAGAGAAAACATCCGTACATTCGAG TTCTCATTGAACCCATACATTTCAACTATTTTTACATAGTTCGTTTTTCATGTGTAAAAT TGTCATCGACGCGCGGAGCATCGGAAAGTTGGAACGTGCGCGATTGCACCAATCCCACT GGGGCCGTGCATTCTGTAGGCAGGAAGCCACTGGACACTCTGCCCGTTCCCACTTGGAAG ATTGGCGTAATTCCACGCTCCTCTATCGATTCTAGCGGGAAAGTTATCTCTCCTGGTAAG TAGGAACATCATGATGCTGCAGTTTCTTTGAAATTTCATATACAGTGTTACCAAGGATAA AGTGGTTAATGCTTATTCGTCATTGAATTTTTATATTTGCTTAAGAGAAGTGACAAAAGA GTGAAGACAGACTATACATCATGAAGGTATGATTTATGATACTATTATTGAGGGGCAACA ACCAGACGTCGTAAAGATTTTAGAAATTTTTTATGGAAAGAAGCAGGAAGACTACCATAT ACTAATTGATGCGTTTGTGGCGTTATTTTTAAACAAACAGAGCGGGTTTACATATACTGT TACTACAAACCGTGAAATTGAAGCAGTTCATATACTTGGAGTATAGTCAATAAAAGACAA GCTTTTTCATCTTCCACTTAATAATTTCTCTAGAGTAATAAACTTCACCCTATTCAAACA TTAATTTTGCAATAGTATACTAACAAATTTTCTTAATAACCTGTTGAAAATTTAAAATAG TTGAACATTTCTTACCCAGTTAACGGGTCTCAAAAGACCTTCGAAATTGATGATGAACAC CGTATTCGTGTTTCTTCGACAAGAGAATCGGTCAAGAAGTCGATGGTGAAGCCGTTGGT ATGAAGCAAGGTGTTTTGTTGCCAACTAGAATCAAGTTGTTGTTGACCAAGAACGTTTCT TGTTACAGACCAAGACGTGATGGTGAAAGAAAGAGAAAGTCCGTCAGAGGTGCCATTGTT GGTCCAGATTTGGCTGTCTTGGCTTTGGTCATTGTCAAGAAGGGTGAGCAAGAATTGGAA GGTCTAACTGACACTACTGTTCCAAAGAGATTGGGTCCAAAGAGAGCTAACAACATCAGA AAGTTCTTCGGTTTGTCCAAGGAAGATGACGTTCGTGATTTCGTCATCAGAAGAGAAGTC ACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAAAGATTGGTTACTCCTCAA AGATTGCAAAGAAGAGACACCAAAGAGCTTTGAAGGTCAGAAACGCTCAAGCTCAAAGA AAGGCTGAAATCAGAAAGAGAGAGGCTTCTTCTTTGAAGGCTTAA

YPL090C, 236 aa (SEQ ID NO 272) MKLNISYPVNGSQKTFEIDDEHRIRVFFDKRIGQEVDGEAVGDEFKGYVFKISGGNDKQG FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAIVGPDLAVLALVIVKKGEQE LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVTKGEKTYTKAPKIQRLVT PQRLQRKRHQRALKVRNAQAQREAAAEYAQLLAKRLSERKAEKAEIRKRRASSLKA

YPL137C, 4331 bp, CDS: 501-4331 (SEQ ID NO 273) GTCTCAGTGATGCAATCATCGCACGGCATTAATTAAGGTTAAGGAACCACTTCTCT ACGCCATACTCCAAACAATAACAATATTAGACCTAGCCAATTGATACCCATGAGCGTGCA GTCATTGCCATGGATTATTCATCTCTTTTCGCTGTTCTCTTTTCTAAGTTTGTCATC ATCATGCCTTCACTTTTGCCTTTCCATCTTTCTTTTTGCTGCAAAATAAAGGGAAGAGGG GTAAAAACGCAAGGAAGAACAAGAAGAAGAAGGGGTAGTGCAAGAAAAAGAAAAGAAGAAAA GAGCGTGTTTTGGGAAATAACACCACAGCATAAAGCTAAAATTCAGTTTATATAATCTAT GTGGAGATAGCATCTAGGTTATGATAACTAACACCGAGTTCGATGTGCCCGTAGATTGGT TGTATAAAGGTAAGAGTAGACGGAAGACAAATACGAAGCCATCGAGGCCTTCTACGTCGC CAGCCTCCTCATCTACGTCCTCTTCGAAAAACGGAGACAATAGCACGAGTGGTAACA GGTCTAGCAATGATAAGCCTCGTGCGAGGTCGTCATCTGTATCCAATGCAGCACTTTGTA ATACTGAGAAACCAGATTTGAAGAGGAACGATGGTAATACCTCTGCATCAGACACTGATA ACATACCGCTACTTACTCCTATTAATAGCGGTAACCGGAGCGATTCCGCTGACATTGATA ATCCGGCTACCGTAGACGCCATAGACCTTATAGATAATGATGACAACGGCTCAAGTACTC AATTTGTAAGGAAAAAACGTTCCACTTCTATATCCAATGCTGTGGTCTCGTCCAAACCAA GACTGGCCAGTTCTGCCATAAACGCCACCGCATCTTCTTCTGTTGGCAAGGGAAAGCACC CGCCAATTTCTTCACCATCTAATGCTACTCTCAAGAGAAGCAACTCGACTAGTGGAGAAA AGACTAAAAGGTCGATTTTTGGATCTTTGTTTAGCAAACGGTCTACCTCTTCTTCAGCTT CCACTGCCAAGAAACCATTACCTGTTGTTAATACTAGCACGACTGAGAATGAGTCTGGTG GCATTAAAGCAGTTGCGACTCCTGATCCACGGGTGAAGGAGATATCATCACCAATGAGAG GAGTGGCACCAACAGCTAGCAAGCCACAGACACCTATACTCCCCTCCCCTGCACTTGCAG TAAAAGACCTATCTACAGTTTCATTGAAAAGGGTCTCGTTTGCCGTCGATAAATTCGAAT CCGATCCTCCCAACACTTCCTTCAAGAACCCCAAAAAAGGGAAACATCCTTATCCCTG ATGACATGATAAGCGAGGTTCCTTCTATTTCCGTGGGTATTTCCAGTAGCAACCAATCGG CCAAGTCAACCAATTCCAACATTAAGGGACCGTTGTACACTAAGAAGTCTAAAGAATATA TACTCGCCCTGGAAAATCAAAAGTTGGCTTTAAGGGAGGCTGCTAAGCATCAGCAAGAAG CTCATTTTGCTGCTAATAGAATAGCCTTTGAAGTAGCCAATTTTAAGACTGCTTCGGATG CAGGCGGTAAGCTTACTGAAAAGTCATCAGAAGGCACCATTACGAAGCAAAGAGAAGAGG TGTCACCTCCAAATGTTGAAGCTGATCGGGAGCTTGAGAATAATAAACTTGCAGAAAACC TCTCAAAAGCCGGCATTGATAAGCCCATTCATATGCATGAGCACTATTTCAAGGAACCTG ATCAAGATAAGTACCAAGACGGTCATTCTATTGAAAATAACGAAGTTACGCTGGATGTTA TTTACACAAGATGCTGCCATTTAAGGGAAATTTTACCCATTCCGTCTACCCTAAGACAAG TAAAGGACAAGACAGCTCCCTTGCAAATATTGAAGTTTTTGAACCCTAAGCCTACCTTGA TCGATATTCTTTCCTTTTGTGATTTCATCACCATTGCTCCCATTCACACGATTGTTTTCG ACAATGTAGCTTTAAACCAGGATATGTTCAGAATAATTATTTCTGCTTTGGTAAACTCCA TATGTAAGTTCCTTTTGCTAAACAAATCACTGAACAAGCTCGACATTTCCCAAACGAAAA TCAAATCTGACCTTGCTGAATCACTATATCGCCATAACATGGATTGGAACTTGTTTACTG ACGTCTTGTCTCAGAGATCTCACAAACCTATAGAAGAATTGTTATTCAATGGTATTCAAT TTAGCAAAATTCCTTACTCATGCTTTGCACGTTTACTGACATCCTTTGCTACCCAAAAAA ACTTTCCAGAATCGGCATCAGGCTTGGTTTAGCAGGTGCCACTACTTCCAATATCTCTC AGGATTGTCTGAAATTTATCTTCAATTGGATGTCTCAATATAACGTCCAGGGTGTGGATC CATATGATAACTTAAGATATTTCATTTTGAACAGCACTAATATTTCGACTTCTTATGATT ATTTGTCGCAATGCTTTCCTGACATTTTACCCTACATGTACAAGTATTTACCAAGATTTC CGAACCTGAAGAGGATACATTTGGATAGCAATAATTTGACATTAAAGGAACTAGCTGTCG TTTGTAATATTTTGATTAAGTGCAAATCGCTCTCGCATGTGTCAATGACTAATCAAAACG TTGAAAACTTCTATCTAATGAACGGCACAGATTCTCCCGTTCAACAAACTAACACAGACG GCGACTTGGATAGTTCGAGCACATTGGACGTTAAGGGCCAATTTGCTAAAAATAGTTTTT CATCCACACTTTACGCATTTGCTAGAGACTCTCCAAACTTGATTGGTTTAGATTTTGACT ATGATTTGATATCAGAAGAGTTCAATCAAGAATAGCACTGTGCTTGATGAGAAATATGA AACGGACCATGGATTCGACTTTCCAGTTAGATGAATTGGATTCGCAAGATGATTTGCTAT TCGATGGCTCTTTAGTAACTATGACCGCTGAAAGTGTTTTAGAAAAACTGAACTTGTTAA GCGATAAGAGTACAAAGGTCAAAAAAGACACCACGAAGAGATATTTGCTGAAAAAATATA

TTGAAAAGTTCCATATCTTGCACCATAATGTTCAGCATACAATAGATACTATGTTCGAAA AAAGGAAATCAGGTGAATTGCCATTGCAAGAAAAAGAAAACCTTGTAAGATTACTCCTTT TGGAACAAACTTATGCAATATACTAGAATTGTTTTCGCATAATCCGAATCTGAATGATG TCCTTGGATCCAGCAGGATGATTCGAAGGAAAGTGTTGACTCCAGCGAAGATTCAAAAT TACCAGCATTGAAGCACGTTGAATCCGGATACCATGTTCCCGAAGAAAAAATACAACCTG AGAATGATGTAATTACAGCAAGACCACATTTAATGGCCACCGATTCTGGTAAAACTATTG **ACGTTTTCACAGGCAAACCATTGGTGTTCAAGCATACATCATCTAGTACTTCTGTAGGTT** GTAAAAAGCAGGAAGAAGAAGAAGGTGAACTACATAAATGGGGTTTCTTCGTTCAGCAGC AGAGGTCTTTATACCCTGAAAATGAATCAACAAGGCAGACACCTTTTGCATCAGGTGATA CGCCTATCAACACAGAAACAGCTGGTAAGTCAACTTCATCTCCTTCAGTTTCAACTTCTA ACAATGAAACTGCTACCACTAGTTTATTTAGCCCAGCTAATCCTAAGATTTTACCAAAAA TTCCATCCGGTGCTGTCTTAAGATCGGCAATCATGAAGGCTAAAGGTATTGATTCTATCG ATGATTTGATTCAGAACGTTAACTCCAACAACATAGAATTGGAGAACATTTATGGTGAAT CCATTCAGAATAGCGCTTCGACATTTACACCAGGCGTGGATTCTGATGTATCTGCGCCCA ATACCGATAAAGGATCCGTAGAAACATTGCCTGCAGTCTCAACTGACGACCCAAATTGTG **AAGTCAAAGTCACTGCTACCTATGACAAACTATTAAATAATTTGTCGATGGAGAGGTCAA** TCAGACTTTGA

YPL137C, 1276 aa (SEQ ID NO 274)

MITNTEFDVPVDWLYKGKSRRKTNTKPSRPSTSPASSSSTSSSKNGDNSTSGNRSSNDKP RARSSSVSNAALCNTEKPDLKRNDGNTSASDTDNIPLLTPINSGNRSDSADIDNPATVDA IDLIDNDDNGSSTQFVRKKRSTSISNAVVSSKPRLASSAINATASSSVGKGKHPPISSPS NATLKRSNSTSGEKTKRSIFGSLFSKRSTSSSASTAKKPLPVVNTSTTENESGGIKAVAT PDPRVKEISSPMRGVAPTASKPOTPILPSPALAVKDLSTVSLKRVSFAVDKFESDPPQQL PSRTPKKGNILIPDDMISEVPSISVGISSSNOSAKSTNSNIKGPLYTKKSKEYILALENO KLALREAAKHQQEAHFAANRIAFEVANFKTASDAGGKLTEKSSEGTITKQREEVSPPNVE ADRELENNKLAENLSKAGIDKPIHMHEHYFKEPDQDKYQDGHSIENNEVTLDVIYTRCCH LREILPIPSTLRQVKDKTAPLQILKFLNPKPTLIDILSFCDFITIAPIHTIVFDNVALNQ DMFRIIISALVNSTVLDKLSLRNVRIDODGWKLLCKFLLLNKSLNKLDISQTKIKSDLAE SLYRHNMDWNLFTDVLSQRSHKPIEELLFNGIQFSKIPYSCFARLLTSFATQKNFPESGI RLGLAGATTSNISQDCLKFIFNWMSQYNVQGVDLAFNDLSTMIKPMVGKLSALSYDNLRY FILNSTNISTSYDLALLLKYLSKLPNLIFLDLSNLSQCFPDILPYMYKYLPRFPNLKRIH LDSNNLTLKELAVVCNILIKCKSLSHVSMTNQNVENFYLMNGTDSPVQQTNTDGDLDSSS TLDVKGQFAKNSFSSTLYAFARDSPNLIGLDFDYDLISEEIQSRIALCLMRNMKRTMDST FQLDELDSQDDLLFDGSLVTMTAESVLEKLNLLSDKSTKVKKDTTKRYLLKKYIEKFHIL HHNVQHTIDTMFEKRKSGELPLQEKENLVRLLLLEQNLCNILELFSHNPNLNDVLGSSRD DSKESVDSSEDSKLPALKHVESGYHVPEEKIQPENDVITARPHLMATDSGKTIDVFTGKP LVFKHTSSSTSVGCKKQEEEGELHKWGFFVQQORSLYPENESTRQTPFASGDTPINTET AGKSTSSPSVSTSNNETATTSLFSPANPKILPKIPSGAVLRSAIMKAKGIDSIDDLIQNV NSNNIELENIYGESIONSASTFTPGVDSDVSAPNTDKGSVETLPAVSTDDPNCEVKVTAT YDKLLNNLSMERSIRL

YPL159C, 1262 bp, CDS: 501-1262 (SEQ ID NO 275) TCAAACAGCATTATATCGCTACCAACAGGTGTGGTCAAGAGGTCATTGACTCTTCCTGTC TCAACGTATCAACCATAAGAACCATAATCATAATAATTGTTTACCTTAATGGCGATATCG CCTTTTATCACCATCGACGATAACAAACGCCTATTCTGTCTACCGTTTCTTTTTTCGCT CGCAATATCAGAATCGTTTATCCCAAAGGGTAGTTATAGCAACTATTTAAATAACTTAGA TGTTTCTTTAACTTATTCCGTCATACGTACACAAACACCCGCTAGATATAGCACTCCTTG CTGTCGAACATTATAAAGGTGCTTTTAAAACTACTAATCGTATATTCAGCAGGTCAGAAC GCAAAGTCGGACGATAAACTATGTTGAAGCTAGCTCGTCCATTTATTCCGCCTTTATCAA GGAACAATGCCATTTCTTCAGGAATAGTTCTCACTTCTAGAAGATTTCAGTCTTCCTTTA CGTTCTTAAGTAACCAGTCTTTACTATCTAAAAATCAAATGAAATCCAAAAGAAAAAAGG GCAGTAAAAAGGCAGCGTACCATCGTCAACCCCCGGAACACGAACATACTGCACCACTTA TAAAGCAAAACAAGACAATCACAAAGAAGAACATAGCGATGTGAGAGGTTCTCATTTAA AAAAGAAAAGAAGCGATTTTTCGTGGCTACCAAGAGTACCATCCACCTCACATTTAAAGC AGAGTGACATGACCACAAATGTACTCTATTCTGGATATAGACCCTTATTCATCAATCCCA ATGACCCGAAGCTAAAGGAAGACACCGGAAGTACGTTATACGAATTTGCGATGAAGCTTG AAGATTTAAATGAACCTCTATCACCATGGATTTCCTCTGCCACTGGACTTGAATTCTTTT

CAGAGTGGGAGAATATACCTAGTGAACTACTGAAAAATTTGAAGCCTTTTCATCCACCTA
AGGAAAAATCAATGAACACAAATGAGCTTATTCATGTAAGTGCTAAGAGAAATACATTAG
TTGACAATAAAACAAGTGAGACGCTTCAGCGGAAAATGGATGAATTTTCAAAGAGAAGAG
GAAAGGGGAGAAAAAAGTCAGTAGTGACGTTGCTCCAAATGAAGAAAAAACTTGAGGGAT
GA

YPL159C, 253 aa (SEQ ID NO 276)
MLKLARPFIPPLSRNNAISSGIVLTSRRFQSSFTFLSNQSLLSKNQMKSKRKKGSKKAAY
HRQPPEHEHTAPLIKQNKTITKKEHSDVRGSHLKKKRSDFSWLPRVPSTSHLKQSDMTTN
VLYSGYRPLFINPNDPKLKEDTGSTLYEFAMKLEDLNEPLSPWISSATGLEFFSEWENIP
SELLKNLKPFHPPKEKSMNTNELIHVSAKRNTLVDNKTSETLQRKMDEFSKRRGKGRKKS
VVTLLOMKKKLEG

YPL175W, 1940 bp, exon1: 501-514, intron1: 515-568. exon2: 569-1940 (SEQ ID NO 277) ACGTTATTTCAAAACACATACGAAATCGCTGGACTTTCTCACTAAAGGCTTCCGGAGCC TGCGGTTCTTCCATCCCCATCTTTCCACATATACCGGGGGTTCTGATGGCATTCCTATA GCTTGCTCAAAGTCCTGCGAGTTTAGCTCATCTTGTGAGTTATTTGCTGGTTCTTCAACA TTCGGAAGAGTAGTGTAGCCCCTAGTATTCACCATATCCTTTGTATACTCATATGCGAAC TTGTCTAATACAATGTATACCAAAAATAACAGCTTGAAAAAAATCTCAGGGTCTTTTCAT TGAATAATCTCATTCTGCTATTTTAAGTTTTTCGTTTGCAACCCGAGACTGTCGAGCTAG AAAATTTCATTGATACGATTTAAAAATAATCGATGCCAGTAATAGCCTCAAAAAACTTAT GCAAAAATACGAGATACTATAAACTACAGCTTAGCTAACTCTAACATTATTATAAAAAC AATGGGCTTCAATATAGCGTATGTCTAGCTCACAGCATGTGTTCCAAATACATTAAAGAA GATCTCTTTTGTTGTTGATACTAACCAGTAAAGTTGAGAGTTATAACAATGAAAATAGGA CGCAGAAACTAATCGATTTGGGCCATTCTGTCGTCATTATAACTCACGCTTACAAAGATC GAGTCGGCGTACGACATCTTACCAACGGTCTAAAGGTCTATCACGTACCATTTTTTTGTGA TTTTCAGAGAAACCACTTTCCCCACTGTTTTTTCAACATTTCCAATAATAAGGAATATTC TTCTCAGAGAGCAGATCCAAATTGTTCATTCTCATGGTAGCGCTTCCACGTTCGCTCACG AGGGAATTCTTCATGCTAATACTATGGGATTGAGAACTGTGTTCACGGACCATTCACTCT ACGGTTTTAATAACTTAACGTCGATTTGGGTGAATAAGTTGCTAACATTTACCTTGACAA ACATAGATCGGGTTATATGTGTTTCTAATACATGCAAAGAAAATATGATTGTTAGAACAG **AATTAAGTCCTGATATAATCTCAGTAATTCCCAACGCAGTGGTGAGCGAAGATTTCAAAC** CAAGGGATCCTACTGGTGGCACCAAGAGAAAACAAAGTAGGGATAAGATAGTGATCGTGG TTTGTTCCTCACATGAAGATGTCGAATTTATAGTAGCGGGCGATGGTCCAAAGTTCATAG ATTTTCAACAAATGATTGAAAGTCATAGACTACAAAAACGTGTGCAACTCTTAGGCTCTG TTCCACATGAGAAAGTCAGGGATGTATTATGTCAAGGTGACATATATTTACACGCTAGTT TAACAGAAGCATTTGGTACAATTCTAGTTGAGGCCGCATCTTGTAATTTGCTAATTGTAA CGACACAAGTCGGAGGAATTCCCGAAGTGTTACCAAATGAGATGACTGTTTATGCAGAAC AGACATCCGTTTCTGACCTTGTTCAAGCAACAAATAAAGCTATCAATATCATAAGAAGTA TAGCCAAAAGGACAGTAGAGATATATACTAATATATCTTCTACTTCTTCCGCTGATGATA AAGATTGGATGAAAATGGTAGCAAATCTTTACAAAAGAGATGGAATCTGGGCTAAACATC TTTATCTGTTATGTGGAATTGTAGAGTACATGCTTTTTTTCCTCTTAGAGTGGCTATACC CCAGGGATGAAATCGATCTAGCTCCAAAATGGCCCAAGAAAACAGTGTCTAACGAGACGA AGGAAGCAAGAGAAACTTAA

YPL175W, 461 aa (SEQ ID NO 278)
MSSSHKVESYNNENRMLCDFFYPQLGGVEFHIYHLSQKLIDLGHSVVIITHAYKDRVGVR
HLTNGLKVYHVPFFVIFRETTFPTVFSTFPIIRNILLREQIQIVHSHGSASTFAHEGILH
ANTMGLRTVFTDHSLYGFNNLTSIWVNKLLTFTLTNIDRVICVSNTCKENMIVRTELSPD
IISVIPNAVVSEDFKPRDPTGGTKRKQSRDKIVIVVIGRLFPNKGSDLLTRIIPKVCSSH
EDVEFIVAGDGPKFIDFQQMIESHRLQKRVQLLGSVPHEKVRDVLCQGDIYLHASLTEAF
GTILVEAASCNLLIVTTQVGGIPEVLPNEMTVYAEQTSVSDLVQATNKAINIIRSKALDT
SSFHDSVSKMYDWMDVAKRTVEIYTNISSTSSADDKDWMKMVANLYKRDGIWAKHLYLLC
GIVEYMLFFLLEWLYPRDEIDLAPKWPKKTVSNETKEARET

YPL180W, 2900 bp, CDS: 501-2900 (SEQ ID NO 279)

CTCAATGGGAATTGAGTGAAGATCAGTCTGATCGAGAGGAATTTGTACGATTCGTGGAAA ACCAGCATTTCGTAGAAAAAGTTGATACGATTTACAACGGTTATAATGAAAGTCTATCAA TGATGGACGACCTGACTAGAGAGTTACTACTATGGGAGAAAAAATATTCAAATAACACTA ATGCCATTCAATAAACGCAAAACACTGCAATATTATTCTCAACCAAAGTATAACTGTAAT GAGGCGAACAAACACATCTATACATATATATACATCTATATGGATATAAAAAACGACTAAT TCAACGTTGTTTTTATCAACCGAGCTTACTCTTGTACGGGTAACCGCAAGGATAGCTAGT TGCGGATGGTATAGCGATTTGGCTGGCACGATGATTAAGGAATCCAAACATCTAATGGAC TAGCACATTCTATCGATTTACGGGTCAGGTAAACATAGATATTGGGATATATCATATATC CTTACTGAGTAACTATAATTATGGTTCATCGAGGAAGGACTTTGAAGTCAGACACTGATG TAACATCTCTTAATGCGTCAACAGTATCACACCAGTCAAAGCCATTTAGACAGTTTTCGA CTAGGTCGAGAGCAAAGAGTAACGCAAGCTTCAAAGGTTTGCGTAGAGTTTTAACACATG ATGGCACCCTGGATAATGATTATTTTAATAAGCACAACGTTTCTCAGAAATGCAAGAGTT CTGATGCACTTTTCAGAAAGCGAACGATTAGTGGGTTGAATATGACAGCTTTAACAAGAG TAAAGTCCAATCAAGGAAAAAGATCAGCATCCTTTCATAGTCCGGTGCATAATACGCTGC TCAGTCCAAAGAACAGCAGTCATTCTAATACTGGAACTGCTGGTTTCGGCCTGAAACCAC GAAGAAGTAAAAGTACCCAATCTGTTCTGAGTCTTCGAGATGCGCAAGAATCTAAAAAGA GTGAATCTACTACTGACGAGGAGGTGGAATGTTTTTCGGAAGACAACATTGAAGATGGAA AGGTGAATAATGATAAAGTAATAGCCGAGCATGTTATGCCTGAAGAAAAAAAGAATGTGC AGCAATTAAATCAGAATGAATTACAATCCCCGGATTCAATAGATGAACAAGAAGAAGATA AATCAGGTACTGATGGAAAGGAAAATCATAGAGCTGTATCCTTACCATTACCTCATTTAT CTTCCAATAACTATTTCGGAGAATCAAGCCATTCTATAGAACATCAGAAAGATGGAGAAA CATCTCCAAGCTCAATTGAAACAAAACTGAATGCAACAAGTGTAATCAATGAAGAGGGGC **AATCAAAGGTGACGAAGGAAGCTGATATTGATGACTTGTCCAGCCATTCTCAAAATTTGA** GGGCCTCATTGGTTAAAGCGGGCGATAATATATCAGAAGCACCATATGATAAAGAAAAAA **AAATTCTTGATGTTGGTAATACCTTAGCTGCACATAAAAGTAATCAAAAACCAAGTCATT** CAGATGAACAGTTTGATCAGGAAGATCACATTGATGCCCCTAGGAGTAATTCATCAAGAA AAAGCGACTCGAGCTTTATGTCTCTTAGGAGACAAAGTTCTAAACAACAAATTATTAA ACGAAGAAGAAGATCTAATCAAGCCTGATGATATTTCTTCCGCTGGTACCAAGGATATTG AAGGGCATAGCTTACTGGAAAATTATGCGCCTAATATGATTCTCTCCCAGTCGACTGGAG TTGAACGTAGATTTGAAAATTCATCATCCATCCAAAATTCGCTTGGGAATGAAATTCATG ACTCGGGTGAGCATATGGCTTCAGGTGATACTTTTAATGAACTGGATGATGGCAAATTGC GCAAGAGCAAGAAAAATGGTGGAAGATCTCAACTTGGCCAAAATATACCGAACTCTCAGT CTACTTTCCCCACCATTGCTAACATCGGTAGTAAAGATAATAATGTACCACAGCACAACT TTTCGACCTCCATATCGAGTTTAACCAATAATTTGAGGAGAGCTGCTCCTGAAAGCTTCC ATGGTTCAAGAATGAATAATATTTTTCACAAGAAAGGTAATCAGAATCTACTTCTGAGAT CCAACGATCTCAACAAAAATTCTGCAGCCCCGGCCTCTCCATTGTCCAACGAACATATTA CATCTAGTACGAACTCCGGTAGCGATGCAAACAGACAATCCAACTCAGGTGCCAAATTTA ATAGCTTCGCCCAGTTCCTTAAATCAGATGGGATTGATGCAGAATCAAGAACACAAAGAA AATTATGGTTGCAGAGGGAGAATTCTATTATGGACTTAAGTTCACAAAATGACGGTAGTG ACTCTATCTTTATGGCAGGAAACATTGATGCGAAAAGGGAGTTTGAGAGAATATCCCATG AATACTCTAATGTAAAAAGATTTTACAACCCATTAGATGAAGCATTGTTGAGAGTACAAC CTATAATAACGGGAAATGCAAATAATATCAGGAAAAAAAGCCATAACGATGCTCAGTCAA TCGCACATTCTAGCAGTGATACAGATCATAAGGATGAGGACGATTTGCTCTTTACTAACT ATGACAAAAATTTGATGATCTTTATCCACATCTTGCAAGTGCAAAGATTCAGGCAGTGT TGTCCGGTATATGGAAAAGCGAAAGTTACTTATTTAACAAGGATGTTAATCCAATCAACA AGAATAGGACAACGAGTACAAACCACAGCGTTGGCCACACTGCTTCACAGAATGCACGTA ACTTGCTGAGGGGCCCGATGGGTTCCAGCACGACTTTGCACCACCAACGCGTCATTAACT CTCTGCAGCCGACTACGAGGCAGTGAATCGCAGGATGGAAAATGTGGGCTACATGCATA CACAGCCACAACAAAGGTGA

YPL180W, 799 aa (SEQ ID NO 280)

MVHRGRTLKSDTDVTSLNASTVSHQSKPFRQFSTRSRAKSNASFKGLRRVLTHDGTLDND
YFNKHNVSQKCKSSDALFRKRTISGLNMTALTRVKSNQGKRSASFHSPVHNTLLSPKNSS
HSNTGTAGFGLKPRRSKSTQSVLSLRDAQESKKSESTTDEEVECFSEDNIEDGKVNNDKV
IAEHVMPEEKKNVQQLNQNELQSPDSIDEQEEDKSGTDGKENHRAVSLPLPHLSSNNYFG
ESSHSIEHQKDGETSPSSIETKLNATSVINEEGQSKVTKEADIDDLSSHSQNLRASLVKA
GDNISEAPYDKEKKILDVGNTLAAHKSNQKPSHSDEQFDQEDHIDAPRSNSSRKSDSSFM
SLRRQSSKQHKLLNEEEDLIKPDDISSAGTKDIEGHSLLENYAPNMILSQSTGVERRFEN
SSSIQNSLGNEIHDSGEHMASGDTFNELDDGKLRKSKKNGGRSQLGQNIPNSQSTFPTIA
NIGSKDNNVPQHNFSTSISSLTNNLRRAAPESFHGSRMNNIFHKKGNQNLLLRSNDLNKN

SAAPASPLSNEHITSSTNSGSDANRQSNSGAKFNSFAQFLKSDGIDAESRTQRKLWLQRE NSIMDLSSQNDGSDSIFMAGNIDAKREFERISHEYSNVKRFYNPLDEALLRVQPIITGNA NNIRKKSHNDAQSIAHSSSDTDHKDEDDLLFTNYDKKFDDLYPHLASAKIQAVLSGIWKS ESYLFNKDVNPINKNRTTSTNHSVGHTASQNARNLLRGPMGSSTTLHHQRVINSLQPTTR AVNRRMENVGYMHTQPQQR

1212 bp, exon1: 501-528, intron1: 529-667, exon2: YPL218W, 668-1212 (SEQ ID NO 281) TGATACAAGACAGGCATTAGGAAACACATGAGTTTTGCATATGTATTATGCAGGTTCATT GGATTTTATTTATTTCTTTTTTAATGCTAAGAAAGTAATTCCGCATAATTAAACGTGTG CTGGCCTCGATAGGTACCTATAGTATACAGAAGCTTACGAAAAGCTCCTGCAGGATGGCA CTTCTAAAATTCGCGCTCAACATGGCCGTATTGTACATTATATCGTTCTATCATTATATC GTATACGCCCGCATTACCCGACAACTCCGTCTGCAACGCGTTGACCAGAAAACTCGAACA AGAGATCGCATAAAAAACCAAAAGGAAACGAATTACTTGTCAAATAGTTATTGTAATGGA TCCTCTAGAAAGGCAAACAGTAGATTTATTTCCTTCTTTTCTAGAAACATCATTATAACT CCTGTTCACGTTTTTCGGATACTTAGTTTTATTCAATGTGGTAAACATTGAATGTTTTCA GCTTAAGATCTATTTTTTTTTTTTTTAGAAGAAATTGCGTCCTTTACTAACTTTATTTTAC TGTACAGTCAGAGATGTGTTGGCTTCCCTTGGTCTGTGGAACAACATGGTAAACTACTT TTCTTGGGTTTGGATAATGCCGGTAAGACCACATTGCTACATATGTTAAAGAACGATAGA TTGGCAACCTTACAACCAACATGGCATCCAACTTCTGAAGAACTGGCTATTGGTAACATT AAGTTTACAACTTTCGATTTGGGTGGTCATATTCAAGCTCGTCGTTTATGGAAGGATTAT TTCCCAGAAGTTAATGGTATCGTCTTTTTAGTCGATGCTGCTGACCCTGAAAGATTTGAT GAAGCACGTGTCGAATTAGATGCTTTATTCAACATTGCCGAATTGAAGGACGTTCCTTTT GTAATTCTTGGTAACAAGATCGATGCTCCAAACGCCGTTTCTGAAGCGGAGCTACGTTCT GCTTTAGGATTATTGAATACCACTGGCTCTCAAAGAATTGAAGGTCAAAGACCAGTTGAA GTTTTCATGTGTTCCGTTGTTATGAGAAATGGTTATTTAGAGGCGTTCCAATGGTTATCT CAATATATTTAA

YPL218W, 190 aa (SEQ ID NO 282) MAGWDIFGWFRDVLASLGLWNKHGKLLFLGLDNAGKTTLLHMLKNDRLATLQPTWHPTSE ELAIGNIKFTTFDLGGHIQARRLWKDYFPEVNGIVFLVDAADPERFDEARVELDALFNIA ELKDVPFVILGNKIDAPNAVSEAELRSALGLLNTTGSQRIEGQRPVEVFMCSVVMRNGYL EAFQWLSQYI

YPR102C, 1025 bp, CDS: 501-1025 (SEQ ID NO 283) TTCTTTACAATTCACCTTGCATTATTGAAGGAGTGCTATTCTTCGTTTTTGCCACCCTTTT GCTGTTTTCCCTCATATCACATAATACCCGGAGAGGCTCTTTCCTGCGACAGCGCAACAT CCAACCATCCTAAAGGTATGGGTGTACTGACGATGCGATTATTTCATTAAGTTCTGTCTT TTTTGTATAAATGAAAAAGAACGGTGAAATCCATAGAAATACAGAGAGCGACGCAAACA GCGCGCAGACTCTACGGGTAATAGACTCACATCCACGTGACCAGTTTCCAATCGAACTTT TTCACTTTGCAGGGAATTATTGTTTCACTAGCAAAGGTAGCCCACTTACCACTCAGCTAT ATTTTATTGTATTTCAACTAATATTATTTTTTTTTCAGTGGAAGGGAAGGTGAACCAAGA ACATACAAACATAGCCAAAGATGTCTGCCAAAGCTCAAAACCCTATGCGTGATTTGAAGA TCGAAAAGTTGGTCTTAAACATTTCTGTTGGTGAATCTGGTGACAGATTGACCAGAGCCT CCAAGGTTTTAGAGCAATTATCTGGTCAAACTCCAGTTCAATCCAAGGCCAGATACACTG TCAGAACTTTCGGTATCAGAAGAAACGAAAAAATTGCTGTTCACGTTACCGTCAGAGGTC CAAAGGCTGAAGAAATTTTGGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA GAAACTTCTCTGCTACCGGTAACTTCGGTTTCGGTATTGACGAACACATTGACTTGGGTA TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTTCTATGTCGTCATGAACAGAC CAGGTGCTAGAGTCACTAGAAGAAGAGATGTAAGGGTACCGTTGGTAACTCCCACAAGA CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAAGTACGATGCTGATGTTTTGGACA AATAA

YPR102C, 174 aa (SEQ ID NO 284) MSAKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIR RNEKIAVHVTVRGPKAEEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI GIFGMDFYVVMNRPGARVTRRKRCKGTVGNSHKTTKEDTVSWFKQKYDADVLDK

YBL003C, 899 bp, CDS: 501-899 (SEQ ID NO 457) TATATGACGGCAAGTGTCTCACTGTTGCATTACGCGATGTTTCTTTTCTTTGTTCTTGTAAG CGCGATTTTACCAGAACTAGATGGCGCTCGTGATCCTGAAAACGGGGAGAAATTTTGAGAAC ACCGCTTTATTAGGCGAAGCGGTGGGCACAGCTCACGCGTAAGGTGTTCCCATTATTTCTCA AAGTGATGCGAATTTCAGAGAACACATTAACCTGGGGGCCATAAACGCGACGTGCTACCATT TTCGTTACGTATACTTAGGCCAGAGATTACAACATGACTACTAATATCAAACATAACTCTAT ATATAAGGGATGAAGATGTATGCTTTCTTAGAATTTCAAACATGTTCCGTTAAAGTTTTACT TCATAAATTCTTGTCTTTTTACATAAGAATTAGGAAAGTACAGAACAAGAGCAAATTTAATA TATAATGTCCGGTGGTAAAGGTGGTAAAGCTGGTTCAGCTGCTAAAGCTTCTCAATCTAGAT CTGCTAAAGCTGGTTTAACATTCCCAGTTGGTAGAGTGCACAGATTGCTAAGAAGAGGTAAC TACGCCCAGAGAATTGGTTCTGGTGCTCCAGTCTATCTAACTGCTGTCTTAGAATATTTGGC TGCTGAAATTTTAGAATTGGCTGGTAATGCTGCTAGAGATAACAAAAAAACCAGAATTATTC CAAGACATTTACAATTGGCCATCAGAAATGATGATGAATTGAACAAGCTATTGGGTAATGTT ACCATCGCCCAAGGTGGTGTTTTGCCAAACATTCACCAAAACTTGTTGCCAAAGAAGTCTGC CAAGACTGCCAAAGCTTCTCAAGAACTGTAA

YBL003C, 132 aa (SEQ ID NO 458) MSGGKGGKAGSAAKASQSRSAKAGLTFPVGRVHRLLRRGNYAQRIGSGAPVYLTAVLEYLAA EILELAGNAARDNKKTRIIPRHLQLAIRNDDELNKLLGNVTIAQGGVLPNIHQNLLPKKSAK TAKASQEL

YDR442W, 893 bp, CDS: 501-893 (SEQ ID NO 459) CTTGTTATTTTGTAAATTGAGCTATGCAACATAAGATTCCTGCGATGTAAGAACTACTTGC TAATCAAGAGAACTTCAACAATTTTCCATCGCAGAGACGAAAAAACTGGAAAAAAATAAAAA GAAAAAATTGAAAAAGAATCGCGACTTCCGATTACATAACCTTATACGGAGTATGATACCAT TCTTGACATCAACACCACCCACGCAGCCCACGTGGCCGCTTCGTGTGCCTTGAAAATAC AGCCTTAAACGCAATCTCATTCGCGTTCTGTGGAAATTGTCTCGGACTACACGCTGGGCGTG CATCACCAGTGAAAATGCCGTACCGCCCCGCTTCCGGTTTTGTTTTTATAAATCCGACTGGA GAAATAGACTTCTGGGTTTACACCCCGGAATAATACTAAAACCAAAACTGGTAAATAGGGCT AAGTAGCGGTATGCACAGTAGCGGCGGAAGTATTAGCAATTTTTACTCTGGTGTGCACAAGA GTGTTCATCATTTTTTCACGGCTAGGATATGCCATGGAATATGGCCATCTTCGCCATCAGA GAGACCGTACCACACGTTTAGAGCAGCCAGGTTGCGAAACTCTTCTAAGATGGTTTCCAGCA ATTGTGTACTATCAGAATGTGGACAGTTTAAAAGGTTGACTGCGAATTTGTCCCAAACCGTA TCACCGTCGCATTTTTTGAATTTGATCAAAGCACCACTCCTAATAGCACAGCGATGCTGTGA GTGTGCCAGTGGGAACGGGTGCTGA

YDR442W, 130 aa (SEQ ID NO 460) MSRKTLPEKVYLSERIIDEEVAVCTVAAEVLAIFTLVCTRVFIIFFTARICHGIWPSSPSER PYHTFRAARLRNSSKMVSSNCVLSECGQFKRLTANLSQTVSPSHFLNLIKAPLLIAQRCCEC ASGNGC

CTGTTGCCATACATATTAGAAGCTGAAGCTGCAGCTAAGGAGGACGAGTTAGACAACAT AGAGGTCTCCAAATGA

YDR529C, 127 aa (SEQ ID NO 462) MPQSFTSIARIGDYILKSPVLSKLCVPVANQFINLAGYKKLGLKFDDLIAEENPIMQTALRR LPEDESYARAYRIIRAHQTELTHHLLPRNEWIKAQEDVPYLLPYILEAEAAAKEKDELDNIE VSK

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 463) TCCTTACTTTAGTCTATTATCAATATCTCTTCCCCCTCTAAATATGTACTCTTTTATTTTT TTTAATTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTTCCTGTGT TAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTCAGGACATTTTAAAC ATCCGTACAACGAGAACCCATACATTACTTTTTTAATATTCTTTTTGTTTTCACCGCCTTC TTTTTATTTTATCCGAAGATCTTTTGGAACCCGCTCTGCGAATAGCGAAGCTAGGATACCA GTGTATTATAACGTTTAGCATCAGTTACCCTTGAAAGCCCAACATATACAAAAATACGCGTC CAAGATGTCTACTAAAGCCCAAAACCCTATGCGTGATTTGAAGATCGAGAAATTGGTCTTGA ACATCTCCGTTGGTGAATCTGGTGACAGATTAACCAGAGCCTCCAAGGTTTTAGAACAATTA TCTGGTCAAACTCCAGTTCAATCCAAGGCCAGATACACTGTCAGAACTTTCGGTATCAGAAG AAACGAAAAATTGCTGTTCACGTTACCGTCAGAGGTCCAAAGGCTGAAGAATTTTGGAAA GAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACAGAAACTTCTCTGCTACCGGTAACTTC GTAAGGGTACTGTTGGTAACTCCCACAAGACAACTAAGGAAGACACCGTCTCTTGGTTCAAG CAAAAGTACGACGCTGATGTGCTCGATAAATAA

YGR085C, 174 aa (SEQ ID NO 464) MSTKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIRRN EKIAVHVTVRGPKAEEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSIGIFG MDFYVVMNRPGARVTRRKRCKGTVGNSHKTTKEDTVSWFKQKYDADVLDK

YGR106C, 1298 bp, CDS: 501-1298 (SEQ ID NO 465) GCAACATTACCACTTTGTACGGAGCGTCAGAAAGAACGCACCTCATCATTATTATGAGAACA GTACGATAACTTCTGTCTGAGATACGCTTCGTTGTTATAATACAAGTGAAACCGCCACGGAT AATTAGCAGCAATTGAACACAAGGGATATCATTTGTGTGACCTTTGTTCCTCTCATAGTTGC TGTGAACCCTTTAGTAACTATTAATGTTTATTTCATGAGACTAGTCAAAACATTCAATAACA ACACTGACTATGCTGCAGTTTCCGCAATAGCAAAATTGTGTCACATTACACGAAAGAAGAA AGAACGCTATTTCTTATAAGAGCAAACTGTTGATAAGTTTATAGCAAGAATAAAAAGGGTAA AAAGTCATTGATAATAACCACTGCTGTGACTATATATAATAAGAATCGAACTGTAAAGTTAA AGCAATGGTGTTCGGTCAGCTGTATGCCCCTTTTCATCTTCACGTTATCATGTTGTATTTCCA AACTGGGATACCATCAGCACTATATCTTCAACGGCAGATGTTATATCATCCGTTGACAGTGC TATCGCTGTTTTTGAATTTGACAATTTCTCATTATTGGACAACTTGATGATTGACGAAGAAT ACCCATTCTTCAATAGATTCTTTGCCAATGATGTCAGTTTAACTGTTCATGACGATTCGCCT TTGAACATCTCTCAATCATTATCTCCCATTATGGAACAATTTACTGTGGATGAATTACCTGA AAGTGCCTCTGACTTACTATATGAATACTCCTTAGATGATAAAAGCATCGTTTTGTTCAAGT TTACCTCGGATGCCTACGATTTGAAAAAATTAGATGAATTTATTGATTCTTGCTTATCGTTT AGATGAAGATGGTGACGATGAATATGCAACAGAAGAGACTTTGAGCCATCATGATAACAACA AGGGTAAAGAAGGCGACGATGATATTTTAAGCTCCATCTGGACTGAAGGACTACTAATGTGT TTAATAGTTTCTGCGTTGCTATTGTTCATTTTGATTGTTGCACTTTCTTGGATATCTAATTT

YGR106C, 265 aa (SEQ ID NO 466) MVFGQLYALFIFTLSCCISKTVQADSSKESSSFISFDKESNWDTISTISSTADVISSVDSAI AVFEFDNFSLLDNLMIDEEYPFFNRFFANDVSLTVHDDSPLNISQSLSPIMEQFTVDELPES ASDLLYEYSLDDKSIVLFKFTSDAYDLKKLDEFIDSCLSFLEDKSGDNLTVVINSLGWAFED EDGDDEYATEETLSHHDNNKGKEGDDDILSSIWTEGLLMCLIVSALLLFILIVALSWISNLDITYGALEKSTNPIKKNN

YGR182C, 117 aa (SEQ ID NO 468) MSRQSAFKFQNGNRHERACLSDVHKILIIILYSTKGKRELGKRITHFMYIHIFCTYLYQASI VQYCSSTLLNVIAFSWYPLNLIYKYEYILRSKLILMVCLDFARSGGVLDSGDVSL

YGR183C, 914 bp, exon1: 501-503, intron1: 504-716, exon2: 717-914 (SEQ ID NO 469) AAATACAAATCCAAGAAACCTCGATGAGGATGACTCTGATGATAATGATGACTCTGATGAGC GAGAGATTTGGTAGATTCAAGCCCTCTACTATGTTTATAGTTGACATATTTGTATAAAA ATACCAACCTAATTACAAATACTTCGAAGTGACTATCATAAGTTTCCTTATCTAGCGAAGGC **AACTTTTGAACTCCCCAGTTGTTAATATGTATCATTATACACGACCCAATCAAACGCGGGGA** AGTCAATGCCGAAAGAATTCTAGGACCTAAAAGCTGCTCAATCCTTGGGCCTTTCCCTAATG ACATCCCCTCTCAAACTTTAGCTTAGCAGTTGTATTTAATGTCCTGTCACGGATAGTCAATA ATCGTTGAAGGTTGATTTTCATATCCTTCGCAATTTCGTAAAGCAACAATAGCAATACGGAC TAAAATGGTATGTTGGTGTGTGTGTGCTGCTTCACATTTCAGGCTAAAAATGTTATCCGT GGAATCTTCCTTAGCCAAGTATCATGGGCTTTGGAAATTAGTTTCCCACCGATGAGCGCAAC GACTTAGCGAAGCTTATGAAATTGGTGACAGCAGCTCTATGAATATGTTCCATGCGTTTCCA TTCAGGTTACTAACAATGCATAAATTATGAGTAGTCTTTTTCATCACTATATAAAACCTTTT TCAAACGAAACGCTGTTTTTGTTGGTACTATCTTTGCAGGTGCCTTTGTTTTCCAAACTGTA TTTGATACTGCTATTACTTCATGGTACGAGAATCACAACAAAGGAAAATTATGGAAAGATGT CAAGGCTCGAATAGCTGCAGGCGATGGAGACGACGATGATGAGTAA

YGR183C, 66 aa (SEQ ID NO 470) MSFSSLYKTFFKRNAVFVGTIFAGAFVFQTVFDTAITSWYENHNKGKLWKDVKARIAAGDGD DDDE

YKR040C, 167 aa (SEQ ID NO 472) MTSFQAVSFALGCNTLVACYAFTVLEKRSLMTSCTNALSFLFFLLTLRRIHRHWYKPYGAFL LIFVLTLRWFRGPIAWVVVDVVFASCNVVFFSPALSDENWPYVSFFGVVVVIAVHIIVVTHI GAFTACCLLKRVSLKSSEEKKKKKKKKKKKKKKKKKK

1343 bp, exon1: 501-513, intron1: 514-927, exon2: 928-1343 (SEQ ID NO 473) TCTTATCTTGTATGCCCGATATAGCAACCTTGTTGGTACCAATCTAACGGTTTCCGTACTTT GCAATGAAGAGATGAGGAGGCATGGGTCACTTATTTAATATGTACGGGTGTTTACATGGAGT TGCTTTCTTTTTTTGTCTCAGCAGTCATTGTGCGCCAAAAAAAGAGAAAACCGTGAGCCGAA GTCCACGCTCTGGAGTTAGGCTCTCCCATTACGGAGAGAAGCATTTCCTCAGCCTGGGAGCC GCACAAGGGGATTTTCTTTCTACCTTCGGCTTGCCTCACTGCGTTGGGGCTTCCCAATGCAA CTTCGTTCGTATGCATACAATCTTTTAGATATTATCTTTTAAAATTATTTTAAAACAATTTT **AAATGTATCTCATATGCTTTTCTTCTGCTGTTGAAAAGGCTAAACAAAGAAGATCAATAAGA** TAAAATGGCTCCATCTGGTATGTGAACTGCAATATTAATAGCACGAGAAAATTGAGAGGAAG CCGACGACAAGAATAGTGCATTAAGGACTTGATTAAGATATGGTGAGCAACGTAATTATCGG GCTCAACAGTTTATTAGCAATCGTTTTGATAGAAGCGTTGATGCTGTGGAAGTTGTTCTTTT GAAAATTATTCCATCCTCATTATACTTTTTTCTTCTATTTCGTGCTCCACGTCGAGGTATCA AGGAACATAGTTTACTAACATTAACGAATTCATCTCCTATGAATTTACTTTTTGTATAGCTA AGGCTACTGCCGCTAAGAAAGCTGTCGTTAAGGGTACTAATGGTAAGAAGGCTTTGAAGGTC AGAACTTCTGCTACCTTCAGACTACCAAAGACCTTGAAGTTGGCTAGAGCTCCAAAATATGC TTCCAAGGCTGTTCCACATTACAACAGATTGGACTCATACAAGGTCATTGAGCAACCAATCA CTTCTGAAACCGCTATGAAGAAGGTTGAAGATGGTAACATTTTGGTTTTCCAAGTTTCCATG AAAGCTAACAAATACCAAATCAAGAAGGCCGTCAAGGAATTATACGAAGTTGACGTATTGAA GGTTAACACTTTGGTTAGACCAAACGGTACCAAGAAGGCTTACGTTAGATTGACTGCTGACT ACGATGCTTTGGACATTGCTAACAGAATCGGTTACATTTAA

YOL127W, 142 aa (SEQ ID NO 474) MAPSAKATAAKKAVVKGTNGKKALKVRTSATFRLPKTLKLARAPKYASKAVPHYNRLDSYKV IEQPITSETAMKKVEDGNILVFQVSMKANKYQIKKAVKELYEVDVLKVNTLVRPNGTKKAYV RLTADYDALDIANRIGYI

FIG. 2:

YBL051C_homolog_1 1229bp PathoSeq: 1..1229; CDS: <1..>1229 (SEQ ID NO 285)

AGAGAACGTATTGAAGAGGAGAAAAGGGGAGAAAAGAGGTCAATTGGAAGAACAACATCGTTCTGCA TCAAATGCTTCTATGGCTTCTTTATTGTCAGCTGCTTCAACTACAGCAGCAACTAAAAATTTGAGT GTGGCTGGCACAAATCCTTCATACCACTGAAAGAATGTTTTTAAATTTACCTTTTAACAATTCC CTGTTCAATGCCCCACCAGTAGAAATTAATTTTAATGATCTTGAAGTTTTGGAATTGTACACTCAA TTAGTATTATACCGAGATGATATTACCAAATCTACTTTTGAATTAGCTATATCACCAGCAAATTTG **AATATTTCTCAACGGAAAATCATATCAATTTTATGTAATTATTTGAATTTATTAGAATTGTTTGAT AATGGGTTGATAATAATTAGAAGAAAACCAGGATACATTGCTCAGTGTATAACTCAACAATCTATT** ATTCCTAATTCTCAACAGGTGTCTGGGCCAACTCACCCGCAACAACATCAACAGAATCAACTTCAA CAATTGGGTGGTACATTAGCTGTTCCAGCGCACCCTGAATTATTAAGATCCCAATCGCAATCAGCA TTACCGTTGCCAAGATTGAGACAGCAAACCTCTACACCAATTCAACAAAATCAACAAGTTCAGCAC CAAAATCAACCACACAACAACAACAACAACAGCATGTTCAACCACAATATAATTATTACAATCAG CAATCTATTCAAAGCCAACCACATTCTGCGAGACCTTATTCTCAATCATATAATATTTATCAACAA CAACAGCAACAGCAACAACAAGCTCAACAAGCTCAACAACAACAACAACAACAATTACAA TATCAACAGGGACACCAGTCACAAGTTTCAACACCTACATTGAATTCTTCTAGTGCTGCCATTA CTTAGATCAAGTAGCAGTAGATCATTTGTTGATGTGAGATCCACACCTCCCACAGTAGTTTTGCT CAACAGCAACAACAACAACAACAACAACAACAGCCGCCACTAACTTCATCAATCCATGATTCT CCAACACCACATCATCATTACCACTTCAACAGCAGCCACCACAACCAAATCATTACCTATCCAAT TACCATCAGGGGGTTGGATCTCAACCAAAAACTCCATTGGC

YBL051C_homolog_2 2153bp public: 1..2153; CDS: 501..2150 (SEQ ID NO 287)

CTGGAAAATCAAAATTGAACTCCAACCAGCAGCGGCGGCGGCGACAGAAAAATATATTAACAGAAT ATTTGATTTGGGAAAAAACAAATTTTATATTTGGAGAATTGAATTTCAATCATTTTAACAAATTCA ATTCATATTACATTGACTTTTGACAAGAGGTATATATAATGGATTTTAGAAATTTATCAACTACAC CGAATCAAATGGGCACTGTAATGCAACGTCGTCCCTCTCTATCATCATTATCGTCAGCCTCGGGCT ATTCTTCCAATTATGGTGGAAATCCTACACCCAATCCCAACAATTCCAATACCAATAACAATA GTAGTGCCAATAGTAATAACAACACTCATGGCAATAACACTCCCAAATTATCAACTCAAAGATTGA CTTGGGTGGAACAGCAACAACAACCCTTGATCTGTTGGAAAATAATACTAAAACAGACTCCA GTAATGATGCTTCTGCTACTAATAATAATAATGTTAATGTTAATGTTAATGCCAATGCCAATGTTA ATGCCAATGCCAATATCCATGCCCAAACCCATGTCAACACAAATGTTAATGCAAACACAACAGCAA CTAGTATTAATGCTTCCACGATTTTAAATACTACACCAAGTATTAATGACACTAATGATAATGCCA **AAAAAATTAATGTTTCCATGATTAGTAATAACAATAACAATAACAGTAACAATAATAACAACAACA** ACGAGTTAATTCCTACTGCGATTGTGATTAAAAATATTCCATTTGCCATTAAAAAAGGAACAATTGT TAGATGTGATGACAAAATTAAACTTGCCATTACCATATGCCTTTAATTATCATTTTGATAATGGTG

YBL051C_homolog_2 550aa (SEQ ID NO 288)
MDFRNLSTTPNQMGTVMQRRPSLSSLSSASGYSSSNYGGNPTPNPNNSNTNNNSSGNSNNNTHGNN
TPKLSTQRLTNNRNLQSLWINQPSIAPSNVVPWVEQQQQQTLDSLENNTKTDSSNDASATNNNNVN
VNVNANANVNANANIHAQTHVNTNVNANTTATSINASTILNTTPSINDTNDNAKKINVSMISNNNN
NNSNNNNNNTNNSSTGSSNIANMLPSVSNATTMNNSNSINSTTNNTTINEADDDELIPTAIVIKNI
PFAIKKEQLLDVMTKLNLPLPYAFNYHFDNGVFRGLAFANFTSTDETSAVVNQLNGREIGGRKLRV
EYKKMLPAQERERIEREKREKRGQLEEQHRSASNASLASLLSAASTTAATKNLSVAGTNPSHTTER
MFLNLPFNNSSFNAPPVEINFNDLEVLELYTQLVLYRDDITKSTFELAISPSIFEYFSTENHINLC
NYLNLLELFDNGLLLIRKKPGSIAQCITQKSIIPNSQQVSGPTHPHHHQKNQLHQQQQQHTSTSTS
LTFIIDDEPSSIGWYISCSSAP

YBL066C_homolog 3254bp PathoSeq: 1..94/2146..3254, public: 95..2145; CDS: 501..3251 (SEO ID NO 289) ATAAAAAAGGAAATACAATTAAAAAAATTTTCCTTCTGTGAAAAGGCAATTTCGGGTCTAGTAGTA AACAAAGCTTAATAATTTCTCCCATTCAAATTTACAACGGACGATGCAGAAAGTAGTTTTCAAATT AATATTCTTTTTAACTTATTTTTCAATCAAGAAGGTACTGAAGATATCAATTAACTCTCAGTTAAA TAATATAAAATTATCACCAAAGCTGCCATCAACGTGTGTCGACAACCAATCGACTCCTCCCTTAAC TAGAACCATAGAACCTCAACATTTGTTTCTATAGAAAAATGAAGTTTGAAAAAGGTAAAGTGAGAA TTTTGCCTAAACCATCCCCTACACCAACCAACCACAAACCCCATTGCCATTACTTCCAGCTCAAA CTAAACCTGTAAACTCAAAAAGAAAATCAGCAGCCAGTACACCTGGAAATGAATCAAAGAAATCAA GAAAATCAAATTCTACAGCTTCAACACCCAACAGTGCTACACCAACATCAGTCGGAACACCTCCAC AGAAAACTTCCAAACCAACAGGTCATAGGCCAGTGACTTCATGTACTTTTTGTCGTCAACATAAAA TCAAATGTAATGCTTCAGATAATTATCCAAACCCATGTGAAAGATGTAAAAAAATGGGTTTGAAAT GTGAAATTGACCCCGAATTTAGACCTCGCAAAGGGTCACAAATCCAATCATTGAAACTGGATGTTG ATGAATTGAAGGCCAAGATTGAAATGTTGACTAAAAATGAATCTTTGCTCACACAAGCTTTGAATC AACACAATTTGAACCACGCTTCGCAACAGCAACAACTGTCTGGATCGCAATCTCAACAACAACATC CTCCAAATCCACAACGTGCATTGTCATATACGTCTGCAAACTCATCACCACAAGTTGCATTTAGCA ATGCATCGCCAATTCCTTCTGTGACAAGTATTCAACAAAATGCACCGTTGACTCACGAAAATTCCG ACAATTCTCCATACGCTTTAAATACACCAGAAAACATTGAAGAATTACAACCAATCTCAGAATTTA TTTTGGGTGACGTTACTTTGCCATTAAACAGGGCCAATGAGTTACACGACAAGTTTATGACCACAC ATTTACCATTTTTGCCAATAATAATATCTCGATCTGCCACCGAATTGTATCATAAATCTCAATTGC TTTTCTGGGCCGTGATTCTTACCGCAAGCTTATCAGAACCAGAACCCAAACTTTATATGTCGTTGG CATCCTTAATTAAACAATTAGCAATTGAAACATGTTGGATTAAAACACCAAGATCAACTCATGTTA TCCAAGCCTTGATCATACTTTCAATATGGCCGTTACCTAATGAAAAAGTTTTGGATGATTGCTCTT ATAGATTTGTTGGATTGGCAAAGAACTTGTCATTACAATTAGGTCTACATCGTGGTGGAGAATTCA TTCAAGAATTTAGTCGGAATCAAGTAAGTCTAGGACCTGATGCAGAAAGGTGGAGGACTCGTTCAT GGTTAGCAGTTTTCTTTTGTGAACAGTTTTGGTCATCATTGTTGGGGTTGCCACCTTCAATAAACA CTACTGATTATTATAGAGAATGCTCGTGTTGATAAATCGTTGCCTAAAAATTTCCGTTGTTTGA

TTTCGCTATCTATTTTCCAATGCAAATTAGTTAATATTATGGGTATTAGCGTTACTAGACCAGACG GTTTATTGGAGCCTCTGAATCGTGCTGGTTCACTTAGTTTATTGGATAGAGAATTGGAAAGATTAA GATTTAAACTTCAATTTGAAGAAGGGGGGCCAATTGAAGTATATTATTTGTATATTAAATTGATGA TCTGCTGCTTTGCCTTTTTACCAGGTACACCTATCGAGGATCAAGTCAAGTATGTCAGTTTTGCAT TGCCAATATATATCAGACAAGCAGTGACATATAGTGTTTTCATGTTGTTCAAATTACATTTGTCAA GAAACACGTTGAGTTCCTGGAAAGATTTGCAAAACGATATTTCTCGAACAGCCAAAGTTCTAGAAA ATTTGAACATGGTGTTGTATAATTATCCTGAAATATTTTTAAATGATCTGGAAAATGAGGATTCAA GTATTATCACCAGAATGAGGTCACATTTGACAGCATCTTTATTCTATGATTTGGTTTGGTGTGTAC ATGAGGCAAGAAGACGATCAGTACTTGATAAGGGGAAAAGACAGGCTCAGCCTAACAAGAAAATCT TGCCCTTGCCATTTTACAACCAAATCACTAAGGATGATTTCAAGACAATTACCACGACATCACCTA ATGGAACTACTATACTACATTAGTTCCAACTGATCAAGCTATGAATCAAGCAAAACTGAAATCTT TTGATTCCAGCAAACCACTTGAAATAAATGGTATTCCCTTACCTATGCTTGAAGCTACTGGTTCAA CAAGAGAAGTTTTAGATTCTTTACCCTCGCAATCTTTACCATCACAAGCACCAACTCTTCAGCAGT ATCCAATGCAGCAAGATCAACAACAAGCAAGAACCATCACAACAACAACAACAAAGCACCTGCAGC AACTGCAGCAATACCAACAACAGCAGCAATCGAATCAACAGCAACCACATCTTCAACATCAAAGAC AGTTTCAACAATCACCACCACCGCAATTTTCAATGATTTCTTCAACGCCGCCCCTTCAGCAACCAC CTTTTATTTTGGCAAACTCACCGTTACCACAAACTTATTTGCCAAAGATTGATGAAAATGAATATGT CACCAGAAGTAAAACAAGAAAACTCTGTTGCTCCATTTGCATCTCAAATCACCAACTTTTTTGATC **ATATGATGCAAGAGAAATAA**

YBL066C_homolog 917aa (SEQ ID NO 290)

MKFEKGKVRILPKPSPTPTNPQTPLPLLPAQTKPVNSKRKSAASTPGNESKKSRKSNSTASTPNSA
TPTSVGTPPQKTSKPTGHRPVTSCTFCRQHKIKCNASDNYPNPCERCKKMGLKCEIDPEFRPRKGS
QIQSLKSDVDELKAKIEMLTKNESLLTQALNQHNLNHASQQQQSSGSQSQQQHPPNPQRALSYTSA
NSSPQVAFSNASPIPSVTSIQQNAPLTHENSDNSPYALNTPENIEELQPISEFILGDVTLPLNRAN
ELHDKFMTTHLPFLPIIISRSATELYHKSQLLFWAVILTASLSEPEPKLYMSLASLIKQLAIETCW
IKTPRSTHVIQALIILSIWPLPNEKVLDDCSYRFVGLAKNLSLQLGLHRGGEFIQEFSRNQVSLGP
DAERWRTRSWLAVFFCEQFWSSLLGLPPSINTTDYLLENARVDKSLPKNFRCLISLSIFQCKLVNI
MGISVTRPDGLLEPSNRAGSLSLLDRELERLRFKLQFEEGGPIEVYYLYIKLMICCFAFLPGTPIE
DQVKYVSFAYLSATRIVTIVSKMVNDISLIELPIYIRQAVTYSVFMLFKLHLSRYLIDKYVDSARQ
SIVTVHRLFRNTLSSWKDLQNDISRTAKVLENLNMVLYNYPEIFLNDSENEDSSIITRMRSHLTAS
LFYDLVWCVHEARRRSVLDKGKRQAQPNKKILPLPFYNQITKDDFKTITTTSPNGTTITTLVPTDQ
AMNQAKSKSFDSSKPLEINGIPLPMLEATGSTREVLDSLPSQSLPSQAPTLQQYPMQQDQQQEPS
QQQQKHSQQSQQYQQQQQSNQQQPHLQHQRQFQQSPPPQFSMISSTPPLQQPPFILANSPLPQTY
LPKIDEMNMSPEVKQENSVAPFASQITNFFDQQTSGWFNNDNODDDFLGWFDVNMMOEK

YBL078C_homolog 908bp public: 1..908; exon 1: 417..449, intron 1: 450..533, exon 2: 534..908 (SEQ ID NO 291) TACATCCCCATCGATTCATCTGACATAATAGTATGTATGATCATACAGAGGGAAAATCACCCTTTT TATTATTACCAAGGTCTCAATGATTAGTGTGGCTAGCGTCTGTTACTACTTACCCCGTGTTTGTAG ATAATTGCCACTCAATCTTTAATTGACCATCGACCACAAAAATAATATGGAAATAATACTAACAGA TGATTTTTAGTCCTCTGAATCTTCCTGATCATCATATACTAACATTTTCGTGGGTGTTATTCTT TAATAGAAAAGACAAGCCGAGGCAGCCAGAATTGCTCAGAGGTTCAAGGATAGAGTACCAGTCA TCTGTGAAAAGGTTGAGAATTCCGATATCCCCGAAATTGATAAACGTAAATATTTAGTGCCAGTGG ATTTGACTGTTGGTCAATTTGTTTACGTTATTAGAAAAAGAATCAAGTTACCAAGCGAAAAAGCCA TTTTCATCTTTGTCAATGACATATTACCCCCAACCGCTGCATTAATCAGTACAATCTACGAAGAAC ACAAGGACGAAGATGGTTTCTTATACGTTTTATACTCTGGAGAGAATACTTTTGGCGAGAAACTAG CAATTGACATTTCATCATTAGATTTCAGTGATATCCCTGATTATGTTTAA

YBL078C_homolog 135aa (SEQ ID NO 292)
MRSQFKDEHPFEKRQAEAARIAQRFKDRVPVICEKVENSDIPEIDKRKYLVPVDLTVGQFVYVIRK
RIKLPSEKAIFIFVNDILPPTAALISTIYEEHKDEDGFLYVLYSGENTFGEKLAIDISSLDFSDIP
DYV

YBR073W_homolog 2891bp PathoSeq: 1..2891; CDS: 501..2888 (SEQ ID NO 293)

GTGGCACATCCCAGGAAGTAGAGCATGGACAGTTCGTATGGTATTGCTGTGCATACGATACAAAAA AAACAGAAACGAGAAAAAAAATCGATCGTCAACCTTTATCAACTCATCTACAGCAGCAGCAAAGTT CGTCCCTAAATATGAGTCAAGTCCAACAGAAACCCAAATCGTTTGGTAGATTGTATACCATGTACT ACTTTCATTTTCCATTTGTTATGCTTACGACAACTGAAACCATGCTACTTCATACGTTTGTATTGA TGTTTGCCTTATTGGTTGCCTATGGGATCTACGCTTATTTGCCTTCAAGTATCATGTTTGCAATCT CCAGAGCATACTATTATGTTTTTGGCATGGATATTAGTACCATCAACGGTTATGCAAAGTAGCGCT GTCTACTTAGTTTTATAGTTTAAAAATTTGTTAATATAAACCCAAAGTTTCTAACAGGCTCTGTTT ATCAAATGAATGTTCGACCTAATGCTCCGTTTCGGCCTCCTAGACCAATAAAGGGGGGGTGTTGCGG TGGTGCAGAAAGTAGTAAAACGAAAATTGCCCACTACCAATCCTAAACCTGCAAAGATTTTGA AGAACTCTGATGGCAAACCTATGGGGAAAAGAGTGTTTACTGCGACACCTAACCTTGACGACGTGA TTAGTGTGGGACCCTATGAATTAGAATTAGACGAAAAAGTAGGGTCTAACTCAACTCCCCAGACAG TGACACGTGTTACCCACCAGTTCAAAAAGGTTGCTCCTCCCACAGCTAGTAGTCGGAAACCGCTTT ATGACGACTGTGCCGATGCCATCGCGTTGCCTCCTCCAAAAGCCAAAGATTATGTCAAAGTAA GTGCAGTGGTAAATAAGGTATTGGTGGTGTGTCCTGTCACGCTTATTTCCAATTGGAGACAGGAGT TTAGGAAATGGTTAGGTGCTAATAAGCTAAACGTGTTGACGCTCAACAACCCAATGTCAAACGAGA **AACAGGATATACTCAATTTTGGAAAGTTGAATGTGTACCAAGTGTTAGTGGTGAATTATGAAAAAC** TTGTGGCACATTTTGATGAACTCTCAGCGGTCAAGTTTGATTTGTTAGTGTGTGACGAGGGCCATC GTTTGAAGAATAGTGCAAATAAAGTATTGAATAATCTTATCAAGCTCAATATTCCGAAGAAAATTG TTTTGACGGGTACGCCGATTCAAAACGAGTTGGTAGAGTTTCACACGTTGATCTCGTTTCTCAACC CGGGTGTGCTTCCCGAGCTAAAATTGTTTCAGCGAAACTTTATAACACCTATATCTAGGGCCCGAG TGACTCAGAGTTTTATTCTTAGACGTACACAAGCGATTTTGGCTAATTACTTGACACAGAAAACTG ACATTTTGTTGTTCTCCACCTACATCGTTGCAGCTCAAGTTGTTCGACTATATAACCAACTTGA AGAAATTTAATCAGTTTGAGGCATTTACCATGATCAATTTGTTTAAAAAGATTTGCAATTCCCCTT CGTTGTTGGCCGACGACGAGTTATTTAAAAAGATTGTTGAAGAAAAGTTTAATTTGGGGATGGCAT CCGGTAAAATAAACATTCTTGTGCCGTTGCTATTGGAAATTGCTTCGCTTGGGGAAAAGATTGTCT TAATTTCCAACTACAAGACTTTGGACTTGTTGGAACAGGTTTTGCGCAAGGTCAGCCTAACAT TTTCGAGATTAGATGGGTCGACCCCAACAATGTGCGTAGCAAGTTGGTTAATCAGTTTAACACGA ACCCCGACATAAACGTATTTTTATTGTCGTCGAAATCTGGCGGGATGGGGATCAACTTGGTCGGGG CTTCGAGGTTGATTTTGTTTGACAATGACTGGAACCCAGCGACCGATTTGCAATCGATGTCGCGAA TTCACAGAGACGGACAATTGAAACCGTGTTTCATTTATAGGCTATTCACCACGGGGTGTATTGACG AGAAAATCTTTCAGCGACAGCTCGTGAAGAACAAATTGAGTTCCAAGTTTTTGGACAATGACGCCA TATCCAATACTCATGATTTATTAGAGTGTGTGTGTGAGGGCGACGGGTCGATGTTGAGTCAGCCAA CCATAGAGGAAAGCGAACCACCCCCAAAACAAGCATGGGTTACTGCATTAGAGCTTAAGAAGAAGA TTGACGATGGTGAGGCGCTAAAGAGGACGGCTGTTAAATTTGCCTTGAACGATTATCGACACTACA ATCCAGAGGTGAACCGTAATTTGGATTTTGATTCTGCGCTACACCGAATTGCTAACAATTCAAGCT ATGAAAATAAGCAATTGCCAATTACATTTATAATGCTGAGAGTAACTAATTAA

YBR073W_homolog 796aa (SEQ ID NO 294)
MFTLFFFTTDQMNVRPNAPFRPPRPIKGGVAVVQKVVKRKLPTTTNPKPAKILTTDPGSTKYVIQW
RKKTSKKNKTWDGDGYAVIKQLENGACEISIKNSDGKPMGKRVFTATPNLDDVISVGPYELELDEK
VGSNSTPQTVTRVTHQFKKVAPPTASSRKPLYDDCADAIALPPPPKAKDYVKVNIDPHLAKVLRPH

QVEGVKFMYECLMGYRGFGGHGCLLADEMGLGKTLMTITTIWTLLKQNPFMEKGAVVNKVLVVCPV
TLISNWRQEFRKWLGANKLNVLTLNNPMSNEKQDILNFGKLNVYQVLVVNYEKLVAHFDELSAVKF
DLLVCDEGHRLKNSANKVLNNLIKLNIPKKIVLTGTPIQNELVEFHTLISFLNPGVLPELKLFQRN
FITPISRARDINCFDPEVKKRGEEISQQLIELTQSFILRRTQAILANYLTQKTDILLFVPPTSLQL
KLFDYITNLKKFNQFEAFTMINLFKKICNSPSLLADDELFKKIVEEKFNLGMASGKINILVPLLLE
IASLGEKIVLISNYTKTLDLLEQVLRKVSLTFSRLDGSTPNNVRSKLVNQFNTNPDINVFLLSSKS
GGMGINLVGASRLILFDNDWNPATDLQSMSRIHRDGQLKPCFIYRLFTTGCIDEKIFQRQLVKNKL
SSKFLDNDATSKSDVFDNDDLKNIFEIDTSTISNTHDLLECVCEGDGSMLSQPTIEESEPPPKQAW
VTALELKKKIDDGEALKRTAVKFALNDYRHYNPEVNRNLDFDSALHRIANNSSYENKQLPITFIMS
RVTN

YBR086C_homolog 2643bp PathoSeq: 1..2643; CDS: 501..>2643 (SEQ ID NO 295)

CTTTGTGTACTCATACGATGGTTGTTATTAGTTAAAGTTGCTTTGCTTTGCTTTTCAATTTCAATT GGTTATTGGTGTTTATTATTTTTTTTGGTTCCTCTTTTTACCCCCCCTTCCGTCTAATTGAGTTA ATTGGATTTGAATTGTTACAATTGAATACTTCAACGAGATGACTTTACCAATTCAGGATTTAGAAC CTGATTATTATATTCCGTCAATTATCCTACCACCGATAATGGATCACCAACCCCACAAGCTGAAA AATCATTGAAAACATTAATTGATTTATTATACGATAAAGGGTTTGCCGCCCAAATTAGACCTGGTG ATTTAGACCATTTGTTAGTCTTTGTTAAATTGTCTTCATACAAGTTTTCTGAAGAAGCTGAAAAAG ATTTAATTAAAAATTATGAATTTGGTGTCACGGGTAAAGATGACGTGTTAGCTTCTAAACTTAGAA TTATTATCAATACTTAACCTATCCACAATCAGTTGGTGGATGTGGTATTACTCCTAATTCTGGGG ATTGGAAATTTGTCACCAGTATTGTTCCAATTACTAATGCCTTTAATGAAACCACTTTAGTTGAAG ATTTAAAAATTAATGTTACTCAACCAAATTTATCAATTGCCACTATCAAAAAGACATATGGAGTTG AAGTTGCTCTTTATTTTGAATATATAAAACATTACACTTTTTTGGTTATTATTGCTTTCTATTATTG GTCTTGTATCTCATTTTAGAAAAGATAAACGATTCCTGTTAACTTTTGCCTTTATCAATTTGCTTT GGGGGGTTTTATTCCTTGCATCATGGCATAGAAGAGAACAACATTTGGTTAATGTATGGGGTGTTC AAAATAGTCATTTAATTGAAGAACATAATTCCGAATTGGCTAAAGTCAATGAAAGATATGAAGAAA AATCAACTTATTCCATGCAAATAATACCAATGGATTCAGATTTTAAAACAATTGGCATTTATCC CCATTGCCTTGGTGTTTGGTGTTTTGATTAGTTATCAATTGAGTTGTTTCTGTATTGAAATCT TTTTAACCGATATTTATGATGGCCCCGGGAAATCTTTATTGACTTTATTACCAACGGTTTTAATCA GTGTATTTGTGCCAATTTTGACCATTGTTTATAATGCTGTCACGGATATTATTATTAAATGGGAAA ATCATGATAACCAATATAGCAAAAATAATTCTATTCTTGTTAAAACCTTTGTGTTGAATTTCTTGA CTGGTTATGTTCCATTAATCATCACTTCATTCATATATTTTACCATTTGCTCATTTGGTGCAACCTC ATTTAGGTGATATTAAAACCACTATTGCCACATATGCTGGTGAAAATAGATTCTACACCAAATACT ATTTCATTGTCACAAATCAAGTTATACAATTGGTATTGAAATATATTCTCCCATTGGGTTTAAGAT TTGTATTTAATTTTATTGAAACGAAAATTCAGAAGAAACCTCAATTACAAACTAAAGATGATAACC CTGATGAATCTATTTGGTTACATAATGTCAGATTATCGTTGAAACTTCCTGAATATAATGTTGATG ATGATTTTAGAGGATTAGTTTTACAATTTGGATATTTGATAATGTTTGGTCCAGTTTGGCCATTGG CACCATTGGTTTGTATTTTCAATTTAATTTTTTTCAAGTTGGATAATTTTAAATTATTGAATG GTAAATATTTCAAACCACCAGTTCCAAGAAGAGTTGATTCTATTCATCCATGGAATTTAGCCCTTT TCTTGTTAGCATGGATCGATTATTTCCCCCGTGGTCACGGCATTTTACCGTCATGGTACTG CTCCACCAAAATCTATGGGTCAATTTGCCCTTGATAAAGCTAGTGTTCATGTTTCATCCTCAGTTT TCTTGGTTTTATTAATGTTTGTTTCAGAACATGGATTTTTGATTTTGAGTTATCTTTTATTTGAAT TCTCTTCTTTGTTCAAGAGTCAAGTTGAATGGGAAAATGATTTTGTTGATAATGATATTAAATTGA GACATGATTATTATTCTGGGAAAGTAAAACCAACTTATAAAGTCCACTCGGATGAGTTGTGGGAGA TTGAAAAAATTGCTTCTACCGAAGATGCTTATCTGACTTCTGCAGAAAAATCTACTACTACTGCTA

YBR086C_homolog 714aa (SEQ ID NO 296)

AA

103/161

MTLPIQDLEPDYYISVNYPTTDNGSPTPQAEKSLKTLIDLLYDKGFAAQIRPGDLDHLLVFVKLSS
YKFSEEAEKDLIKNYEFGVTGKDDVLASKLRIIYQYLTYPQSVGGCGITPNSGDWKFVTSIVPITN
AFNETTLVEDLKINVTQPNLSIATIKKTYGVEVALYFEYIKHYTFWLLLLSIIGLVSHFRKDKRFS
LTFAFINLLWGVLFLASWHRREQHLVNVWGVQNSHLIEEHNSELAKVNERYEEKSTYFHANNTNGF
RFLKQLAFIPIALVFVGVLISYQLSCFCIEIFLTDIYDGPGKSLLTLLPTVLISVFVPILTIVYNA
VTDIIIKWENHDNQYSKNNSILVKTFVLNFLTGYVPLIITSFIYLPFAHLVQPHLGDIKTTIATYA
GENRFYTKYLLKLKSQEEFKINQGRLDAQFFYFIVTNQVIQLVLKYILPLGLRFVFNFIETKIQKK
PQLQTKDDNPDESIWLHNVRLSLKLPEYNVDDDFRGLVLQFGYLIMFGPVWPLAPLVCIIFNLIFF
KLDNFKLLNGKYFKPPVPRRVDSIHPWNLALFLLAWIGSIISPVVTAFYRHGTAPPKSMGQFALDK
ASVHVSSSVFLVLLMFVSEHGFLILSYLLFEFSSLFKSQVEWENDFVDNDIKLRHDYYSGKVKPTY
KVHSDELWEKFTPQSTLNFTGPKPTAETDDKVEKIASTEDAYSTSAEKSTTTAT

YBR093C_homolog_1 1784bp public: 1..607, PathoSeq: 608..1784; CDS: 399.1781 (SEQ ID NO 297) CGGTAATTATGTCACAAAAACAACAATCAACATATTAAATCGTTATCCCAACTTTGTCAGTTTTA GGGCTCTGTTTAGTTTAACTTCTTGTAGTTTTATTATTCCGATTGGGTTAGCTCAATAACTGCATT TCGTACAATAATGTTAATTCAATTCTAAATTCCGATGAACCGAACACACAAAAAAACATCCAGTTCT GGAGAGATTTTTCAAAACTTCTATTATAAATAGAACCCTATAAGTCCATAATAATTCAATTGAAGG TCATGGTTTCTGTTTCTAAATTAATCAATAACGGGTTGTTATTAACTAGTCAAAGTGTTTTCCAAG ATGTTGCTACTCCGCAACAAGCTTCTGTGCAACAATACAATATACTCAATTTTCTTGGCGGTAGTG CCCCTTATATTCAAAGAAACGGATATGGGATTTCTACTGATATCCCTGCTGGTTGTGAAATTGCTC **AAATTCAATTGTATTCAAGACATGGTGAAAGATACCCAAGTAAAAGTAATGGTAAAAGTTAGAAG** CAATTTATGCTAAATTTGAAAACTACAAAGGTACTTTTAAAGGTGATTTGTCATTCTTAAATGATT ACACTTATTTTGTCAAAGACCAGAGTAACTATGCTAAGGAAACTAGCCCAAAAAATTCTGAAGGAA CCTATGCCGGTACAACCAATGCCTTGCGTCATGGTGCTGCGTTTAGAGCCAAATATGGATCCTTAT ACAAGGAAAACTCAACTTTACCAATCTTCACATCCAATTCTAACAGAGTACATGAAACTTCAAAGT ATTTCGCTAGAGGGTTTTTAGGTGATGATTATGAAGAGGTAAAACTGTCAAGTTTAACATCATCT CTGAAGATGCTGATCTTGGTGCCAATAGTTTGACTCCTAGAAGTGCATGTTCCAAGAACAAAGAAC TGAGCAGTAGTACTGCCAAAAAATATAACACAACATATTTAAATGCTATTGCTGAAAGATTAGTTA AACCAAACCCAGGTTTGAATTTGACTACAAGTGATGTCAACAATTTATTCAGTTGGTGTGCTTATG **AAATCAACGTCAGAGGAAGTTCACCATTCTGTGATTTATTCACCAATGAAGAATTCATTAAGAACT** CTTATGGTAACGATCTTTCCAAATATTATTCTAATGGTGCTGGTAATAATTACACCAGAATCATTG GTTCAGTGATTTTGAATTCATCCTTGGAACTTTTGAAGGACACTAAGAACTCTAATCAAGTATGGT TATCATTTGCTCATGATACTGATTTGGAAATTTTCCATTCTGCTTTAGGATTATTGGAACCAGCTG AAGATTTACCAACATCTTACATCCCATTCCCTAACCCATACGTCCATTCTTCTATTGTTCCACAAG GTGCCAGAATATACACAGAAAAACTTCAATGTGGAAACGATGCTTATGTTAGATACATTATCAACG ATGCTGTCGTGCCAATTCCAAAATGTGCTACTGGTCCAGGGTTCTCTTGTAAACTTGATGATTTTG AAAATTTCGTTAAAGAAAGAATTGGAGATGTTGACTTTGTTAAACAATGTGGTGTCAATAGTACCT ACCCATCTGAGCTTACTTTCTACTGGGATTATAAAAATGTCACTTACAGTGCTCCTTTAGAATTGT

YBR093C_homolog_1 461aa (SEQ ID NO 298)
MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHGERYPSKSNGKSLEAIYAKFENYKGTFKGDLSFLNDYTYFVKDQSNYAKETSPKNSEGT
YAGTTNALRHGAAFRAKYGSLYKENSTLPIFTSNSNRVHETSKYFARGFLGDDYEEGKTVKFNIIS
EDADLGANSLTPRSACSKNKESSSSTAKKYNTTYLNAIAERLVKPNPGLNLTTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKNSYGNDLSKYYSNGAGNNYTRIIGSVILNSSLELLKDTKNSNQVWL
SFAHDTDLEIFHSALGLLEPAEDLPTSYIPFPNPYVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFVKQCGVNSTYPSELTFYWDYKNVTYSAPLEL

YBR093C_homolog_2 1871bp public: 1..1752, PathoSeq: 1753..1871; CDS: 501..1868 (SEQ ID NO 299) GAGTTTTATGGGATTGGGTTTTTCAATTAAAGACTCTTCGTGATAATGCAATACCAAAACCAAAAT TTATTTAACGATGCAATAATTATTTCAATGTGAGCTATCCATGAATCAGTGAGAATCTTTATTATG

GAAGAAATTGGTCAAAATTTGACAATGTTTAGTAACTTTATATCTTGGTGTTGGGATGGTGCCACA AATGGAGATTGTTGAGTGTACATGAAAAATACGTAGTTAAATTTTGTTTCTTGTTTTTATTATTTA GCCACTTTTTTATCCGATTCTTCATATTACCTTTGGTAAAGTGATAAGATTAATATCATATTAGTA AAACACCCCCAATGATGAATGTTTGTATTTATAGCCAGACTATAAAAATTACGGGGATTTAATTCG CGACTCACCCACGTTCTCACACAGTATGTGCTTTTTTCATAAGTATGATTTGAACCCTAAAATATC CTGGGTTTATTCTAAGTGGACAATCTGTTTTCCAGGATGTTGCTGCCCCACATCAAGCATCAATTG **AACAATATAATATTGTCAAGTACCTTGGTGGCAGCGGTCCATATATTCAAAATTCAGGGTATGGGA** TTTCTACTGATATACCAGAAAAATGCACTATTGAACAAGTTCAAATGATTAGTAGACATGGTGAGC GATTTCCTAGTAAAGGAGATGGGAAATACTTTAATTCAGTGATGGAAGTTTTCAAGAGATATGGTG **AATTTCATGGAGATTTATCTTTTTTAAATGACTATGAGTATTTCGTTACTAATCCAGATTATTATG** AAAAGGAGACTACTCCTAAAAACTCAAAAGGTCCATATTTTGGAACTACAAATTTATTACGACATG GAGCTTATTTTAGAAAAAGATATCAATCACTATTTGACCAAAAGGAGAAGCTTGTTGTGTTTACTA GTAATTCTGGAAGGTGTTATCAAAGTGGTGTCTATTTCGCTCGAGGATTTTTTAGGAGATGATTACT CAGAAGATACAGTTGAATTTGTTGTTGTTGATGAAGACAAAAAAATGGGTGGTAATTCATTGACAC CAAGATACGCTTGTAAAACTTTGAATCAAGATTTACACAAAGATTTGGTGAATCAGTACGATAAGA CTTATTTGGACGATATTTTATCTAGATGGCTAGTAGACAATCCTGGATTAGATTTAAGTGCAGATC AGGTCTCGTCATTATTTCTTTGGTGTGCCTTTGAGATTAACGTTAGGGGGGTATTCTCCATTCTGCA **ATCTATTTACAAAAGATGAATTTATCAGAAGTGGGTACCGAAACGATGTTGGTAATTACTATCAAA** CTGGTCCAGGTAATAATATGACAAAGGTAATTGGCTCACCTATGGTGGAAGCGTCGTTGAAAATGC TTCAAGAAGATTCAAAAATTTGGTTGACATTTACCCATGATACTGATATTGAGATGTATTTGACAT CTTTGGGATTGATTGTTCCACCAGGGGATTTGCCCGTTGATCGAGTACCATTTCCCAATCCATATA ATGCAGCAGAATTTTTCCCTCAAGGTGCTAGAACTTACACTGAAAAATTGAAATGTGGTGAAAAGC AATATGTTAGATTATTGTGAATGATGCAGTTTATCCATATCCGGATTGTAGTGGAGGTCCTGGGT TTACTTGTGAATTGAATGATTTTATCAAATTAGTTAAAAGTCGTTTACATGATGTTGACTATAAGC TTCAATGTGAAGTGGACGGACCAGCGGAATTGACATTTTATTGGGATTATAAAGACAGAAAGTATA **ATGCGCCGTTAATAGATCAGTAA**

YBR093C_homolog_2 456aa (SEQ ID NO 300)
MVGLSRVLNAGFILSGQSVFQDVAAPHQASIEQYNIVKYLGGSGPYIQNSGYGISTDIPEKCTIEQ
VQMISRHGERFPSKGDGKYFNSVMEVFKRYGEFHGDLSFLNDYEYFVTNPDYYEKETTPKNSKGPY
FGTTNLLRHGAYFRKRYQSLFDQKEKLVVFTSNSGRCYQSGVYFARGFLGDDYSEDTVEFVVVDED
KKMGGNSLTPRYACKTLNQDLHKDLVNQYDKTYLDDILSRWLVDNPGLDLSADQVSSLFLWCAFEI
NVRGYSPFCNLFTKDEFIRSGYRNDVGNYYQTGPGNNMTKVIGSPMVEASLKMLQEDSKIWLTFTH
DTDIEMYLTSLGLIVPPGDLPVDRVPFPNPYNAAEFFPQGARTYTEKLKCGEKQYVRFIVNDAVYP
YPDCSGGPGFTCELNDFIKLVKSRLHDVDYKLQCEVDGPAELTFYWDYKDRKYNAPLIDO

YBR093C_homolog_3 1888bp PathoSeq: 1..1656, public: 1657..1888; CDS: 500..1885 (SEQ ID NO 301) TCAATATATATCTTGTGAATAATAACTTCGTTCTAATTCACTATACACAACTAGACGTGTACACGC TCAATCTCAGGTAAAGAAAGTTTATATTCCATCACTATATAACAACAATCAGGCTTTGCAAAAAA CATTTAAAACTAATACTGGTAATATGGAAATATAACGCCTCGTAGTTCTACGCACGTGGCATCCTT TATCTATTTATTCAATTTACCCCTAATTTATGAATTAGCTTAATAAGAGCAGTCAAATTAACACGG CTCAATTAATAGTACTTAATAATATGAAGCCGATCAATTAACCGATCCTTTGAATAATTTGAAAAT TTTCCTAAACAGCAACAACAACTTGAAATTCAAAAATGGTTTCTGTTTCTAAATTATTGAACAA TGGATTGTTATTAGCTGGTCAAAGTGTCTTCCAAGATGTTGCTACTCCACAGCAAGCTTCTGTGCA ACAATATAACATCGTCAATTCTCTTGGCGGTAGTGCCCCTTATATTCAAAGAAACGGATATGGGAT TTCTACTGATATCCCTGCTGGTTGTGAAATTGCTCAAATTCAATTGTATTCAAGACATGGTGAAAG ATACCCAAGTAAAAGTAATGGTAAAAGTTTAGAAGCAATTTATGCTAAATTTGAAAACTACAAAGG TACTTTTAAAGGTGATTTGGCTTTCTTAAATGATTATTACTTATTTTGTTACTGATAAAAACAATTA CGAAAAGGAAACTAGCCCAAAAAATTCTGAAGGAACCTATGCCGGTACAACCAATGCCTTGCGTCA CGGTGCTGCGTTTAGAGCCAAATATGGATCCTTATACAAGGAAAATTCAACATTACCAGTTTTCTC TTCCAATTCAGGTAGATGTTACCAAACTTCAAGATATTTTGCTAGAGGATTTTTAGGTGATGACTT TAAAGAAGGTAAAACTGTCAAGTTTAACATCATTTCTGAAGATGCTGATGTTGGTGCCAATAGTTT

YBR093C_homolog_3 462aa (SEQ ID NO 302)

MVSVSKLLNNGLLLAGQSVFQDVATPQQASVQQYNIVNSLGGSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHGERYPSKSNGKSLEAIYAKFENYKGTFKGDLAFLNDYTYFVTDKNNYEKETSPKNSEGT
YAGTTNALRHGAAFRAKYGSLYKENSTLPVFSSNSGRCYQTSRYFARGFLGDDFKEGKTVKFNIIS
EDADVGANSLTPRSACSKNKERSSSTAKKYNTTYLNAITERLVKPNPGLNLTTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKYSYGNDLSNYYSNGAGNNYTRIIGSVILNSSLELLKDTKNSNQVWL
SFAHDTDLEIFHSALGLLEPAEDLPTSYIPFPNPYVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFVKQCGVNSTYPSELTFYWDYKNVTYNAPLGDF

YBR093C_homolog_4 1886bp PAthoSeq: 1..102/1038..1062/1078..1886, public: 103..1037/1063..1077; CDS: 501..1883 (SEQ ID NO 303) ACTACTTAAATTGGCATATCCAAACAAACTTGAAGTAGGAGTTTCCTTATTTTTATTTTGTATTTA ACATATTAAATCGTTATCCCAACTTTGTCAGTTTTACTAACACCTTTTATTTTGTGTTATACAAAT TGCACAATCAATTACTATAACTTTTTTTTGAAACGTGGGCTCTGTTTAGTTTAACTTCTTGTAGTT TTATTATTCCGATTGGGTTAGCTCAATAACTGCATTTCGTACAATAATGTTAATTCAATTCTAAAT TCCGATGAACCGAACACACAAAAAACATCCAGTTCTGGAGAGATTTTTCAAAACTTCTATTATAAA TAGAACCCTATAAGTCCATAATAATTCAATTGAAGGATTATTTTCTTTTTCCCTTTTCTGATTACTT TCACCAATTTTCTTCTCCCAAAAAAAACACCTTCTTCATGGTTTCTGTTTCTAAATTAATCAATA ACGGGTTGTTATTAACTAGTCAAAGTGTTTTCCAAGATGTTGCTACTCCGCAACAAGCTTCTGTGC AACAATACAATATACTCAATTTTCTTGGCGGTAGTGCCCCTTATATTCAAAGAAACGGATATGGGA TTTCTACTGATATCCCTGCTGGTTGTGAAATTGCTCAAATTCAATTGTACTCAAGACATGGTGAAA GATTCCCAACAGCAAGTAGTGGGAAAGATTATGAGAAAATTTATGCTAAATTTAAAAACTACAATG GTACATTCAAAGGTGATTTGTCATTCTTAAATGATTACACTTATTTTGTCAAAGACCAGAGTAACT ATGCTAAGGAAACTAGCCCAAAAAATTCTGAAGGAACCTATGCCGGTACAACCAATGCCTTGCGTC ATGGTGCTGCGTTTAGAGCCAAATATGGATCCTTATACAAGGAAAACTCAACTTTACCAATCTTCA CATCCAATTCTAACAGAGTACATGAAACTTCAAAGTATTTCGCTAGAGGGTTTTTTAGGTGATGATT ATGAAGAAGCTAAAACTGTCAAGTTTAACATCATCTCTGAAGATGCTGATCTTGGTGCCAATAGTT TGACTCCTAGAAGTGCATGTTCCAAGAACAAAGAACTGAGCAGTAGTACTGCCAAAAAATATAACA CAACATATTTAAATGCTATTGCTGAAAGATTAGTTAAACCAAACCCAGGTTTGAATTTGACTACAA GTGATGTCAACAATTTATTCAGTTGGTGTGTTATGAAATCAACGTCAGAGGAAGTTCACCATTCT GTGATTATTCACCAATGAAGAATTCATTAAGAACTCTTATGGTAATGATCTTTCCAAATATTATT CTAATGGTGCTGGTAATAATTACACCAGAATCATTGGTTCAGTGATTTTGAATTCATCCTTGGAAC TTTTAAAAGACACCGAGAACTCTAATCAAGTATGGTTATCATTTGCTCATGATACTGATTTAGAAA TTTTCCATTCTGCTTTAGGATTATTGGAACCAGCTGAAGATTTACCAACATCTTACATCCCATTCC CTAACCCATACGTCCATTCTTCTATTGTTCCACAAGGTGCCAGAATATACACAGAAAAACTTCAAT GTGGAAACGATGCTTATGTTAGATACATTATCAACGATGCTGTCGTGCCAAATTCCAAAATGTGCTA TTGACTTTATTAAACAATGTGGTGTCAATAGTACCTACCCATCTGAGCTTACTTTCTACTGGGATT ATAAAAATGTCACTTACAATGCTCCTTTAGAATTGTAA

YBR093C_homolog_4 461aa (SEQ ID NO 304)

MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ IQLYSRHGERFPTASSGKDYEKIYAKFKNYNGTFKGDLSFLNDYTYFVKDQSNYAKETSPKNSEGT YAGTTNALRHGAAFRAKYGSLYKENSTLPIFTSNSNRVHETSKYFARGFLGDDYEEGKTVKFNIIS EDADLGANSLTPRSACSKNKESSSSTAKKYNTTYLNAIAERLVKPNPGLNLTTSDVNNLFSWCAYE INVRGSSPFCDLFTNEEFIKNSYGNDLSKYYSNGAGNNYTRIIGSVILNSSLELLKDTENSNQVWL SFAHDTDLEIFHSALGLLEPAEDLPTSYIPFPNPYVHSSIVPQGARIYTEKLQCGNDAYVRYIIND AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFIKQCGVNSTYPSELTFYWDYKNVTYNAPLEL

YBR181C_YPL090C_homolog 1635bp public: 1..938, PathoSeq: 939..1635; exon 1: 500..505, intron 1: 506..930, exon 2: 931..1632 (SEO ID NO 305)

ATATATATATATTATGTATTTTTTTATTGTTGTTCAGGAATTTTAAACATGTTCATGAATAATGA TAATCTATGAACAAATTAAAGAACTCTTTGGTTTCATTTGCAACCAATGTGCGTGACTTAGGGCTA TAGCCCTACTTTTACTTGTACGATACTGCATATTTTGTTGTTGTGCGAATAGTTAGCGTAATAATC TTTTTTTTTGTGTGTGTGCGGTTTACTTACTCTTCTTCTCTCGCACATATTTTATTAGAGCTTAC AGTTGTTTGTATAGTGAGAGTTTCACTAACAAAGCTTCAACAATACTAACAAATTTTCGCACGC AGTTAATTTTCAGACAGGCACAAAGGAATTAATCACCATGAAGGTATGTGATTGAATATAACCTAT AGAGTAGGAGTTTTAAACAGGATAATTGGATTCAATAAGAGGAAAAATTTTTTATCGTCGTGATTA TAACAAATACAAAGAAATTAAGCAATGAAGTGATATAAGCAAATGAAGGACTAGTTTATTAGGGGT **AACTACAAATCAATTTAGTTAACTTCAATAATGACAATAATTTTAATCACTGAAAACAATAAACAT** TTTTAGTTAAACATCTCATATCCAGCCAACGGTACTCAAAAATCTATGGATATCGATGATGACACA AAATTACGTGTTTCTACGGAAAAAAGAATGGGTCAAGAAGTTGAAGGTGACTCAGTTGGAGATGAA TTCAAAGGTTACATCTTCAAAATCACTGGTGGTAACGATAAACAAGGTGTCCCAATGAAACAAGGT GTTATGCACCCAACCAGAGTTAGATTATTATTATCTAAAGGTCACTCTTGTTACAGACCAAGAAGA ACTGGTGAAAGAAAAGAAAATCCGTTAGAGGTTGTATTGTTGCTCAAGATTTGTCAGTTTTGGCT TTGTCTATTGTTAAACAAGGTGACAATGAAATTGAAGGATTAACTGACACCACTGTTCCAAAAAGA TTAGGTCCAAAGAGAGCTAACCACATTAGAAAATTCTTTGGTTTAACTAAAGAAGATGATGTTAGA GATTTCGTTGTTAGAAGAGAAGTTACTAAAGGTGACAAAACTTACACCAAAGCTCCAAAGATTCAA AGATTAGTTACTCCACAAACTTTACAAAGAAAGAGAGCTTTGAAAGCTAAAAAAGTCAAGAATGCT GAAGAAGAGCTGAAATTAAAAAGAAGAGAGCTGAATCTTTAAAGAACTAA

YBR181C_YPL090C_homolog 236aa (SEQ ID NO 306)
MKLNISYPANGTQKSMDIDDDTKLRVSTEKRMGQEVEGDSVGDEFKGYIFKITGGNDKQGVPMKQG
VMHPTRVRLLLSKGHSCYRPRRTGERKRKSVRGCIVAQDLSVLALSIVKQGDNEIEGLTDTTVPKR
LGPKRANHIRKFFGLTKEDDVRDFVVRREVTKGDKTYTKAPKIQRLVTPQTLQRKRALKAKKVKNA
QQQRDAAAEYAQLLAKRLHERKEERAEIKKKRAESLKN

YCL016C_homolog 1520bp public: 1..1079/1081..1520, PathoSeq: 1080; CDS 501..1517 (SEQ ID NO 307)

YCL016C_homolog 339aa (SEQ ID NO 308)
MSEYSVYQQLNEDTNATKYTYKLLQLPSKILNQLESKSTNLYIKSDINSLALCTDSETFKLRQMNH
SNTVLLLNKEPDNKLIGFQKTSYEYELTEIKGSIDTSDIPIFNGQTAQQPIDLIALEDNSICSHQE
FLSNWYELGGCEIDNGAYIMSADIITELLYLLITKLMSLQVHEFSPEDVSSIITPPYNDSMVTSII
HKFCTIESEKYQLNDLKITQWFGIVEMSKINHKMTDISEFLLNWKTSLPSFYNPPLDISQLAGYYC
SPIENKILYVDPESLSENLSQRFKELFELDKSWNYDEFIPFIKKFVPAGKKVDSIILKYGKKKKVG
RDRFIVCPR

YCR073WA_homolog 710bp PathoSeq: 1..710; CDS: 315..707 (SEQ ID NO 309)

YCR073WA_homolog 131aa (SEQ ID NO 310) VKLPLFDLFLLGCAPDGHIASLFPNHGEQLREKLAWVLPVSNAPSGPENRITLSIPVICHSARVTF VVEGLTKAPIIKTIMERPEKGLPSSIVNEGAAGRVSWFVDDDALNDLFDITKKKYKYLSIPEPSH

YDL010W_homolog 1190bp PathoSeq: 1..1190; CDS: 501..1187 (SEQ ID NO 311)

TATTAGAAAAATATGATATAACACCAGCACCAAATGTTGTTGAATTAGATCGATATGAATATGGAG CTGAATTACAAAGTTATTTGACAGAGAAGAGTGGGAGAAGAACTGTGCCAAACGTATTGGTTAGATAAACATTTGATTAGATTTGAAAAAACTTCATAAAGATAATGATTTGATTAAATGATTTGAATTAGATT

YDL010W_homolog 229aa (SEQ ID NO 312)
MAGVRQLRIIALTAFVLGLIFTLHKVGSNAASLVHAQASDQQPNKHNTKSTTYTATNDESVANLID
SKNDPQTDDKINQKISQDQDEAINGNKDTNKDTTKVKPDNGEYDPISDLIKIRSLSPMTIFSKSYC
PYSKKIKQLLLEKYDITPAPNVVELDRYEYGAELQSYLTEKSGRRTVPNVLVGKSFESRGGCDEFE
KLHKDNDLIKLLVEWGSGRLQVAKKNTPSNA

YDL083C_YMR143W_homolog 1256bp PathoSeq: 1..1256; exon 1: 501..521, intron 1: 522..848, exon 2: 849..1253 (SEO ID NO 313) AGTGGTTGTTCAATAATGGTAAGTTCTTGGAAATAGCCATTGTTGCTTTCTGGTGGTTAGACTTGT AGGAAGTAGAACTGTTTTCCAATGAAAAGTAGTTTTAATTAGAAAAATTTTCAAAGTGCGTGAAGC TGCTCAAAACTATATGTACTGTACACAATCTAGGGCTATAGCCCTAATATTGTACAGGAAGAACTT TGTTGTTAGTAGAGAGTGTCTCGCACTAACAGAACATTTTTTTCAGAACAGGAAAATTTTTGAAAT CTAACATCTTTTACTGAAAGCCAAGCATCAACACAATAATGTCAACCCAATCTGTTCAAGTATGTA **AACGAATTGAAATAAAGAGATAGAGAGATGTTTTATTATCAAAATACGAAAGGAAAGGCAATTAAA** AATAACCAGAAAACGATAATATTTTAGCGACCATTAAATGACACTTGAAGGCTCACTGGGCCAATA GAATATCTCCATATACACTTTTGAACTATTTACTAACAATTTACTTTTGTTTCTAGACTTTTTGGTA CCCCAATCACCTTGGTCCAACCAGAAATCTTAAGATTCAAAGTTTACGAACCATTGACTTTGGTTG GTTTAGATAAATTCCAAGGTATCGACATCAGAGTTAAAGTCACTGGTGGTGGTCACGTTTCTCAAG TCTACGCCATCAGACAAGCTATTGCTAAAGGTTTGGTTGCTTACCACCAAAAATACGTTGACGAAG CTTCTAAGAACGAATTAAAGAAAATTTTCGCTTCTTACGATAAGACCTTGTTAGTTGCCGACTCAA GAAGAATGGAACCAAAGAAATTCGGTGGTCGTGGTGCCAGAGCAAGATTCCAAAAATCTTACCGTT

YDL083C_YMR143W_homolog 142aa (SEQ ID NO 314)
MSTQSVQTFGKKKTATAVAHVKAGKGLIKINGSPITLVQPEILRFKVYEPLTLVGLDKFQGIDIRV
KVTGGGHVSQVYAIRQAIAKGLVAYHQKYVDEASKNELKKIFASYDKTLLVADSRRMEPKKFGGRG
ARARFOKSYR

YDL125C_homolog 959bp public: 1..959; CDS: 501..956 (SEQ ID NO 315)

GTGTTGGTTGGCCTGCTGAAGCCACTGATTTTGATAAATTAGGAAAATTGCATGAGAAATTAAAGGAAGATTGGCTAAGGTAGATAATGAAAAATTATAA

YDL125C_homolog 152aa (SEQ ID NO 316)
MASHASCIFCKIIKGEIPSFKLIETAKTYSFLDIQPIAEAHVLIIPKHHGAKLHNIPDDYLSDILP
VVKKLTKVLKLDENNTPEGEGYNVLQNNGRIAHQVVDHVHFHLIPKKDEATGLGVGWPAEATDFDK
LGKLHEKLKEELAKVDNEKL

YDL133CA_YDL184C_homolog 297bp PathoSeq: 1..297; CDS: 220..294 (SEO ID NO 317)

YDL133CA_YDL184C_homolog 25aa (SEQ ID NO 318) MRDKWRKKRVRRLKRKRKVRARSK

YDL136W_YDL191W_homolog 1303bp PathoSeq: 1..1303; exon 1: 501..503, intron 1: 504..943, exon 2: 944..1300 (SEQ ID NO 319) TATTGTCTGATGCTATACGGAATGGGCGTTACAAATATACAAACTTATATTTGAAAGTAAATTCTA TTATTTTCTTCTATCGTATGCATACCGATTATTATCACAAGGACAATTGCCTATTGTTGTGGGAA TAAATTTAAAATCCTTCTTATTGGTGTCTAGACTTTGCTTTTTGTGGTGATTAGGGCTTTAGCCCT CAATTAACGCTTAGATCCAATACAGTTTTGGTAACTTGTACACGAACAAAATCTCAAATTTGTTAC TGTGTGAACCAACGAAGGAAGAAAAAAAACCCATACAAAAATTTTTCAGTATCAAGGAATTAGA AGAGACGTTTAAATCAACAAAGTTCAAATCTATCAACAATGGTATGTTTAATATCGATATTATCCA TAGATGTACATGTATCCTAATGGGTTTCATTATTTGGAAAGTTATGTTTATGGGAGTTCTATTTAT CTTTCCCTCCACTATTCAATATACTCAACAACATTATCAAGTTAAAAGTTCAGAAGATACACGTAA ATGAAAAGTTAATACCAAGAAGAATACAAATTACCAGTCCATACCGTGTTTGGGTTTAGATTACTA TATTTTACAAGAAACATATTATATGAAATGATACCCAATCCACAGCGACTTTTCAGATAGCCAAAT CTTTTTTTTTATTATTAGGCCGGTGTTAAAACTTTCGAATTAAGAACTAAATCTAAGGAACAATT AGAATCTCAATTGGTTGAATTGAAACAAGAATTGGCCACTTTAAAAGTTCAAAAATTACAAAGACC AAGTTTACCAAGAATTCACACTGTTCGTAAAAACATTGCTAGAGTATTGACTGTTATTAACTTGAA TCAAAGAGAAAATGTTCGTGCCTTTTACGCTGGTAAAAAATACATTCCAAAAGATTTAAGAGCTAA AAAGACTAGAGCTTTAAGAAGAAAATTGACTAAATTTGAAGCTTCTCAAGAAACTGAAAAAGCTAG AAAACAAAGAATTGCTTTTCCACAAAGAAAATTTGCTATTAAAGCTTAA

YDL136W_YDL191W_homolog 120aa (SEQ ID NO 320) MAGVKTFELRTKSKEQLESQLVELKQELATLKVQKLQRPSLPRIHTVRKNIARVLTVINLNQRENV RAFYAGKKYIPKDLRAKKTRALRRKLTKFEASQETEKARKQRIAFPQRKFAIKA

TTTCTACTACCTGTGATGACTCGCCGACATTTGTCACTAAGGATTCTTCCGAGTTAATTGAATTTG CTTGGGAAACAGTCGATAGTGTCACTTTGGAAACTTTATACAAAGGATCAAACTTGGTTCGTCCAA CCAACACCTATCACACCTTACTGCTCGAAGATTCATAGAATAACATGGGACAATGTCAAAAATG CTGGGTCGTTCAAAGACGCCATCACAAACTTTGATCAATACGTACAAGAACACATAATTTCCAAGA **AAAAGGAGTTTTCAATTGTGATGTTTGACATTTCCAAATTGAGAGTTCAGTTGGTTCGTGAAGCTA** GAGACAAATCCGTGGTTTTACCCTCGTATCTACAACATCCAAGGATTTTTGATTTACCAAGAGAAT ATTTAAATTGGCAATCTAGCCACCCTGAAACATTATCATACCCCCCAACTTCTTTAACTAATATTA TTACTGCATTAGAAGTTGAGGTTGAGAATATATCTGAATATGTCGACTTGCCAAACTTTTCTTCCA CACCATCACCATCAAAAGCTTCAGCAACAACGACGACGACAACTGCAAATGTCACAGCCATTGACG TCCTTTCCAGTGAAACAGAACCAAATGGTAAAGTCATTGCAAATTTGCACGCCAAAATTGCCAAAC AATTGATCAAAAAATCCATCCTGTTGAGAATCACCCTAATGTATTTACAAGACCTTTTGATTCGG CTCAAGATATCACTGCTTTTACATCAGAAAGATCAAAAGTACTCTATCTTTCCAACTTGCCAAACG ACACCACACTCAGGGTTGGAATCATGGTTCACTCAGTATGGTGGAAGACCAGGTGGGTTTTGGA CTTTTAAGTCTGCAGATGATAACAATAATAATAACAACAACAATAGCAATGGCGGGAAAGGATATC AGAATGCGAGAAAATATGGTATTTCAGGGTTTGTGGCCTTTAATACTCATGAGGAAGCAGTTGATT GTTTAGCTTTGAATGGGAGAGTGTTGAATGATCGTCCTATTGAAGTTCAAGCGTCTTCTAGTAAAG TGTTTGATATGGCCATGGATAAATTGTTGTTGACTCTGTTCCCACTCTCAAAGAACAGACCTAGAC CCGGGGATTGGACTTGTTTATCTTGTGGGTTTTCCAATTTCCAGAGAAGAACACTGTTTCAGGT GCTCTTTTGCGGCAGTGGCGTTTCAGGATGTTTTTAACAGTAATACAGGCAATGCCAACGGTAATG GCAATGTTAGCGGCAACCACAACCACAACCACATAGTGGAGCTCGCCGTGGCATGAATTTACAGC CTGCTCAAGCTAATGAGAAAATTGGAACAGGCAATATTAGTATTCCTTCTTACAACGATCCAATCA AGGGTCCAACAGGTAATGTCACTAATCACCTCAACAATTCTGAGACCAATTTACTGAACAACACTA **ATCTTAACAACAACAATCATCATAGTAATAATTATCACAATAACTACCATCACCACAACAACAATA** ATAACAATCATGGGAATAGCAATGGTAACACCATACATGGTCGTTCCCATTATAACAATAGTGTTC CATTTAGAGCAGGTGACTGGAAATGTGAAAATTGCATGTATCACAATTTCGCCAAAAATTTGTGTT ATTCAACGGCCGCTGCCATAGCTGCAGCAACAGCCAGTGGTCAACCTTTAAACTTGAATAATAATG ATTCTCGTAACAACAATGCTTCTGGGGCATCAAAGTTCAACAATGGCTACAACCAAAGAATCAGT ATTACAATAATAATAGCAAGAATCTTAGCAACAATTTTGGTCTTAATGGTATGCATCAGCAAAACC ATGGAAGTAGCTCTTCCCATCAACTGAAACTTCAATTGAATAATACTTGA

AGAACAACAAATCAAAGTTTCAAGACTATCTCAAATCTTGTTGTCACCATAACTATCAATTGTTCA CCTCTTGAACCAACATCAAATTGAATAAACATAGGATCATGAGTGACAGTGGTTATACATTAATCT ATGAGCCTAATACGGCTACGAAAGTATCTGTCAATGAATTTAAAAATTTGTTGGAAAAGGGTAAAG ATGATGTGAAAGTAGATACCATGAAGAAGATTTTGATTACCATATTAAATGGAGACCCCTTACCTG **ACTTGTTGATGCATATAATCAGATTTGTCATGCCTTCCAGAAATAAAGAATTGAAAAAGTTGTTGT** ATCATTATTGGGAGGTTTGTCCAAAAATGGATGAATCAGGTAAAATGAGACATGAAATGATTCTTG TGTGTAATGCCATCCAACGTGATTTACAGCATCCAAATGAATATATTCGAGGCAATACTTTGAGAT ATTTGACGAAATTGAAAGAGCCAGAATTATTGGAAACTTTAGTTCCTAATGTCCGTCAATGTTTAG **AACACCGTCATGCCTATGTCAGAAAAAATGCTGTTTTCGCATTATGGTCTATTCATAAAGTCAGTG** ATCATTTAGCTCCTGATGCTGACGAGTTAATTTACAGATTTTTGTATGAGGAAAACGATTCTGTTT GTAAAAGAAATGCTTTTGTTTGTCTTGGAGACTTGAATAGAGAAGCTGCTTTGCAATATATTCAGG ATAATATTCAGTTATTGAGACTTTGGATCCATTGATACAATTGGCTTTTATTGAGTTTATCAAAA AGGACTCTATTCAAAATCCAGCTTTAAAGCAACAATATGCCCAATTAATGACAGAAATTATTGAAA GCTCTTCAAATGTTGTTATGTATGAAGCTGCTAACACGTTGACTGTTTTGACTTCAAACCCACAAT CAATTTTGTTGGCAGGAAACAAGTTTGTTGAATTGGCTACTAGAGAGTCTGATAATAACGTTAAAA TTATCACTTTAGAGAGAATAAATCAATTACACAAGCAACATCCTGGTGTGTTACAAGACTTGTCAT TGGCTATTAAATTTGTGGAGGTTGCTGCCAATGTCATTGATTTATTGTTGGATTCTATAGCCGATT TGAATACCACTGCCGCCTACGAGGTTATCACATTTGTTAAAGAAGTTGTTGAGAAATTCCCAGATT TAAGGGACGCTATTTTGAGAAGATTGATTTTGGCTTTGCCACATGTGAAAAGTGGTAAAGTTTTTCC GTGGTGCATTATGGGTTATTGGTGAGTATGCCTTAGAGGAATCATTAATACAAGAATCTTGGAAAT ATATTAGAGGAAGTATTGGTGAAGTACCAATTATTGCTAGTGAATTGAAACTGAAAAAGCGTGATG ATACTGAGGAATCACAAGAGGAAGAAACCGAGTATGATGGTAAACCTCGCAGAAAGGGTCCAGTTG TATTGCCAGATGGTACCTACGCTACTGAGTCAGCATTGACAAGCGAAACAACTGACTCTTTGGAAA GTGACAGCAAGACTCCTATCAGAAAGCAAATTCTTGCTGGTGATTTCTACTTAGGTGCTGTATTAG ACGGATTAAAAGCAGAAGCATTGTTGATTATGGTTTCGATTTTAAGAGTTGGGGAATCTAGCTTGG TTTCTAAGAAAATTGATGAGGATTCTGCTGACAGAATTTTGTCTTACATCAAGATTTTGAACGATG AAGAAGACCTTCAGGAAATCAAGACAAGCTTCCTTGAAGATACTAAAGATGCATTTAAAGCACAAA TTAATAATGCTGAATTGAAGAAAGCAGAAGCATTGGCTAAGGATTTGCATGATAACGCTGAACAAA TTGACGATGCAATTGTTTTTAGACAGTTGGATAAAGATAACAAAAAGAGTAAAGCTTCTGTGGATG TTATACAATTGACTGGGTTTTCCGATCCTATTTACGCAGAGGCATTTGTCAAAGTTCATCAATACG ATGTTGTGTTAGATGTCTTGCTAGTGAATCAAACCAACTACTTTAAGAAACTTATCAGTTGAAT TTGCTACATTGGGTGATTTGAAAGTGGTTGATAAACCAACTACCGCAAATATTGGACCTCATGGTT TCTACAAAGTTCAAACAACTATTAAAGTTACTTCGGCTGATACTGGTGTCATCTTTGGTAACATAG TGTATGACGGTCAACACTCGGACGATTCACGTATAGTTATTTTGAATGACGTTCACGTTGACATTA TGGATTACATTAAGCCAGCCACTTGTTCAGAAAGTCAATTCCGTAAAATGTGGAACGAATTTGAAT GGGAGAATAAGATAACCATTAAATCACCTATTGAAACATTGAAAGAGTACTTGGATGAATTAATGA AGGGTACAAATATGCAATGCTTGACACCGGGTGCGGTAATTGGAGAAGAATGTCAATTTTTATCAG CAAACTTGTACTCAAGGTCAAGCTTTGGTGAAGATGCATTGGCTAATTTATGTATAGAGAAACAGA GTGATGGACCAATAATTGGTCATGTCAGAATAAGATCAAAAGGTCAAGGTTTGGCTTTGTCATTGG GTGATAGAGTAGCTTCCATTTCAAGAAAAGGTAAGAAGGCAACTATTGCTCGTGTTTAA

YDR238C_homolog 952aa (SEQ ID NO 324)
MSDSGYTLIYEPNTATKVSVNEFKNLLEKGKDDVKVDTMKKILITILNGDPLPDLLMHIIRFVMPS
RNKELKKLLYHYWEVCPKMDESGKMRHEMILVCNAIQRDLQHPNEYIRGNTLRYLTKLKEPELLET
LVPNVRQCLEHRHAYVRKNAVFALWSIHKVSDHLAPDADELIYRFLYEENDSVCKRNAFVCLGDLN
REAALQYIQDNISVIETLDPLIQLAFIEFIKKDSIQNPALKQQYAQLMTEIIESSSNVVMYEAANT
LTVLTSNPQSILLAGNKFVELATRESDNNVKIITLERINQLHKQHPGVLQDLSLEILRGLSSQDLD
VKKKALDVTLQFITTRNVEDVVKLLKKELQSTALSNDDKNADYRQLLINAIHQLAIKFVEVAANVI
DLLLDSIADLNTTAAYEVITFVKEVVEKFPDLRDAILRRLILALPHVKSGKVFRGALWVIGEYALE
ESLIQESWKYIRGSIGEVPIIASELKSKKRDDTEESQEEETEYDGKPRRKGPVVLPDGTYATESAL
TSETTDSLESDSKTPIRKQILAGDFYLGAVLASTLVKLILRLQSLKQTQEKILNGLKAEALLIMVS

ILRVGESSLVSKKIDEDSADRILSYIKILNDEEDLQEIKTSFLEDTKDAFKAQINNAELKKAEALA KDLHDNAEQIDDAIVFRQLDKDNKKSKASVDDVAAASGSNELKKENLSSRLNKIIQLTGFSDPIYA EAFVKVHQYDVVLDVLLVNQTTTTLRNLSVEFATLGDLKVVDKPTTANIGPHGFYKVQTTIKVTSA DTGVIFGNIVYDGQHSDDSRIVILNDVHVDIMDYIKPATCSESQFRKMWNEFEWENKITIKSPIET LKEYLDELMKGTNMQCLTPGAVIGEECQFLSANLYSRSSFGEDALANLCIEKQSDGPIIGHVRIRS KGOGLALSLGDRVASISRKGKKATIARV

YDR294C_homolog 2270bp public: 1..278/280..2270, PathoSeq: 279; CDS: 501..2267 (SEQ ID NO 325)

AAAAGCAGAACACAAAACATGGAATTTGAAAACAATTTTGTAATTCAATCGATCCGAGACTTCCAT AGCAAAGTTAACAAGCACAATTGTCATTTTAACTTAATTGGTGGATTAATCGGGATCAATCTGAAT TGTTTCCCGTATTGTTTAAAACCAAAGAAAAAGGATAATCAAAACTAAATCTTTCATATTAACACT AAAGAAAAAAGCTCTCTCTCCCCCAAAAGAAAAGCAAAGGTAATTCCTTCATACACCCTT **TGATATCTTTCCTCTTAGACTTTTCTTTTAATACTTGCATCAATTGGAATATTACTTGTTCATACT** GGAGTTTTCATTGAACTAAATATTATTAAAATATTATTATGCTTGAATTGAATTCAATTACGATTC CTCGGAATTTCACTGAATTCCAACTCACAGCATTAAAGATCTACTATCAACTTAAGATTTTATTTC TTGCCACATACTGTGCTCAAGGATCATTTGGCTTGAACGGTTCAGTCTGTTTAGCAAGAGATATTT TTGTTGGCTATGTTGTATACACTCAATTATTAAAGCTTTTATCGAGTATTAAGAGGGTACGGTATTG TAGATTCTATTCGAAGGTTATACCTATATGTTAGTTCTACGGTGTCATCTCAAATCTTTTCACTAC CATTTATTAAATCCAAAATTGACAAGGAATTGCAAGCGACTATTGGCAAAGTAGAAGAAGAGATTA TGAAAAACGATCCACAGTTATTACAGTTTCCCGAATTGCCAGAACAGGGTATTGACGCTGACAATG TTTCCTTGGAGTTGGATAAATTACAAAACTTGAAACATTCTGACTGGATCAATGGAAGAGTCAGTG GAGCAGTTTATCATGGAGGTGAGAATCTATTGTCATTACAAGTTGAAGCTTACAAGAAATACTCGG TGGCCAATCAATTGCATCCCGATGTTTTCCCAGGTGTGCGTAAGATGGAGGCCGAAGTAGTTCATA TGGTTTTGGATATCTTTAATGCTCCGAGTGACGGGTGTGGATCGACAACTTCGGGAGGTACTGAGT CGTTATTGTTAGCCGGGTTGTCAGCTAGAGAATATGGGAAGAAATATCGTGGAATAACTGAGCCTG AAGTCATTGCCCCCGTGACAATACATGCGGGAATTGAAAAAGCCTGTTTTTATTTTGGAATGAAAT TACATAAAGTTGACTTAGATCCGGTTACCTTTCAAGTTGACGTTAAGAAAGTAGAAAGATTGATCA ATAGTAATACAGTTTTAATCTGTGGATCAGCCCCAAATTATCCTCATGGAATAATTGATGATATAG AGTCCTTATCCAAGTTGGCAGTCAAGTATAATATCCCGTTGCACGTTGATGCATGTTTGGGGGTCAT TTATTGTTTCGTTTTTAGAAAAATCAAAAGTACATGGCGATAGGAAATTGCCCATATTTGATTTTC GATTACCAGGTGTCACGTCAATCTCATGTGATACTCACAAATATGGGTTTGCTCCCAAGGGGTCAT CAATAATTATGTACCGTTCGCCAAAATTACGTGAGTGTCAATACTATATTGCAAGTGATTGGACGG GTGGAATGTATGGTTCTCCAACTTTGGCTGGTTCTAGGCCAGGTGCTCTTGTAGTTGGATGCTGGG CTACATTAATCAATATTGGGAAACAAGGATACACCAAGTTTTGTTACGATATTGTGCTGGCGTCAA TGAAAGTTAAACGAGCAATTGAAACTGACCCGATACTATCCAAACATTTACAAATTATTGGTGATC CAATTGGGTCGGTAATTTCGTTTCAACTTGCACCTCAGCAATCGGGAAATTTAAGTATTTACGAGA TTAGTGATTTGTTGACCAAAAAAGGTTGGCATTTTGCAACTTTACAAAACCCATCAGCATTACATT AAGAAGCGGTGGCAATTGCCGAGGAACACAAAAAGAATGGAGTGACCAAAGCTCCAGGTGATACTG CTGCGTTATATGGTATAGCTGGCAGTGTACATACAGCAGGGTTGGCTGATAGATTAATTGTTGCAT TTTTAGATACCTTATACAAAATTTGA

YDR294C_homolog 589aa (SEQ ID NO 326)
MLELNSITIPRNFTEFQLTALKIYYQLKILFLATYCAQGSFGLNGSVCLARDIFVGYVVYTQLLKL
YRVLRGYGIVDSIRRLYLYVSSTVSSQIFSLPFIKSKIDKELQATIGKVEEEIMKNDPQLLQFPEL
PEQGIDADNVSLELDKLQNLKHSDWINGRVSGAVYHGGENLLSLQVEAYKKYSVANQLHPDVFPGV
RKMEAEVVHMVLDIFNAPSDGCGSTTSGGTESLLLAGLSAREYGKKYRGITEPEVIAPVTIHAGIE
KACFYFGMKLHKVDLDPVTFQVDVKKVERLINSNTVLICGSAPNYPHGIIDDIESLSKLAVKYNIP
LHVDACLGSFIVSFLEKSKVHGDRKLPIFDFRLPGVTSISCDTHKYGFAPKGSSIIMYRSPKLREC
QYYIASDWTGGMYGSPTLAGSRPGALVVGCWATLINIGKQGYTKFCYDIVSASMKVKRAIETDPIL
SKHLQIIGDPIGSVISFQLAPQQSGNLSIYEISDLLTKKGWHFATLQNPSALHFAFTRLTVPVVDE
LIADLVEATKEAVAIAEEHKKNGVTKAPGDTAALYGIAGSVHTAGLADRLIVAFLDTLYKI

YDR430C_homolog 3605bp PathoSeq: 1..330/1927, public: 331..1926/1928..3605; CDS: 501..3602 (SEQ ID NO 327) **AATTTATAAAACCGGATAGGGCCGTTATCGCAGGACGTGTCCCATGATCAATCTACAATGAAATGA** TTCACATGAAATATGTTACAATTCCACACTTGCTGCTAAAAAGCAACAGTTTTGCAATAGAGAAAA GCATGATATACTATCGATAATATCTTTCGATAAGAACTTAAATGTAGCAACGTTGAATTTTAAAAT CTCGTTGAAATCATCTCCATTCTTTTTCCACGTCTTTGTTGAAAACTTTGCAACCTAAAAAAAT AAGAATCACTCCAACAAGTTTAAACTACATTATCAATTATGTTGAAAACTAGATTAAAACAAAGCA GGGCCATAAGTCGGGTTGTAAGAAGATATGCATGCTCACACCCCATTTCTCCCAATCTTGATAAGT ACCCAGTTGGTCTAAAATTGCATGGTTACGAAGTTACCCAAACATCACCTATCCCAGAATTTTCCC TCACTGCTGTATCATTAAAACACACAGAGAGTGGTGCAACTCACTTACATTTGGATTCCCCTAATG ACAGTAATAATGTATTTCTGATTGCCTTCAAAACAAATCCTCCAGATAATACTGGGGTTCCCCATA TTTTAGAACATACAACTTTGTGTGGTAGTAAAAAGTTTCCGGTCCGTGATCCATTTTTTAAAATGA CCAACAGGTCGTTGAGTAACTTTATGAATGCAATGACAGGCCATGATTACACATTTTATCCATTTG CTACCACCAATTCAAAGGATTTTGAAAACCTAATGGATGTGTATTTATCGTCAGTGTTTGAACCGC **AATTAAACCATACCGATTTCTTGCAAGAAGGATGGAGAATAGAAAATCAAAATGTTCATGACATAT** CGTCCAAGCTTGAATTCAAGGGAGTTGTATATAATGAAATGAAGGGCCAGTATTCGAACTCTGCAT ATGCAAAAACATTTACTTATGGAAAATTACCATTGGAAGACAGTTTAAGTAAAATAAGCAAATACT ATGAATCATTCGAAAAAAAGGTGTCTTCAGTTGACGTCAAACAACCTATATTTTCTACAGATAAAT AGTACTGCACATCTATCACCTGGAACTTGGGTAATCCATTGGATCCAAACATGCAGTATGATATTT TTAAATGGAAAATATTGAGCTCATTATTGTTTGATGGACACACTCTCCTTTCTATCAAGAGTTAA TTGAAAGTGGATACGGTGACGATTTTTCTGCAAATACTGGGTTGGACTCAACCACCGCGTTGCTTT CGTTTACTGTTGGTCTCAACTACTTAACCAAGCAAAAAGTTGATAATTTTAATGAAAAAGTTATGG AAATCATTAATAATAAAATCATTCCCGAATTAAGTAACGAAGAGTCCTCTTCATATCATGGTAGAA TTGATGCTATATTGCATCAAATAGAAATAGGATTCAAAAGACACAAGCCCGATTTTGGATTTGGAT TATTGAGCTCTATTGTTCCGTCATGGGTGAATGGAGTTGATCCAATTGACACCTTGCAAGTGGAAA AGATATTGTCGCATTTTAAAGAAGATTATAAACAAAATGGTTTAAGGATCTTTAAAGAATTATTAG AAAAGACATTGTGTAACCCTCATTCGCAAAAATTTAAATTCACCATGGAGCCAAGAGAAGATTTTA CCAAACAATTGGTAAAAGATGAGAATTTGATGATCGAGAAAAGAGTAAGTGAACTCACAGAAGATA ACAAGAAGCCAATCTATGAGCAAAACTTGGAATTAGCTAAATTACAATTGGAGGATCAAAATACAG AAGTTTTACCCACATTGACTATTGATGACATTCCAAAGAGAGGTGATTTTTATGCCATTGATTTGG GCCAAGTAAATAAGAAAGTTGTACATGAAAGGGTAGTTGATACCAATGGCTTGGTTTATGCCAACG CTTTAAAAGATATTTCCTATTTACCCACCAAACTTTACAAGTACCTTCCATTGTTTAACAACTGTT TGACGAACCTTGCTGGAACAGAAAACACCCCATTACGGAGTTGGAAACTAAAATACAAATGTTAA CTGGCGGATAACATTTAGTTCTAAAATATCGACTGACCCCTATAATATTGAGCAACTAAAATTAC AGTATGTGTTAAGTGGAATGGCTTTGAAAGAAAAGTCATCCTCAGTTTATGATTTATGGTTGGAGA TTTTAACTACCAAATTCGACACCAGTGATGAGGTATTAGAAAAGTTGTCAGTTTTGATTAAAA ACATGGGACAAAACCAAATCAATAATATTGCTGATCGCGGTCATTCTTATGCGGCTGCTGTGAGCT CACTGAAATTGACACCGCTGAAATACATCAGTGACATCGTTTCAGGTTTGAGTCAAGTTCAATTTG TAATGGAGTTGAACTCCAAATTAGAATCAGAAGGGAAAGAGTACTTGGCCAAAGAGATTATTCCGA TATTGCAAGAAATACAAAAGTATGTATTGCAAGGTGAATTCAGGTATAGACTAGTTGGAAATCAAG AGATTATTGTTGAAAACGAAAAGCTTATTGAGAAATTTGATAAGGATATTTCTTCGAACAGACCAA CTTTATCGTTAACAGTAACAGATGGTTTACTGGCATTGTTGAACTCATTCAATTACAATCATACAA GTGAAAATGTCTTAGTTAACTTACCATTTCAAGTGGGATACTCTTCATTAGGTAAGATTGGCTCTT CGTATTCATCAAAGGATGGTGCTTCTTTACAAATATTATCTCAGTTATATTCCTTTAAAAATCTAC ATTCCAAAATAAGAGAAAGCAATGGTGCATATGGAGGTGGTTTGACATATGATGGGTTGAACGGGA CATTAAACTTTTATTCGTATCGTGATCCTAATCCTGTTAAGTCGATTCAAACTTTTAGAGATTCCT TACTGTATGGACTTGATGCTAATTGGAACGATAAGGATTTACAAGAGGCTAAGTTGCGGGTTTTCC AAAGCGTCGATGCTCCAATTAATATCTCTTCTCAGGGTGCTAGTGCCTTCTTTGAAAATATAGATG ATTACTTGAGACAGGAAAGAGAAAACTTTTTGGGTACCACTTTAAAGGATCTCAGAGATGTGA

CTGAAAAGTATCTTGTTGATAACCAAAACAACCTTGTCACTGTTATTGGTGACAATGAAATTTTAA ATGTCGATAATAAATGGCAAATTAGAAATTTTCAAGTATAG

YDR430C_homolog 1034aa (SEQ ID NO 328) MLKTRLKQSRAISRVVRRYACSHPISPNLDKYPVGLKLHGYEVTQTSPIPEFSLTAVSLKHTESGA THLHLDSPNDSNNVFSIAFKTNPPDNTGVPHILEHTTLCGSKKFPVRDPFFKMTNRSLSNFMNAMT GHDYTFYPFATTNSKDFENLMDVYLSSVFEPQLNHTDFLQEGWRIENQNVHDISSKLEFKGVVYNE MKGQYSNSAYYFYIKFLESIYPSLNNSGGDPKKIVDLSYEGLLEFHSKNYHPSNAKTFTYGKLPLE DSLSKISKYYESFEKKVSSVDVKQPIFSTDKSEIFDVTIPGPVDTMNGKETSEQYCTSITWNLGNP LDPNMQYDIFKWKILSSLLFDGHNSPFYQELIESGYGDDFSANTGLDSTTALLSFTVGLNYLTKQK VDNFNEKVMEIINNKIIPELSNEESSSYHGRIDAILHQIEIGFKRHKPDFGFGLLSSIVPSWVNGV DPIDTLQVEKILSHFKEDYKQNGLRIFKELLEKTLCNPHSQKFKFTMEPREDFTKQLVKDENLMIE KRVSELTEDNKKAIYEQNLELAKLQLEDQNTEVLPTLTIDDIPKRGDFYAIDLGQVNKKVVHERVV DTNGLVYANALKDISYLPTKLYKYLPLFNNCLTNLAGTENTPITELETKIOMLTGGITFSSKISTD PYNIEQLKLQYVLSGMALKEKSSSVYDLWLEILTTTKFDTSDEVLEKLSVLIKNMGQNQINNIADR GHSYAAAVSSSKLTPSKYISDIVSGLSQVQFVMELNSKLESEGKEYLAKEIIPILQEIQKYVLQGE FRYRLVGNQEIIVENEKLIEKFDKDISSNRPTLSLTVTDGLSALLNSFNYNHTSENVLVNLPFQVG YSSLGKIGSSYSSKDGASLQILSQLYSFKNLHSKIRESNGAYGGGLTYDGLNGTLNFYSYRDPNPV KSIQTFRDSLSYGLDANWNDKDLQEAKLRVFQSVDAPINISSQGASAFFENIDDYLRQERRENFLG TTLKDLRDVTEKYLVDNQNNLVTVIGDNEILNVDNKWQIRNFQV

YDR450W_YML026C_homolog 1366bp public: 1..1366; exon 1: 501..548, intron 1: 549..976, exon 2: 977..1363 (SEQ ID NO 329) TTAAGAACTAGCAGATGTAAAATGTTTTATGTCATTATAATATTTGTTAATACATGTATATAGATT TTTTAATGAATGTATTCCCTAAATAGAACAGAATTATGATGCTGTTACAGCAAAAACTGGTTTGAG GCGCGCGATTCTTCCTGCTAGAGGTTTTTCTTTTTGTATGTCTGTAACAGTGCGACTCACATAGTT AAGTAATTTTAAAGCCAGAGATTGTGTACAGTCGCACGCCCCTAATCACATAGTTAATTCTCAAA TTTTGTATAGTTCAGTTTAACAACACCAGTAATCAAACATGCCATTAGTTGTCCAAGAACAAGGTT CATTCCAACACATTTTACGGTATGTGAGTGTATTATAAGATTATTTGAATGAGATAGAAAAGGGTT AAGGAAGGAAAGAAATTATCCAACTACTGTTTTGGGAAAGATTAATCAGAAATTTGAATGCAATGA **AAAAACTTTTTCAAGAGATGGATATGGAACAAGATTCGATTGTTATCAACAAATATAAAGAAAAGC AATGATTTACTACTGTTTGGGAAAGATTTTGGATATGTGTATCAACAATACTACTATTTACTTTGG** AGTAATATGTTTTCAATATTATCAGAGACTTATCAAAATTTATGAGTTTATTATTATTGAAGTTCA ATACCATCAAGCCTTTTTTTAACCATCACTCTATTCAACAATCATTTAAATATTAAAGTCTTTTT TTTCCCTGTTTAAAGTATTCGATTTACTAACATTATGAATTATTATTATAGTTTGTTAAACACCAA CATTGATGGTAGAATCAAGATCATGTACGCCTTGACCAAGATCAGAGGTGTCGGTAGAAGATATGC CAACTTGGTTTGTAAAAAAGCCGATGTTGAATTAACCAAAAGAGCTGGTGAATTGACCCAAGAAGA CAGACAAAAAGATCAAGTTGATGGTAAAGATTACCATGTTTTAGCTAACAACTTGGAATCTAAATT GAGAGATGATTTGGAAAGATTGAAGAAAATCAGATCTCACAGAGGTATTAGACACTTCTGGGGATT GAAAGTTAGAGGTCAACATACTAAAACTACTTCTCGTGGTCGTTAA

YDR450W_YML026C_homolog 145aa (SEQ ID NO 330)
MPLVVQEQGSFQHILRLLNTNIDGRIKIMYALTKIRGVGRRYANLVCKKADVELTKRAGELTQEEL
ERIVTIMQNPTNYKIPAWFLNRQKDQVDGKDYHVLANNLESKLRDDLERLKKIRSHRGIRHFWGLK
VRGQHTKTTSRGR

TTTTCACACTAAGTTAAGGAGAGTGCGAAAAATTTAGTACTAACAAAATTGTATTGTGTTGTGTGT TTATTGTATTAACATTTTAAGATATCAAGAAACTAAAAATGGCTAAGTTCATCAAATCTGGTAAAG TTGGTATGTAAAAATGAGTACCTATATGGGTAGACAATGATAGATTTATTGGCCAACTATGAATGG GATAGATATATATGATATGGGAGAGAATTTTGAAGGATTGAAATATTTTATATAAAAGAGAGAAGC GAAGATTTAAATGATTACCATCGTAATAAATTTATTGGAATTTGGGAGATTCTTTTGGAGTTAAGA **AAAAAGCAAGTGATTGATCAATCACTATGGAGCCGTCACAGACATCAACGAATCCCACAACATTT** TTATTTATTCATATCCATCATATGGCAGTAACAATCATGAATCTACAAATTACATTTAAAAAAAGC ATTATACTAACTAAATTTTTTAGCTATTGTTGTAAGAGGTCGTTACGCTGGTAAAAAAGTAGTCAT TGTGAAACCACATGATGAAGGTACCAAATCTCACCCATTCCCACATGCCATTGTTGCTGGTATTGA AAGAGCTCCATTGAAGGTTACCAAGAAGATGGATGCTAAAAAAGTTACCAAAAGAACTAAAGTCAA GCCATTTGTTAAATTAGTAAACTACAACCATTTAATGCCAACTAGATACTCATTAGATGTTGAATC ATTCAAATCTGCTGTCACTTCTGAAGCTTTAGAAGAACCATCTCAAAGAGAAGAAGCTAAAAAAGT TGTCAAGAAGGCTTTTGAAGAAAAACATCAAGCTGGTAAGAACAAATGGTTCTTCCAAAAATTACA CTTTTAA

YDR471W_YHR010W_homolog 136aa (SEQ ID NO 332)
MAKFIKSGKVAIVVRGRYAGKKVVIVKPHDEGTKSHPFPHAIVAGIERAPLKVTKKMDAKKVTKRT
KVKPFVKLVNYNHLMPTRYSLDVESFKSAVTSEALEEPSQREEAKKVVKKAFEEKHQAGKNKWFFQ
KLHF

YDR486C_homolog 1157bp PathoSeq: 1..1157; CDS: 501..1154 (SEQ ID NO 333)

TTCCAGTCATTCCGAAATGCATAAGCAAGACGTTAGTTGTATTGTGGTTGTTTAGTCTAATCCAAA AATACTTGCCATGACGACCCACTGAAGTAACAACTGCATTTGTTAAGGCTTTTCTCATCTTATTCA ATTCTTTTTCAGCATCATTCGTATCTTTAAGCACAGGGAATAGCAATGGATCATGTAACAAATTCA AGTTAGTCGTCAAGAAAATAATTCAGTGTTAAAGTCTGTACCTTAAGCGTCAAACGTACTTCTGCA GGAGGTTTTAGAAGGCAAAACCAAATCTAGACAAGGAGATGAACAGATTATTCGGAACGAAAAGCA CTGCGCCCAAACCATCTTTGAATGATGCAATCAAGGGAATCGATGAAAGAGTGGGGTCTTTGGATG TTAAATTAAGCAAGATCAACTCGGAATTATCCACATACCAACAAAAGATAAGCAGAATGAGAGACG GACCCGGGAAGTCGGCACTAAAACAAAAAGCAATCAAGTTACTAAGACAGAGGAAGCAGATAGAAG CTCAAAAGGATCAGTTAGAGAATCAATCTTGGAATATGACACAAGCTTCCATGACAACAGATAACT GAAAAATTAATATCGATGAATTGGAAGATCTTCAAGATGAAATGTTGGATTTGATTAAATCAA ATGAACTACAGGAGGCACTTCTGACGAGCTATGATGTACCCGATGACATCAGTGAGCTGGAGTTGG ATGCTGAATTAGAAGCTCTTGGCGAAGAAATTGATTTTGAAAATGAAATGGCAGAGAGTGGGATAG GTGCACCTAGTTACTTAAATGATACAGAACCTACAGCAGCAGATAAATTGCCTACATTTATTGACG AACAACCAGAAGAAGCTCAAAAAATCGCAAACTAG

YDR486C_homolog 218aa (SEQ ID NO 334)
MNRLFGTKSTAPKPSLNDAIKGIDERVGSLDVKLSKINSELSTYQQKISRMRDGPGKSALKQKAIK
LLRQRKQIEAQKDQLENQSWNMTQASMTTDNLQNTMVTINAMKTANKSLKQTYGKINIDELEDLQD
EMLDLIDKSNELQEALSTSYDVPDDISESELDAELEALGEEIDFENEMAESGIGAPSYLNDTEPTA
ADKLPTFIDEOPEEAOKIAN

TCATTTGTTGACTTTTGAAAGTTTTATTCATCCATATTCTTCAAGTTAAAATAGTGTTCAATATCT GTCCAACCAAGAAGAAAACCAATAAACAACATCAATTCCAACTTTGTTTACATCAAACAGAAACAA AAAACAGATAATTTATAGACACCTTCATTCATTCGTTATTTTTTTCCAAGTACTACACGTCTTTAT CGTCATCGATTATGTCCCAATCAAATCATAATCATCCACAGAAGATCGGACCTTGGAAATTAGGTA **AAACTTTAGGAAGAGGTGCCACCGGTAGAGTCTTATTAGCTACTCATCAAACTACTGGTCAAAAAG** CTGCCGTTAAAGTAGTTTCCAAATCCGAATTACAAGACGAAGAAACCGAGAAAAATGGAGATGGAT TATATGATGTATGGGAAACATCTAAGGCTCTTTATCTTGTTCTAGAATACGTTGAAGGTGGAGAAT TATTTGATTTATTGGTGGAACGTGGTCCATTACCTGAAGTCGAGGCTATCAAGTATTTCCGTCAAA TCATATTGGGTACGGCTTATTGTCATGCTCTTGGTATATGTCACAGAGATTTAAAACCAGAGAATT TGTTACTAGATTCTCAATTGAATGTAAAATTAGCCGATTTTGGAATGGCAGCTTTAGAAAGTAACG GCAAATTATTAGAGACTTCTTGTGGTTCACCTCATTATGCTGCTCCAGAAATCGTTAGTGGATTGA **AATATCATGGAGCTGCTTCTGATGTTTTGGTCTTGTGGGGGTTATATTATTTTGCCTTGTTGACAGGTA** GATTACCCTTTGATGATGAAAATATTAGAAATTTACTTCTTAAAGTCCAGGCTGGTAACTTTGAAA TGCCCGTTGATGAAGTTAGCAGAGAAGCTAGAGATTTAATTGCTAGAATGTTAGAGGTTGATCCTA TGAGAAGAATATCTACTGAAAAAATCTTAAGACACCCATTGTTAACCAAATACCCAATGTCAAACG **AAGATTTAATCAGTGAAAAATCATTACCACATCCACATACTGGTTACAAATCTTTAGGGTCAGTTA** GAAACATTGATAAACAGATTTTATCAAACTTGACAATTTTATGGAATGATAGACCCGAAGAGGAAA TTGTTGATTGTCTTTTGAAAGATGGATCCAATCCAGAAAAAACATTCTATGCATTATTGATGAGAT ACAAGCATAATCAAGACGATAACACTAATAACAATTCACCAAAGAAATCAACGAGTTTCAATAATA AAGTGGTACGCAGTGGGTCCAAATACAGTCTTAATGGAACCCCTAGAAGAAAAAGAGCCAGTCACA TAAGTGTGTCAAGACCAACATCTTTCCAATACAAGTCTAATCCTGGCGCTGGTGCAACAGCAAATA GAAACTCCGTTGCCAGACATTCTGTGGCTTCCTCGGCCAACAATTCTCCTCGTAAATCACCATACA AGTCACCATACAGATCACCTTATAGATCACCATATAAATCGCCTTCTAAGAGATATTCATATAATC AATCCCCAACTAAATCTCCTTACGGAAGAGATCAAATTCACAAAGACAATTTGAAAATGAACCAT TAAAGGCAAAGCCAAGAAATATTTACAATGAGATTGTTGATGCACAAAGCAACTTTTCTCTACCTC CATCGCTTCCACCTTCCTTACCTTCAAAAGATTCTCGTTATATGATCGATGAACCCAATCAACCCC AGTTGCAACAACCTGCTTTAAGTCAAGTCCCTGAAAATCCTATTGTTGATGAATCCCCTGATTTAA TGCAGTCAGCAAAAATTTCTAGTGGAAAGAGAAATTCAATAATAGGAAAGAACAACAACAACAGCA ACAGCAACAAGAGAATGTCTAAGAGAAAATCAATTCGTGCATCTATGACCACGGGATTGAAAAAGAA ATTCCATAACCATGAAATTGTTATCTACTTATGCTAAATTATCAGGTGATGACGACTGGGAATACA TGGATAAACAAACAAAAGAACATCGGCTACTTTTGCAGCATTGTGTGACAAAATATTTAATCAAG **AAGACTATGACGAAGAAGACGAACAATTAGTTGATCCTGAAGAAAAGGAAGCCAAGGAATATGAAA** GGTTAATGGAATTGGAAAGAAAGAAACATGAAGCTGAGTTGAAAGCTAGAAGAGAATTAGAAAAGA AGAAAAGAAGACAAAAGAGACGTTCCATTTTGAGTTCTAAGAAATTAAGTATTATTGTCAAGAATG **ATGCTGATCCAAATAATAGTGAACAAGAGTTGGTCGATGAAGGTATAAAACAACCAAAACGTCAAT** CCAAAAACTTGACCGCTTTAAGAGCATTATCTGAAGGAAATCATGCATCTGAAGAATTGACATTGG AAGACGTTGAGAATTTGAAGAGACGATCAGCATCACCAGCCGGTTCCAAAAAGAAGACAAACTCCGG TTTTGACAAGAAGACCTGTATCAAGATTAGATCCATTATGGCAAGCACACGAGAATGAACAGTTAG ATAGAGCAAAAGATGCCTTGGAACAAGAATGGAGGGATTCACAAAAGAGAAGTTCTACTGTTAGTC GTAAAAAAGTCAACAGAGAGTCGATGATATCAGTTATGGATGATATTGTTGAAGAGGACCAAGGCC GTGTCAACAGGAGATCAACACGAAACACTTACTATGAAAGGGAAAGAGACTATGAATTACCAGAAC CAACTGTGGAAGATTCCAACTTGACTGATGACTACATGACAGAAAATCAGAAAATCAAGACTTTTGA ACAGTCAGTTAAATGTTAGGGATCCACTTAATGAAAAAAGAAAATCTGAACCCAAGACTCTTATTA GCAATGTTCAAATACCGAGTGTTACTAGAAAATCAAGAAATTTCACTACTTCCAACAAAAGGTTGT CGGTATTGTCTATGTATTCAACAAAGGAATCATACCGTGATTTGAATTCTATAATTAACTCACCAG ATGAAAACCCCGAACAGCATCAAAACATGAACAAGCCAGCGTTACGAACCAGTATTGCTGATCGTT TGGATAAAGCTGGATTGGCTGAACCAGAATATGAAACTGAGACTGATGGTGAAGATAAAGTGTCTG TTATTGATTTGGATGATCATTTAGCTGATAGAAGGACTTCCTATTATGATGGATCTGGAAAGAGAG CATCTAGAGCTTCAACAACTAAACGTTACAATGTTCATTCCAGTTCAGAAAAAAGACCAAAATCCA AAGTTCCTGATTTGCCAAAGAATGATTATGATGACACATTTGTCAGTAATAGTGATGAAGTTCATA AGCGTCAGTATAAATCGATGGTTTCTGATGAGTCTAGTGCATCTGATGATGTATTTGATAAGATTA AATTACCAGATGGTAAATCAACTAAATCTTCCATTGATGAATTGGCTAACGGCACGTCTACAAGTG GTCATAGAAAACCAAAGATAAGACATTCTCAACCGGGCCCAGAAATGTTGATTCCTCATTTGAATG GAGGTATTGAGTCGTCTCAACCAATGTCTAAAGTTCGTGGTAACAATTCAAGTGGTCATGATGATA

YDR507C_homolog 1349aa (SEQ ID NO 336) MPHSRQPSISSSIMSQSNHNHPQKIGPWKLGKTLGRGATGRVLLATHQTTGQKAAVKVVSKSELQD EETEKNGDGLPYGIEREIIIMKLLTHPNVLRLYDVWETSKALYLVLEYVEGGELFDLLVERGPLPE VEAIKYFRQIILGTAYCHALGICHRDLKPENLLLDSQLNVKLADFGMAALESNGKLLETSCGSPHY AAPEIVSGLKYHGAASDVWSCGVILFALLTGRLPFDDENIRNLLLKVQAGNFEMPVDEVSREARDL IARMLEVDPMRRISTEKILRHPLLTKYPMSNEDLISEKSLPHPHTGYKSLGSVRNIDKQILSNLTI LWNDRPEEEIVDCLLKDGSNPEKTFYALLMRYKHNQDDNTNNNSPKKSTSFNNKVVRSGSKYSLNG TPRRKRASHISVSRPTSFQYKSNPGAGATANRNSVARHSVASSANNSPRKSPYKSPYRSPYK SPSKRYSYNQSPTKSPYGRRSNSQRQFENEPLKAKPRNIYNEIVDAQSNFSLPPSLPPSLPSKDSR YMIDEPNQPQLQQPALSQVPENPIVDESPDLMQSAKISSGKRNSIIGKNNNNSNSNKRMSKRKSIR ASMTTGLKRNSITMKLLSTYAKLSGDDDWEYMDKQTKRTSATFAALCDKIFNQEDYDEEDEQLVDP **EEKEAKEYERLMELERKKHEAELKARRELEKKKRRQKRRSILSSKKLSIIVKNDADPNNSEQELVD** EGIKQPKRQSKNLTALRALSEGNHASEELTLEDVENLKRRSASQPVPKRRQTPVLTRRPVSRLDPL WQAHENEQLDRAKDALEQEWRDSQKRSSTVSRKKVNRESMISVMDDIVEEDQGRVNRRSTRNTYYE RERDYELPEPTVEDSNLTDDYMTEIRKSRLLNSQLNVRDPLNEKRKSEPKTLISNVQIPSVTRKSR NFTTSNKRLSVLSMYSTKESYRDLNSIINSPDENPEQHQNMNKPALRTSIADRLDKAGLAEPEYET ETDGEDKVSVIDLDDHLADRRTSYYDGSGKRASRASTTKRYNVHSSSEKRPKSKVPDLPKNDYDDT ${\tt FVSNSDEVHKRQYKSMVSDESSASDDVFDKIKLPDGKSTKSSIDELANGTSTSGHRKPKIRHSQPG}$ PEMLIPHLNGGIESSOPMSKVRGNNSSGHDDSVPPPPPAHKVNKKPLDDKTNFPPPEVDPKRKGSF FRKLSWGSKKTIENNTNAATNTTTQQQLPSPAESKEEKPKSSFFRWFSSSNTPSAAEIRKFNTILP KHEMSTALFALLNSWSNFGLKDLRNDQVGYYITGAISKHNSFNLKSCKFRIKINQRDFNQKSEIVC VRVKGSKVTTDTLFCEIEKVLLKEGGLDK

YER102W_YBL072W_homolog 1121bp public: 1..1121; CDS: 501..1118 (SEO ID NO 337)

AAAATTTTCATAATTTAGAAGTTTCATTTACAGTCTTTTTTCAATTAACAGTGATACAAGAGTGTA TGTAAAGACAACATGTACTAGCAACTATAATATGATTTACCAATGATTGGGATCACAATAAATGTG TTAATATGAATGAGAGAAGGATAGTGAATAAGAGATTACGAAAGAATAGATTCAACAAGTTCAGAA TGGTATACAACTAAAATGGAATTATTTTCAAATATGCAACTATCATTATGACTACTACGACAACAA TTTTAATCGAGAGAAGATCATTAGATCAAGAGTTGGGAAACTAATACCAAGGAAATATCATTAAGA **ATTAATAGCTTTGCAAAAATTGGTTTTACTCATATTATTTGTTTTAGTTGGAAAGCGATTACATCA** TGGAACAAAGTTTACTAACAACATTGTTATAGGTAAAAATGGGTATTTCTAGAGATTCACGTCACA AACCAGCCAACACCAAGATTGGTCCAAAAAGAATTCACTCTGTCAGAACCAGAGGTGGTAACCAAA **AATTCAGAGCTTTGAGAGTTGAAACCGGTAACTTCTCTTGGGGTTTCCGAAGGTGTTTTCCAGAAAAA** CCAGAATTGCTGGTGTCGTTTACCATCCATCTAATAACGAATTGGTTAGAACCAACACCTTGACCA **AATCTGCTGTTGTTCAAATTGATGCTACTCCATTCAGACAATGGTACGAAAACCACTACGGTGCTA** CTTTAGGTAAAAAGAAGGTGGTGCTCATGCTGCTCACGCTGCTGAAGTTGCCGATGCCAAGAGAT CAAGAAAAGTCGAAAGAAAATTGGCTGCTAGATCTGGTGCTGCTGCCATTGAATCCGCTGTTGACT CTCAATTCGGTTCTGGTAGATTATACGCTGTCATTTCTTCAAGACCAGGTCAATCTGGTAGATGTG ATGGTTACATCTTGGAAGGTGAAGAATTAGCCTTCTACTTGAGAAGATTAACTGCTAAGAAAATAA

YER102W_YBL072W_homolog 206aa (SEQ ID NO 338)
MGISRDSRHKRSATGAKRAQFRKKRKFELGRQPANTKIGPKRIHSVRTRGGNQKFRALRVETGNFS
WGSEGVSRKTRIAGVVYHPSNNELVRTNTLTKSAVVQIDATPFRQWYENHYGATLGKKKGGAHAAH

AAEVADAKRSRKVERKLAARSGAAAIESAVDSQFGSGRLYAVISSRPGQSGRCDGYILEGEELAFY LRRLTAKK

YFL014W_homolog_1 819bp PathoSeq: 1..819; CDS: 419..816 (SEQ ID NO 339)

TTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTTGTG
TACTACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTCGTCCA
AATTGAGACCCTCAATTACATTTTGTCAAAAAAAATTGGTCCCTAGTGTTGCTATCGATAACGAAGG
TGAAGGCAGTTTAGCTTGGAGACATTTAGAGAACTTAGTTACATCTCATCTTCCGTTTCGAGAAAT
CGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCCCAGCACCACAGCAATATAGCAA
TCATAAATAAATTGCCCCGCGGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTTGCCCCCCTC
TCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGGTAAATTCTTTGAATCTTTGTTTTTTT
TCGACATACACCATAAATCCCATAGAAAACTGCAAAATGTCTGACGCCGGAAGAAAAAACATTTCT
ACTAAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGTCTACCTTGGAAAAAGGGCAAGGAACAA
GTCACCAGTACCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAAATCTTTCACTCAA
ACTGTTGCAGACAGCGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCGAA
CAAGCAGAGGGCGAACAAAGACCCTTGCTGAAACAGCTCAAAGAATATGTCGAGGTTGCCAAAACTG
AAATTGGAAAGGCTGCTGAATACGTGA

YFL014W_homolog_1 106aa (SEQ ID NO 340) MSDAGRKNISTKINEAITPESEKSTLEKGKEQVTSTLDKAVGSNVPDNQKSFTQTVADSVQQGSDN AKADLKKQSEQAEGEQRPLSKQLKNMSRLPKSKLERSSNT

YFL014W_homolog_2 884bp public: 1..884; CDS: 501..881 (SEQ ID NO 341)

CCTTCTCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTTG
TGTACTACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTCGTC
CAAATTGAGACCCTCAATTACATTTTGTCAAAAAAATTGGTCCCTAGTGTTGCTATCGATAACGAA
GGTGAAGGCAGTTTAGCTTGGAGGCATTTAGAGAACTTAGTTACATCTCATCTTCCGTTTCGAGAA
ATCGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCCCAGCACCACAGCAATATAGC
AATCATAAATAAATTGCCCCGCGGTTGACAGTGTATATCTTCGAGGAATGCCAACCTTTGCCCCC
TCTCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTCTTTGAATCTTGTTTTT
TTTCGACAAACACCATAAATCCCATAGAAAACTGCAAAAATGTCTGACGCCGGAAGAAAAAACATTT
CTACTAAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGTCTACCTTGGAAAAAGGGCAAGGAAC
AAGTCACCAGTACCCTTGACAAAGGTTTGGCTCAAATGTTCCAGATAACCAAAAATCTTTCACTC
AAACTGTTGCAGACAACGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCG
AACAAGCAGAGGGCGAAGCAAAGACCCTTGCTGAAACAGCTCAAGAATATGTCGAGGTTGCCAAAA
CTGAAATTGGAAAGGCTGCTGAATACGTGAGTTGTCACCGGTGCTACCGAAGGTTGCCAAAA

YFL014W_homolog_2 127aa (SEQ ID NO 342)
MSDAGRKNISTKINEAITPESEKSTLEKGKEQVTSTLDKAVGSNVPDNQKSFTQTVADNVQQGSDN
AKADLKKQSEQAEGEAKTLAETAQEYVEVAKTEIGKAAEYVSGVVTGATEGAKTGADSTKK

YGL011C_homolog 1244bp PathoSeq: 1..1244; CDS: 501..1241 (SEQ ID NO 343)

PCT/BE00/00077

TCCCAGATAAGTTATTAGATCCTAAAACCGTGTCATATATTTTTAAAATCACTCCTAGTATAGGAA
TGGTTGCCACTGGATCAATTGCTGATGCTAGAGCTCAAGCCATGAGAGCAAGATCTGAAGCTACAG
AATTTAGATATAAATATGGTTACGAAATGCCGGTGGAAAGTTTATCAAGAAGAATAGCGAATATAT
CTCAATTGTATACTCAAAGAGCTTATATGAGACCATTGGGTGTTGCTTTAACTTTTATTCAAGTTG
ATTTTGCTGATGAAGGTAGAGGTCCACAAATTTTTAAATGTGATCCTGCTGGATATTTCACTGGGG
TGAAAGCCGTGGCCACTGGTCCAAAACAACAAGAAGCAACGACTTATTTAGAGAAAAAATTCAAAA
AAACCGATGCTGTTAAAGGAGATTGGCAAAAAAACTGTTGAATTTGCAATAATTGCCTTGAGTTCTG
TGATTGGAACTGAATTCAGAAAAAAATTGATATTGAAATTGGCCACTGAAGGAGAATTTAGAA
TTTTGACACCAGAAGAAAAATAGACGAAAGATTCAATAGCTGAACAAGATTAG

YGL011C_homolog 247aa (SEQ ID NO 344)
MSNSAGFDRHITIFSPEGRLYQVEYAFKAINSANITSLGITGQDSAVIISQKKIPDKLLDPKTVSY
IFKITPSIGMVATGSIADARAQAMRARSEATEFRYKYGYEMPVESLSRRMANISQLYTQRAYMRPL
GVALTFIQVDFADEGRGPQIFKCDPAGYFTGVKAVATGPKQQEATTYLEKKFKKTDAVKGDWQKTV
EFAIIALSSVIGTEFRKNDIEIGVATEGEFRILTPEEIDERLISIAEQD

YGL031C_YGR148C_homolog 155aa (SEQ ID NO 346) MKIEVDSFSGSKIYPGRGTLFVRGDSKIFRFQSSKSASLFQQRKNPRRISWTVLYRRHHKKGISEE AAKKRTRKTVKHQRAIVGASLELIKERRSQKPSDRKAARDSKLAKDKEAKKAAKAARKAEKAKAVA SGASVVSKQQAKGSFQKVKATSR

YGL043W_homolog 1418bp public: 1..436, PathoSeq: 437..1418; CDS: 501..1415 (SEQ ID NO 347) AATCTACCATTAGGCAATGTCATATAATTTAGATTACGAACAGCTGATGACGCAGTTTCATTATCT CCATAATTTATAATGGCATACCCTTTGGATTTACCTGTTAATTCATCAAATAATAACTTCACATCT AATACTGGTCCAACTGATCTTGCAATATCCCGCACCTGTTCTTCAGTGTAATCAAATGGAAATTTA CCTATTGAAACACAAGTGCTTTTACTATCCATATTTAGTTTGAGCTGCCTAGTTTTCCTGATTCTT GGTAACAAAAACTATAATTATTAACAAATTATCGATAGAATCTCTTCCAAAGTACAACCAATTT CGATACATTTTTTCTATGAGATGTTTTTTTTCCCCTTTGTCTTTTAACTAATGTATTTGGGTACACT TTTGCATATATTACTAATATTTATCTTACCCTTTCATCATGGATACAAAGGAAATAAGATCTACCG TATCTAATCTTGAAAAAGCAGTAGATGACACCACCATTTTAAAGTTGTTGAATATCTTGAATGATG GGGTTAAACCATCCGAAAAACTCTTGAGAGAAACCAAAGTAGGTGTAGCTGTCAACAAATTCAGAA GTCACGACAGTGCCGAAATCAACGGTTTAGTTAAAAAAATGATCAGAAATTGGAGAGATGCCGTGC AAGCCGAAAAGAACAACAAAAAGAAGTTAGCAATAGCAGCTGGAACAGGAACAGCTTCAA GCTCAGCAATTTCGCCATCATCATCGGGTTCTGGAAGTACAACACCAAAACCATCAGAGTCAACCA CACCATCGGCTGCCCGTAAAGGTCCAAGAAATCCAAAAACTGACGGTGTAAATACTCAATTATACG AAAATGATACCAGAAATGCATCGGTTAGTGCTTTATACACGTCGTTAGCAGTTGATCGTGACGATT

YGL043W_homolog 305aa (SEQ ID NO 348)
MDTKEIRSTVSNLEKAVDDTTILKLLNILNDGVKPSEKLLRETKVGVAVNKFRSHDSAEINGLVKK
MIRNWRDAVQAEKNNKKKLAIAAGTGTGTPSSSAISPSSSGSGSTTPKPSESTTPSAARKGPRNPK
TDGVNTQLYENDTRNASVSALYTSLAVDRDDSPKHILRIAIEIEAEVYKSEYSKVSDSYRNRLRSF
TMNLRNKKNPELRERILSKQILPAAFIKMTPNEMAPEALKKEIEKLHKQNLFDAQGATEKRAVTDR
FTCGKCKHKKVSYYQMQTRSADEPLTTFCTCENCGNRWKFS

YGL103W_homolog 1301bp public: 1..688, PathoSeq: 689..1301; exon 1: 501..548, intron 1: 549..899, exon 2: 900..1298 (SEQ ID NO 349) ACATTTATTGTTGGCTATACTTTCCCAGTTTTAAAGGAATGGTTAGGCGGGTCAGTCTACTTTATT TTTACTGTAATGTGTTGTGCCAGTGTATGGTTTATCAAGACTAAAGTTCCTGAGACAAAGGGTAAG CATTCGTACCAGGAAGTCTGGAATTAAACGGTAGTTACTTCCAGTATATATGGTGTTCATTGTGTT TGTAGATCGCATAGTGTGAGCGCGCACACACACACACTTTGTAGTGCTACAGTTTCTCTCTTTC CCATACACTCTCGCAGTCGCACGCTTGACAAAAGTTAATTAGAAATAGAAAAATTTCTCATTCCTT TTGAGTTTTCCACCATAATCAACTAGTAATAACCAACAATGCCTACTAGATTAACTAAAACCAGAA **AACACAGAGGTAATGTTTCTGGTATGTACAATTTCACTAAAGTTTTAACGGATGAAAGAGTATTGA** TCATACAACCAAAGCAATGAATATGAGTAGTTTGGGAAACCACAACATACGAGTTATTTTCAGAA CAATCAAGTTTATCATTTACAGAAGACAGTTCCATCAATATGTCCAAAATACTCTTTGAAGTCAAT ACAGAAAGCACCCGGGTGGTAGAGGTAAAGCTGGTGGTCAACATCATCACAGAACCAACTTGGATA GGAGACCAGAAATCAACTTGGACAAATTGTGGACTTTGGTTGATTCTGAAAAGAAGAAGACGAATACT TGAGCAAATCATCTGCTTCTGCTGCTCCAGTCATCGACACCTTGGCTCACGGTTACGGTAAAGTTT TGGGTAAAGGTAGATTACCAGAAGTTCCAGTCATTGTCAAAGCCAGATTTGTTTCTAAATTAGCTG AAGAAAAATCAGAGCTGTTGGTGGTGTTGTCGAATTAGTTGCTTAA

YGL103W_homolog 149aa (SEQ ID NO 350)
MPTRLTKTRKHRGNVSAGKGRIGKHRKHPGGRGKAGGQHHHRTNLDKYHPGYFGKVGMRYFHKQQN
HFWRPEINLDKLWTLVDSEKKDEYLSKSSASAAPVIDTLAHGYGKVLGKGRLPEVPVIVKARFVSK
LAEEKIRAVGGVVELVA

YGL147C_homolog 423bp PathoSeq: 1..423; CDS: <1..420 (SEQ ID NO 351)

GCTATCAAAATCACTGTTCACAATGGTGACAGAAAACACGTTGCTGCTTTAAGAACTGTCAAATCT
TTGATTGCTAACTTGATCACTGGTGTCACTAAAGGTTACAAATACAAGATGAGATTTGTTTATGCG
CATTTCCCAATTAACGTTAACATTATTAAAAAAGATGGTCAAGATTACGTTGAAATTAGAAATTTC
TTGGGTGAAAAAAGAGTTAGAGAAGTTAAAATCCATGAAGGTGTCACCATGGAAATTTCTTCTACT
CAAAAGGATGAATTGATTGTTTCTGGTAACTCCTTGGAAGCTGTTTCTCAAAATGCTGCTGATATT
CAACAAATCTGTCGTGTCAGAAACAAGGATATCCGTAAATTCTTGGATGGTATTTATGTTTCTGAA
AGAGGTACCATTGTTGAAGAAACAA

YGL147C_homolog 140aa (SEO ID NO 352)

AIKITVHNGDRKHVAALRTVKSLIANLITGVTKGYKYKMRFVYAHFPINVNIIKKDGQDYVEIRNF LGEKRVREVKIHEGVTMEISSTQKDELIVSGNSLEAVSQNAADIQQICRVRNKDIRKFLDGIYVSE RGTIVEEI

YGL213C_homolog 1655bp PathoSeq: 1..1655; CDS: 501..1652 (SEQ ID NO 353)

GATGATCGCTAACAAGGTACCCGATTTATTCATCAACAAAGAAGCTACTTCATAGAATTGATTCTC **AACCTTAAATAGCTTGTAGTTTTTATGATTGGGACTAATTGTGCAGCATCGAACAATATTGCCAGT** TGCATAGAATAAATCGGTATTATTACGGCATACCAATCGATTGTAGGGGGTTGAAGCTGGTGCTAA TTCTGGGGTTGTTGCATTTCCAGTCCATAAACGTTGAAACACAAATTGCTGTAATTTGGTGAAT GAATTGATCAGATGATCCTATGGGTGGCATTGTTAAGGTTGTTCGCTACGATGTATTTCTAGGATA TTGTCGTTGTAGCAAGAAGAAAAAAAAAGTGTCTTCACAAGTCTTGGACTCAATTTTCACCCCT CCACAAACTCAATTCAATTAACTATCAATAATCCAATATGGGTAAACAGTATATATCTACCGTCA GTGCATCTCAGGCTCATAAGCTGGATATTCTTGGTGTAGCTATTACCAATAAGTTCACTGTATCCG TTGTCCAACTGGTATTTATAGATAAAAGCGGAATCCATGCGGTGGCTGCTTACGAAAATGTTTTGC CAAGCTCTACATTGAAAGTGACATTATTAGCATTTGCATGTTTCAATGGATCTATCATCTTCAGAT ATTATATCAATGATGACTTTTCAACTATCGAAAGTCTAACTGATGATATAAAATCATTTGAAAGCA ATTGTTGGACCCCTGGCTTTTATCGCGATCCAGAATCCAAACAAGACTATTTTATTACAACCAAGA CCAATGGCACTACAGAGGTTCATTTATTGAATATTGTTGATGAAAATGAGAAGGCTGTAATCACAT TTGAAAAGTTTGGGCAATTAAAAGGAAACTCTTCTTCTTTCCCAAATTCTTTGGCTATATGTCCAA CAGAGAATAAAAAATGTGCTGTGGGGTACATCAATGGTGATGTCTTGTTATATGACTTTGTTAGCT TGAAATTGATATACACATTTCGTTCGAGTGATTTGGTGACCAGTAGAAATTCCCAATCGACGTCTA TACCTAGGGTGTTGGCATTTTCCCCTGGTGGAACCTTGTTGGCTGTGGCAAGAGACAATCAAGCTG CTGGGTCAATTACATTATACGACGTTGAGCATGGTGAGAATGTGGGGGTCTTTGGCCACACCCTCAC ACTCGGCCAAATCTGTTGGTGGGTTTGCACATCAAGGCTGGATTTTGGGGTTGAGTTTTGATG AGGAAGGTAAGCACTTGGCTAGTTGTGGATTTGACAAATGCATAAGAGTCTGGAATTTAGAAACAA GCGAAAGGGAAGCAACAATTAGTATATCTATATCAGACTTAGATGATACTACACATAATGATCAAG ACGAGAGTGTCGCTTCTGGTGTTTTTTTTTAAAAAGGGGGGTTAGAGGTGGCTCTGGTGGTGACA GCAATGAAGGATTATGTGTCGTGAGTTTCGATAGAGGAATAAGATGGTACCGAGAGGCAGGAGGAA TATAG

YGL213C_homolog 384aa (SEQ ID NO 354)
MGKQYISTVSASQAHKSDILGVAITNKFTVSVSSDGYAKFWDNKQDEVHSPKEFVQSVFIDKSGIH
AVAAYENVLPSSTLKVTLLAFACFNGSIIFRYYINDDFSTIESLTDDIKSFESNCWTPGFYRDPES
KQDYFITTKTNGTTEVHLLNIVDENEKAVITFEKFGQLKGNSSSFPNSLAICPTENKKCAVGYING
DVLLYDFVSLKLIYTFRSSDLVTSRNSQSTSIPRVLAFSPGGTLLAVARDNQAAGSITLYDVEHGE
NVGSLATPSHSAKSVVGGFAHQGWILGLSFDEEGKHLASCGFDKCIRVWNLETSEREATISISISD
LDDTTHNDQDESVASGVAFIKKGVRGGSGGDSNEGLCVVSFDRGIRWYREAGGI

YGR085C_YPR102C_homolog 174aa (SEQ ID NO 356)
MSDKSQNVMRELRIEKLVLNICVGESGDRLTRAAKVLEQLSGQTPVQSKARYTVRTFGIRRNEKIA
VHVTVRGPKAEEILERGLKVKEYQLRSKNFSATGNFGFGIDEHIDLGIKYDPSIGIYGMDFYVVMG
RAGARVTRRKRARSTIGNSHKTNKEDTIQWFKTRYDAEVLDK

YGR118W_YPR132W_homolog 919bp PathoSeq: 1..919; CDS: 482..916 (SEQ ID NO 357)

YGR118W_YPR132W_homolog 145aa (SEQ ID NO 358)
MGKGKPRGLNSARKLRVHRRNNRWADQAYKARLLGTAFKSSPFGGSSHAKGIVLEKIGIESKQPNS
AIRKCVRVQLIKNGKKVTAFVPNDGCLNFVDENDEVLLAGFGRRGKAKGDIPGVRFKVVKVSGVSL
LALWKEKKEKPRS

TTGAATCCAGTTATATTCATTAAAGATCCTATAAAATACGATTATTCACAATTTATTATATCTTTA CTCCCGAAATTCATTAATTGTAATCGTATTGATTTAGTTATACTTTGTCAAATCACCGAATCAAAT Caattgaatgaaattttatgtttttatcaattaattcgtaatcataagaataatggagatact GATGGAGATACCGACAGTTTGCCTATGTTTGATTATCGATTTGAAATTAATATATTATTTAATTTA TCAACAAAAAAATTGAATCAATTATGTTTAAATAATTGGAATCATGGATATATTGCGGAAGGTGAT **AATGATAACAGTACTAACTTGTCATCTTTGCCATTGTCAATAACACAAATATCAAACATTGAAATT** CCAACAATCCAATCAAGAGCAAATAGTAGTAGTGCTTATAATGATGAGGATGATAAAATTACTACT AGTCGGCAATATCAACAATTTAAAACTACTGCTGTAGGTGGAACATTTGATCATTTACATGATGGT TCTAATTTATTAATTAATAAAAAATTTAAATCTCAATTACAAACTTTTAATCAAAGACAAAATTTA ATTAATGATGTTTGTGGTCCAACTGGTTATATTAATGATATTGATAATTTAATAATATATCTCAAGAA ACTAAATCTGGTGGTGAATTTGTTAACAAATTTCGTAAAGATCATGGATTTAAATTATTAGATATT ACAATAATTAAAGTGATTGGTGGGAATATTGAAGAAAATTCATGGAAAGGTAAATTAAGTTCAA

CTGATATTAGAGAACAAGAATATAATCGATTATTAAATCAATAA

YGR277C_homolog 322aa (SEQ ID NO 360)

MLNPVIFIKDPIKYDYSQFIISLLPKFINCNRIDLVILCQITESNQLNEILCFYYQLIRNHKNNGD TDGDTDSLPMFDYRFEINILFNLSTKKLNQLCLNNWNHGYIAEGDNDNSTNLSSLPLSITQISNIE IPTIQSRANSSSAYNDEDDKITTSRQYQQFKTTAVGGTFDHLHDGHKILLSMAIFLTSNKLIIGIT GSNLLINKKFKSQLQTFNQRQNLVIQFINLLLLSETSVIFFEIYEINDVCGPTGYINDIDNLIISQ ETKSGGEFVNKFRKDHGFKLLDITIIKVIGGNIEENSWKGKLSSTDIREQEYNRLLNQ

YGR284C_homolog 1427bp public: 1..1427; CDS: 501..1424 (SEQ ID NO 361)

CAAGAGTAAAATCTAAATCGTTCCAATGATTTTGGACAGCTCATAGGTTAAGAGGTCTACATGTGT TGGTGGCAGTAGTATTGGTATTAAGTGGGTGGGTCATGGTATTAGAGAGTGGGTGTTATAAAAGAA GGTTGTGATTTTTTTTTCCACTGGTGGTGGTGGTGCTGATTGTACTGCTGTTCACTTTATTGTTT TTTGTATTAGTTGTTCTTTTTTGTTTTTTTTTTACTTGTTCAAAGTTTCATATAATAATAATATTCT TGTTTTCATATTTTTTTTTTCAGAACAAGAACAAATACAACTTATATAATTTGATCTTACTCTTAT TTGAGGAGTATCATTAATTTAAATTATATCAGTTAACAATGTCGTATCGTGGTCCTAATCAATTTG GTAATCAACCTCCACATCATGGAATACCTTCTCAACCTCAACCACATATTGGTCCAATATCTTCCA GCAAAAGTCCTTTAGAACAATTTGAAGATGTTGCTAAAAAAGTTGAAGATTGGATCGATGATTATT TTAAAGTCTTGAAACCATACGTCCCAGCAATTGGTAGAGCATTTTTGGTGGCCACTTTCTATGAGG ATACTTTAAGAATCTTCACTCAATGGAATGAACAAGTTTATTACTTGCACAACTATAGACACTATT GGCGTTGGTTGACCGTTTTATTCTTGATCAATAATATGGTGGTTATGACAGTTGCATCCACTTTAG TAATTGCCAGAAAAAAGAATAACATTGCTACTATTGCATTGATCGTTGTTGTTATTATACAAGGTA TTGGGTATGGTTTATTGTTTGATGCTCAATTTGTTTTGAGAAACTTGTCCGTTGTTGGAGGGTTAG TATTAGCATTTTCCGATAGTATTGTTAGAGATAAAAGATCCTTAAACATGCCAGGTTTACCGATGT TGAACAATCAAGACAACAAAAAGTATTTCCTTTTAGCTGGTAGAATTTTGTTAGTATTATTATTTT TGGGATTCGTCTTTCTTCTGATTGGTCATTGGGTAGAGTTTTCATTATTATAATCGGGTTAACTT CTTGTGCTTCAATTGTTGTTGGTTACAAGACAAAGTTTTCAGCTGCTATCATGCTTATTGTTTTAT TCTTATACAATGTGTTCACTAACCAATTCTGGGCTTATGCATCTCAAGATGCTAGACGTGACTTTT TGAGATATGAATTCTTCCAAGTTTTGTCAATTGTGGGAGGATTATTGTTAGTGGTTAATGCAGGTG CTGGTGAATTCTCCATCGATGAAAAGAAAAAGATTTATTAA

YGR284C_homolog 308aa (SEQ ID NO 362)
MSYRGPNQFGNQPPHHGIPSQPQPHIGPISSSKSPLEQFEDVAKKVEDWIDDYFKVLKPYVPAIGR
AFLVATFYEDTLRIFTQWNEQVYYLHNYRHYWRWLTVLFLINNMVVMTVASTLVIARKKNNIATIA
LIVVVIIQGIGYGLLFDAQFVLRNLSVVGGLVLAFSDSIVRDKRSLNMPGLPMLNNQDNKKYFLLA
GRILLVLLFLGFVFSSDWSLGRVFIIIIGLTSCASIVVGYKTKFSAAIMLIVLFLYNVFTNQFWAY
ASQDARRDFLRYEFFQVLSIVGGLLLVVNAGAGEFSIDEKKKIY

AACATCATCCAGATAAAAAATCCGCTAGTGGTGGATTAGAAAACGATGGATTTTTCAAAATTATTC AAAAAGCCTTTGAAGTTATGTTGGACCCAGTCAAGAGAAGACAATACGATTCTATTGATGTTGAAA ATGATCCAAAACCACCAGCTCCAAAATCCAAATACGATTTCTTTGAAGCTTGGGGTCCAGTATTTG AAAGTGAAGCAAGATTTTCTACTAAACAACCAGTTCCATTGTTGGGAAATTTAGAAAGCACCAAAG AAGAAGTTGATGCTTTCTACAGTTTCTGGGGAAGATTTGACTCTTGGAAGACTTTTGAATTCAAAG ATGAAGATGTTCCAGATGACACTGCCAACAGAGATCACAAACGTTATATTGAACGTAAGAATATTG CCCAACAGAAAGAAATTGAAGCAAGAAGATCACAAGAGATTATCGAATTGGTCGAAAGAGCTCATG AAAAAGAATCTGGATCAAGAAAAGCTGCTGAAGAGGCTGCTGCCAAAAAGGCTGCTGAAGAGGCCG CTGCTAAGAAAGCCGCCGAAGAAGCCGCCGCTTTGAAAGCCAACTCTAAAAAAGCTAAAGAAGCTG CTAAAGCTGCTAAAAAGAAAAACAAGAGAAACATCAGAGCTGCTGTTAAAGACAATAATTACTTTG GTGACTCAGCTAAATCTGCCGACATTGATGCTGATGTCGATTTGTTAATCGAAAAATTCGACGATG TCAAATTAGGTGAAGTTGCTGATAAAGTTAAAGATGCTGATGCTTCAGTGAAATCTACTTTTG TTGAAGTTGCAAAGGAATTGGTTGGAGCTGGTTCTTTAGATGCTTCCTATTTGAAATATTTTAACT AGATTTTTTTTTTGTAGGAAAATAATATATATAGAATGTAAACTATCAAAAACAATTATACAGAAG CTGAACTCAAACAAGACTAAACAGCAAG

YGR285C_homolog 427aa (SEQ ID NO 364)
MSIVLPSGTTDGFKAVSKYSAPVRRPIEPVGRYFLAHASRTLRGHTWSEFEKLEAEKNVKQIEVNE
DEDLGDEEQSEELLEHDPREWKTANLYAVLGLSHLRSKATEDQIRRAHRKQVLKHHPDKKSASGGL
ENDGFFKIIQKAFEVMLDPVKRRQYDSIDVENDPKPPAPKSKYDFFEAWGPVFESEARFSTKQPVP
LLGNLESTKEEVDAFYSFWGRFDSWKTFEFKDEDVPDDTANRDHKRYIERKNIAQQKEIEARRSQE
IIELVERAHAEDPRIKLFKEKAKKEKAAKKWEKESGSRKAAEEAAAKKAAEEAAAKKAAEEAAALK
ANSKKAKEAAKAAKKNKRNIRAAVKDNNYFGDSAKSADIDADVDLLIEKFDDVKLGEVADKVKDA
DAASVKSTFVEVAKELVGAGSLDASYLKYFN

YHR021C_homolog 1178bp public: 1..537/917..1178, PathoSeq: 538..916; exon 1: 501..503, intron 1: 504..932, exon 2: 933..1175 (SEQ ID NO 365) ACATCTCAAATTGGTAGTAGAAGAATTCAACCTTGGGACAGTATTCTCTGCTTAAAATGAGTTTAC TGATCAAATAAAATATTGGCTCAACCATTGAAAAGCTATTCTTGACACTTTTTGCAGTTTTAGTTT TGGTTGTTTCACAATTGAAAAAAAAATGTTGAGCCCTAATAGCCCTAATTGTTTGCACGTGATGT AGTTTTTGAATTATACATATTAGAGAAACAAGTTAACAATGGTATGTTCATTAGATTTACCATGAG TTATGGAGGGATATTCCTGGATGATCAGAATATCATAATATAGGAGTATACTATTTTACTGGAATC **AAGATATAATTGAATTGAAATAAAAATTGAATAAGAGGAAGCATAGAATACGGAATGATGATTAAC** AAATCAGAAAACATTGTACTACCGAATAATGAATTAGGATCAACATATTAATATCAACTACTACTT TAAAAGAACAGGAAAATGAGAAGAGAATCAGCATGAAAGTTACCACCTCAGAAAAACGTCAAAGAAA TATACTTTTGGTGTGGATCCATGTGTTATTACTGAAATCATCGAAACGAATATAACCCTCCTTTTC TCGTATAGGTTTAGTTCAAGATTTATTACATCCATCTCCAGCCACTGAAGCTAAACAACACAAAT TGAAAACTTTAGTTCAACAACCAAGATCTTTCTTTATGGACGTTAAATGTCAAGGATGTCTTAATA TCACCACTGTTTTCAGTCACGCTCAAACTGCTGTCACTTGTGACTCTTGTTCTACTGTTTTTGTGTA

YHR021C_homolog 82aa (SEQ ID NO 366)
MVLVQDLLHPSPATEAKQHKLKTLVQQPRSFFMDVKCQGCLNITTVFSHAQTAVTCDSCSTVLCTP
TGGKAKLTEGCSFRRK

YHR141C_YNL162W_homolog 1179bp PathoSeq: 1..1179; xon 1: 501..503, intron 1: 504..861, exon 2: 862..1176 (SEQ ID NO 367) TTTATATTGTTTTTTGTTTCTATGTATAGTAATTATTTAATTTGATGTTCCATTATTCATGTAATT GTGATGTATTTTTTTTTGTTGGTCCTTCTTTGTGTTTTGATATTTTGCAGCTGGTCGGATCATACAA TTAGGTGAACAAAATTAATGTGTGAGCGTGTACATGCACAATTTTCAATTGGTTATTCTCACGCA TTAGTTCACTAGTAACTTTCGAAGACAACATAGACAAGATGGGTATGTTCCAGTATAGCAATATTC AACAATGAGATACAAGATATTCCTCCAATACAAAGAGATTAATGGTGTTTTTGATAGAGTGTAAAAG CCATGTGTTTAATAAGAATGATTTGTCAAGGGATAAGATGAAAAGTGGAAATTGTCCAAACAACAT TGAAACGAATTITCTGGGATAGCGTTCAAACAATCAAACCTATCCAGGTTTCTTATGACAATTAAG **AAAACAAGTCAATATTATCAAAGATGGAGTTTTATAAGGAGAGATATTGAAACATCAAATTGTTGA** AAGAAATAGCCAACTATTTGGCACCATTTCCTGTGATCATAGAAATACTAACAATCCTCTTGTGTT ATAGTTAACGTTCCAAAAACTAGAAAGACCTACTGTAAAGGTAAAGAATGCCGTAAACATACCCAA CACAAAGTTACCCAATACAAAGCTGGTAAAGCTTCTTTGTTCGCTCAAGGTAAAAGAAGATATGAC AGAAAACAATCCGGTTATGGTGGTCAAACCAAACAAATTTTCCACAAGAAAGCCAAGACTACCAAA **AAAGTTGTTTTGAGATTGGAATGTGTTGTCTGTAAAACCAAGGCTCAATTACCATTGAAAAAGATGT** AAACATTTCGAATTGGGTGGTGACAAAAAACAAAAAGGTCAAGCTTTACAATTTTAA

YHR141C_YNL162W_homolog 106aa (SEQ ID NO 368) MVNVPKTRKTYCKGKECRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGYGGQTKQIFHKKAKTTK KVVLRLECVVCKTKAQLPLKRCKHFELGGDKKQKGQALQF

YIL112W_homolog 3583bp PathoSeq: 1..3583; CDS: 365..3580 (SEQ ID NO 369)

GTGCGAATAATACAAGCGATCGTTTGAATAATCCAATGATTAGCTCTGATCAACGAATTCAAAATT TTCCCCTCAAGGACGTAGTACAACAAGAGATGAGAAGGGGTTTGAACTGTTTGATTTCAGAGGAGA TGACGGTGCAAAAAGATCTACCACCAAAGAAGCACATAATTTTTTGAATGATTCACGAAAGAGTTC CATTAGTGATATCTCAAGCCAAAAATTTTCAAGGGAAAGTTCCCGTAATGTTTCACGGGAAAGCAG CAGGCGAAGTTCAATAATAAAAATTGATCATCATACTAATGTGGACGTGTCAACGAAACCGGAAAA TATAAATAGCAGAGATAACAAAACTGAGAAGAATATGACTTTGAGTTCAGAGTCAACCAAACCGAG AAAATCTGCCAAAACTAAGGCTAAAGAAGAAAAGGTAACAATCGAAAAAAGTGACAAAACGATTAA TTCAGAAGAACGAAAAACGGAACCAATTCAACAAAGCGAGCAACTTTTAACGGACAAAAAGGATAA TAAACTGGAACCCAATAGTGAAGTAAATTTGAAAGACAATAATGACGACCTGAAAGCTACAGCTGG CTGTGCCCTAGGACCTGATAAGAATACTGGAAAAAACGATTCAGATAAATCAGAAACGACTCAACC AAAACTTGCCCGCTCAGAATCATTTGCCGATACATCATTATTGTCTCCAGTTAATGAAAGTGATAC TGATTTCAATTCAATGAGTTAGCAGAGATACCGGAAGCAAAGGATGGTTCAGTTGTGGCAGCAAA TGTGCTGGAGAACATTGATGAGAATGAAAATATTTCAGAAGCTGAAACTGTTATAGCAGATGACCT GAAGAAAACAAAATTGAATACTATTTTTAGTTCCGATGAAGAGGAGGAGGAGATTCAAGAACCAGA TTTCAAACTCCAAGAACCAGAAAAACTACCAGAAGATGACCAACATCCTGATTTTCAAAATTCAAA AGCAACAACAGAAATCAGTAACGATAAAACAGAAGTAAATAAGCCAGAAGTGAAAGAGGTTGGCGA GAAAGAGAAATCACCAACTAGAAGATAGATTACCAATTAAAAAAGAGAAAATGCGGTCGGAGAA TGCAAAGACATCTGAAAACGGTGTCAGTTCAAAATCAGAATCTAAGATTTCAAAGTCGAAGAAACT ACCTTACAAAGTTAAACGTGATTCAAGTGGTCGATCATTATTACAACGAGCTTGCAAGAAGGGTAA TTTTGCAGATGTCCAAGATTACATAGAGAGGGGTGCTAGTGCCAATGAAAAGGATTTCTGTGGATT CACATGCTTGCATGAGGCAGCATTGGAAGGTCATACACAAATTGTGAAATATCTCATCGAAAATGG TGCTAATGTAAATGCGAAAGCTGATGAAGCTGGTGATTCCGAGACACCATTGATCGATGCAGCTGA AAACAACATCTTGATTGTGTTAAAGTGTTACTAGAAAATGATGCTGATCCTACTATTTTCAATAT TGATGGATTCACCGCTTTAACTAAGATTTATAATGAACATGAAGGAGAAGAAGGATATGATGAAAAT TATTCAAGTTCTAGAAGAAGCAACTGCAAACTATAACAGTCGTTTACCAAGAGAAGTTCAGTTTGT

ATCAGATGCTCCTATTGGTAGTGGACCAATCATGGAGGATCCAAATGACAACTATTTTGCAGAGCT **AATTAAAGGTAAGGGAATATATAAATACGCTGCAGAGAATTCAAAAGAGAAAACAGCAGAATATTT** TGTTGCTGGTCATAATTTAGAAGGAAAACCAGATATTTTAATTTTAGCTGCTAGAAACGGCCACAC AGAACTTGTTGATATTATACTAGGGCTAAACCCTACACCTTTTAATATTGATACCGAGTCAAGTTG TGGTGTTACTGCATTATTGGCCAGTATTGGACGCGGTCATTTTGAAGTTGTCGATTCCTTGTTGTC CAAAGGTGCTGATCCATTCAAGACAAGAAAAAAAGATGGGTTGAATGCTTTAGAAATTGCACAACA CTCGCCACATTTTGATTCACGGGAAGTTAGTGTAATAATGAAATTCATGGAGAAGAAGAAGTGGAAC CAAAATTTTGTCTGGTATTCCGTCAAGGGTAGTATCTCGTGCAACATCTCGTGCACCTTCTGTTCC TGCTGAAAAGAAGCTGGAGGATAAAATCACGAAAACAGTTAATGAGCATGTCAGCAATCGGAAACC ATGGTCAGACGATGAACCTAAAGAACCACATCTTTTGAAGAAGTCAAAGTCTGATTTGAAATTGAA ATCACTACATAGAGAATTCACTTCTGATGATCACCACACCAGTGAAAGCCATTCAGATTCTTTTGC AGAAAAAAGAAAACATTTATCGGCAACGCCACCTGCTCCGCCACCACCACCACCACCACCTTC TCAAGCAGTTATCAAGGCACAAGAAGAACAAAAAATCAAAGATGCTGAAGAAGCTAGATTGTGGCA AGAAAAGGTCGAAGCTAAAAAGAGGGCTCGAAGAGAAATGTTTTTAAAGTCCGAGAAAGAGAAAGA GCAGAAACGGAAAGAAGAAGAATTGCGAGCACAAGAAGAAAAACGAATTGCCAAAGCAAAACA GGGGTTGCGACAACAGTTGACATTAGATCATTATCCGGTTGGATTGCGTTATTGCAAGTTTGATGG AAACCCAAATATCTCGGCTGTTGATAAATTTTTGCCTTTCTATGTATTTGTAATCGACGATAAAAA GTATGCTGTTGATTTGCAAGTCTCCTTGATCACGTCAACGGTTGTCAGCAAGGTTATCAATACTGT ACAACCTCATCAGAAGAGAGAAATAAATGCAACTGAAAAAAGCAAATTGTGGAAGCTCTTTTTCAA GTTTATTGGTATTGATCCTAGGAATCCAAATTGTGATCAAAGAAGCTCAATAACAAATGGTCAAAA ACAGTTTCAAAATTTGTTGCTTCATTTTGTGGAGGTAGATTTAGCTGAAGAATTTTTAAAGGAATT TCCAGAAGTACACTCAAAAGCAAAAGATAACCAAATTGATGTTAGTTTAGAGTCTTTGAGTGGGTT TTCTGATTGCGTCAAGGATGATATAATAGTTGATGGAAATCTTGAAATTGATATTGATTCCAAGAA AATCGAAAAGTTTATTCCTCCTCATTTGAATACTAGGAAAGACATTATTAGGACTGTCAGTACTTT **AGCACACCCACTATGGTGA**

YIL112W_homolog 1072aa (SEQ ID NO 370) MTLSSESTKPSVEEVSKSLKPTITKKTSFTDYLKSAKTKAKEEKVTIEKSDKTINSEERKTEPIQQ SEQLLTDKKDNKSEPNSEVNLKDNNDDSKATAGCALGPDKNTGKNDSDKSETTOPKLARSESFADT SLLSPVNESDTDFNFNELAEIPEAKDGSVVAANVSENIDENENISEAETVIADDLPRLDEGKKLLR EQTADVKRHKLKKTKLNTIFSSDEEEEEIQEPDFKLQEPEKLPEDDQHPDFQNSKATTEISNDKTE VNKPEVKEVGEKERNHQLEDRLPIKKEKMRSENAKTSENGVSSKSESKISKSKKLPYKVKRDSSGR SLLQRACKKGNFADVQDYIERGASANEKDFCGFTCLHEAALEGHTQIVKYLIENGANVNAKADEAG DSETPLIDAAENKHLDCVKVLLENDADPTIFNIDGFTALTKIYNEHEGEEGYDEIIQVLEEATANY NSRLPREVQFVSDAPIGSGPIMEDPNDNYFAELIKGKGIYKYAAENSKEKTAEYFVAGHNLEGKPD ILILAARNGHTELVDIILGLNPTPFNIDTESSCGVTALLASIGRGHFEVVDSLLSKGADPFKTRKK DGLNALEIAQHSPHFDSREVSVIMKFMEKKSGTKILSGIPSRVVSRATSRAPSVPVSSDEDDVVEE KEITAHTENKSAEKKSEDKITKTVNEHVSNRKPHESTGRKLEKTHSNEERKRKREWSDDEPKEPHL LKKSKSDLKLKSLHREFTSDDHHTSESHSDSFAEKRKHLSATPPAPPPPPPPPPPSQAVIKAQEEQK IKDAEEARLWQEKVEAKKRARREMFLKSEKEKEQKRKEEEELRAQEEKRIAKAKQEEQERLAREAE EKSKELEEKKVGLRQQLTLDHYPVGLRYCKFDGNPNISAVDKFLPFYVFVIDDKKYAVDLQVSLIT STVVSKVINTVQPHQKREINATEKSKLWKLFFKFIGIDPRNPNCDQRSSITNGQKQFQNLLLHFVE VDLAEEFLKEFPEVHSKAKDNQIDVSLESLSGFSDCVKDDIIVDGNLEIDIDSKKIEKFIPPHLNT RKDIIRTVSTLAHPLW

YIL148W_YKR094C_homolog 659bp PathoSeq: 1..659; CDS: 501..656 (SEQ ID NO 371)

YIL148W_YKR094C_homolog 52aa (SEQ ID NO 372) MIEPSLKALASKYNCEKSICRKCYARLPPRATNCRKRKCGHTNQLRPKKKLK

YIL150C_homolog 2297bp PathoSeq: 1..1162, public: 1163..2297; CDS: 501..2294 (SEQ ID NO 373) ACTCAGCCTTTTGAAATTCACTTTTGGTAAAAGGATATGTAATTGAATCCGCATAATGGACTTTCT CTAACTCCATATTGTTGTTCCTACCCTCTTGCGATAGAGACTTTGATCGTGACATTTTGTAAGTGG TAGAGGTATGGGTAAGATTATTTTCACCACCGTTTTCCTTTAGCAAATAGTCTAAAGCATTTTCTG **AATTGTTGAGTTTCGGTACATCATTAGCTATCTTTTGTACAATTGATTTGCTTCTACCTCTAGTCA** ${\tt GTGTGTTTTTTTTTTTTTCCAGCATTTTGTCTTGTTCTAAAAATGAAACAGCGCAATGAT}$ TCTTTTCATAGTTTTTTTTTTCCATACATAACTTCTGACGCGTGCACTATATCTGCTAACATACTC GGCAACAACAAAGAAAGAGAATTTGAACTAATCCGAAGATGAACGACCCCAGAGATGAACAAATTG ACTCCGATGATGTATTAACAGAAGATTCATCTGATGAATTGAAGGACTTGGTGCAGGAGTTTGAAT TGAAATATGCAGAATTAAAGAAGAACAAAGCCTTGAAAAAACGTCGTTCACAGTCACCACTGGAAG ACATGCTGAATAAACAGAAACCCCATCAACCGGAGGTCCCCAGAACCCCAGAAAAAGCTAAAGTCC ATTTGGATAAGGTAGTAGAAGAACCAAAGCAAAGAATTTTTACCAAGAAGGAGCCTCGGGATTCCA AGATAAAAGAATCAAACTTCTTAAACAAACTCTACGAGACAAGTAATAAGCATGATAAAGAAGATG CCCATAAAATAGATTTCAGTAAAAGAAGGTTTGAGTTTCAATTGGATAAGTATACTTTTACGCCAA AAGACGTTGTTGATGATTTAGAACCGATATCCAAGCTTTACTTGCGCAGAAGATACCTTGCCCAAC TGCAAATTGCCGACATTATTGCCGAAACTGATAGCAACATGAAATTCCTTAAAATTGACAAGTTTT TAGCGAAAACCCATAAATCAAACAACTATGCTGAACCCAAGTATTGTAATTGGTGTCTTGTTGCCT TTGTGGTGCGCAAGGACCCAGTGCAGGTTGCTGCCAACAACTCTAAATACATCAAGTTGAAGGTTG GAAATTTTATGAATTCTGTAGACTTGATGCTTTTTGATAAGGCTTTTCAGAAAAACGGGAAAATCC **AACCGGGTGATTTATTATTCATTTTGAATCCATTGATCAACAAGTATGAAATACAAGTTGGCAAGG** GCCAGTTTCAGTCTGGGTTCAATTTGAAAGTAGAAAACACCAATGTGTCAAGTATTTTAGAGATAG GATCGTTAAGAGATTTTGGGTTTTGCAAGTTTACTAGAAAGCTAGATAATAGCAGATGCAAAAGGG CCATCAACACAAGGACGCAAGAATTCTGCGATATACATTTGGATATGAAGTTTAAGTCTAGTACAA GAATGGAATTAAATGGAAGTGTTTCGATTAGATCCCCGCAAAAAAACAAGAAAAAAGATGTACATGA ATAAAAATGGGTCTGGCTTTATTAAGCAATATAACGAGGAGAGTACTGTTATAGGAACAAGCTACG GTTCTCCTCTTGATCCAAAAAGGTACCAAGACCCGAAAGTACTCCAGAACCAAATCAAGCGGCGCA **AACTAATAGACGACAAGGCAAAGGAGATGCTTGAACAAAAGCTATCGAAACTAGGTTCGGCTTCAT** TATTGAACAATTTACAATTATCTAAGAAAGAAGCAACAGATAAACTTGCGAGTGATCGTCTGAAGA GCAAAGGATTCACCAACACAATGATTTCACATATTGGGTTTGATCCAACAGGTACATCTTTGAACC AAAATAGTACCCTGCTTGGCAGCAAGCTGATGGAAAAATCTCGAGCACGGGAATTGCATGATTTGA GTGTTGAAACATCTGGTCATAAGTCGTTGTCTTCGTCTAAACAAGATCGCCAGTCGAAAGTTGCAA CCTCTCGTCGGTTACAGAATCTTGTAGGAAAGCAAACACACGCTACACTAGTAGATAAAAGGAAAA GAGTGGTTGTCTCAGATGAACAACCGGGGATGGAAGAAGATGAAGAAGACATTGAAATCCAGT TTGACGACGAAAAGTCTAAGATGTCCTACATGAAAATGACTGGAGCCAGGTAA

YIL150C_homolog 598aa (SEQ ID NO 374)
MNDPRDEQIDSDDVLTEDSSDELKDLVQEFELKYAELKKNKALKKRRSQSPSEDMSNKQKPHQPEV
PRTPEKAKVHLDKVVEEPKQRIFTKKEPRDSKIKESNFLNKLYETSNKHDKEDAHKIDFSKRRFEF
QLDKYTFTPKDVVDDLEPISKLYLRRRYLAQSQIADIIAETDSNMKFLKIDKFLAKTHKSNNYAEP
KYCNWCLVAFVVRKDPVQVAANNSKYIKLKVGNFMNSVDLMLFDKAFQKNGKIQPGDLLFILNPLI
NKYEIQVGKGQFQSGFNLKVENTNVSSILEIGSLRDFGFCKFTRKLDNSRCKRAINTRTQEFCDIH

LDMKFKSSTRMELNGSVSIRSPQKNKKKMYMNKNGSGFIKQYNEESTVIGTSYGSPLDPKRYQDPK VLQNQIKRRKLIDDKAKEMLEQKLSKLGSASLLNNLQLSKKEATDKLASDRSKSKGFTNTMISHIG FDPTGTSLNQNSTSLGSKSMEKSRARELHDLSVETSGHKSLSSSKQDRQSKVAKWNTNIRTLQNYD RRVASHSLSTSRRLQNLVGKQTHATLVDKRKRVVVSDDEQPGMEEDEEDIEIQFDDEKSKMSYMKM TGAR

YIL167W_YIL168W_homolog 1499bp public: 1..1499; CDS: 501..1496 (SEQ ID NO 375)

TTTCTTCATCAACTTGCTCAAATGTCTTTGAAAGTGAAAGCTTACTTTTTTTGGTTTCGTTTAGGTG GCATCAAGGTAAAGGAGGGAGTTTTGGTATAGTTAGGTTTTTGACTTATTTCCTTTTTTTGAGTAGA TATAACAGAACTACCAAAAGTGAGCCCACATCTGTTAATCTTGAAAAGCAAAATTGAGAAAACCAT TTATGCAAGTCGTGTACTGGTGATATTCTTGGTCAATTGCTACACTTTTGTAATGAATACTGTAAT GTAGCCGACGTGGGTTGAANAATATATTTAAGTATATAGAATCAGGTCAATATAAAATGTTTGA **AATATAACAAAATGTTTCAATGTAAACTGATGGTTAAGGGATTATAAATCAAACTGAGTAGTGCTT** TTGTTCCTAAAAAACCCATCGTGGTGGTAACGTCAGGAGACCGCGACATCAAATGGAATTCACACA TTGTTGAGGTTACAGACAAACTTCCTACAAAGCCTCCGTGCAGGGTGTTTTTCAAGAATGAGTATG CCAGAAAACTTGGCAAATCGAACGTAGCAGTTTTTTCGTCATCTGGTGGTAATGCAGGATTAGCAG CTGCTTATGCCAGCCAGTTTTTTGGAGTATCGTGCACTGTGGTGTTGCCTGAAAGTTCGAAGCCAA CTGTTATAGAAAAGTTGAAATCCTTGGGTGCAGATGTCATTATTCATGGGAAACATTGGGGAGAGG CCGATAACTATTTAACTGATTTTGTTATTAAAAATCTTGACAAAACAGTCTATCCGGTCTATTGTC ACCCTTTTGATGACCCATTGTTGTGGGAGGGTCATAGTAAGATCATCACGGAAATCATCGATCAAA AGCAATTACCCAACTTTGATAAAGTTAAGGGGGTCATTTGTTCGGTAGGAGGGGGGTGGCTTATACA ACGGAATAGTTGAAGGTTTGGAAAATCATAAGGAGATACCAGTGTTGGCAATTGAAACTAAACAAG CGGCCACGTTTCACGAGGCGGTCAAAGAAGGTAAAGTTGTTCATTTACAAAAAGTGCAAACTTTGG CCACTTCTTTGGCTTCGCCGTACCTTTCTTCCAAGGCATTAGCAAACTATATTGAGCGTCCTACAG TTCTTGCTGAAATTGATGACTTGGACGCTGTTAAAGGTGTTGTTGATGTATACGACCATTTCGGAT ATATGGTTGAGCCTGCATGTGCATCCGTTGCATCAGTGATGCACAGGCAAGATTTATTGAATA AATTTGGTACATTAAGTCCAGATGATATTATCATTGTTGTCATATGTGGTGGATCGGCTATCAACA AGTATATTATAGACGAATATAGAAGTTTATTAGAAAAAGACTCTTGA

YIL167W_YIL168W_homolog 332aa (SEQ ID NO 376)
MKEPSITTTFVEVTDKLPTKPPCRVFFKNEYEQPSGSVKLRGMGHLVGQSIDVARKLGKSNVAVFS
SSGGNAGLAAAYASQFFGVSCTVVLPESSKPTVIEKLKSLGADVIIHGKHWGEADNYLTDFVIKNL
DKTVYPVYCHPFDDPLLWEGHSKIITEIIDQKQLPNFDKVKGVICSVGGGGLYNGIVEGLENHKEI
PVLAIETKQAATFHEAVKEGKVVHLQKVQTLATSLASPYLSSKALANYIERPTVLAEIDDLDAVKG
VVDVYDHFGYMVEPACGASVASVMHRQDLLNKFGTLSPDDIIIVVICGGSAINKYIIDEYRSLLEK
DS

GTTTGAAATATAATGACGCCCCCCCAAAAGGAACTTAAACATTTGCCTTACAAAATTGAAAATA AGGGTAACAAACCAGTTGTTAAAGTTGAATACCAAGGTGAAGAAAAACTTTCTCCCCTGAAGAAA TTTCATCTATGGTTTTGGGTAAAATGAAGAGTATTGCTGAAGATTACCTTGGCAAAAAAGTTACTC ATGCCGTTGTCACTGTTCCAGCTTATTTCAACGATGCTCAAAGACAAGCTACTAAAGATGCCGGTA CTATTGCTGGTTTGAACGTTTTGAGAATTGTCAATGAACCTACTGCTGCCGCTATTGCCTATGGAT TAGACAAAGGCGACCAAGAAAAACAAATTATTGTTTACGATTTGGGTGGTGGTACTTTTGATGTTT CTTTATTGTCCATTGAAGGTGTTTTTCGAAGTCTTGGCTACTGCTGGTGATACTCACTTGGGTG GTGAAGATTTTGATTTCAAGATTGTCAGATACTTGGCCAAACAATTCAAGAAGAAGCACAATATTG TATCTTCTCAAATGAGTACTAGAGTTGAAATCGACTCCTTTGTTGATGGTATTGACTTTTCTGAAA CTCTTTCAAGAGCCAAGTTTGAAGAATTGAACATTGCTGCTTTCAGAAAGACTTTGAAACCAGTTG CCACCAGAATTCCAAAAGTTCAAGAATTATTGGAAGGATTCTTTGATGGTAAAAAGGCTTCTAAAG GTATTAACCCAGATGAAGCTGTTGCTTATGGTGCCGCTGTTCAAGCAGGTGTTTTGAGTGGTGAAG AAGGTGTTGATGACATTGTTTTGTTGGATGTTAACCCATTGACTTTAGGTATTGAAACTTCTGGTG CTGCTGCTGATAACCAACCAACTGTTTTGATCCAAGTCTATGAAGGTGAAAGAACCATGGCTAAAG ACAACAACAGATTGGGCAAATTCGAATTGACTGGTATTCCACCAGCTCCAAGAGGGTGTCCCACAAA TTGAAGTCACTTTCTCATTGGATGCCAATGGTATCTTGAAAGTTGAAGCTGCTGATAAGGGAACTG GTAAATCTGAATCCATTACTATCACCAACGAAAAGGGTAGATTATCCAAGGATGAAATTGATAGAA ACTCATTAGAAAACTATGCTCATGTCTTGAGAGGTCAATTGAGTGATACTTCTGAAACCGGTTTAG GTTCTAAATTGGATGACGATGACAAGGAAACTTTGGATGACGCTATCAAGGAAACTTTAGAATTTA TTGCTAACCCAATCACAGCAAAATTATACGGTGGAGCTGCTGGTGAAGGTGCTGGTGGCGCTGGGG ATGCCAAATTCGGTGATGATGATTCAGATGAATTCGATCACGATGAATTGTAG

YJL034W_homolog 687aa (SEQ ID NO 378)
MRSSQSSWLPRIGLLYVALVILIPFLVSPKHAFAVAAVSDDESSTDNYGTVIGIDLGTTYSCVGVM
KNGKVEILANDQGNRITPSYVSFNGDERLVGDAAKNQASSNVNNTVFDIKRLIGLKYNDDTVQKEL
KHLPYKIENKGNKPVVKVEYQGEEKTFSPEEISSMVLGKMKSIAEDYLGKKVTHAVVTVPAYFNDA
QRQATKDAGTIAGLNVLRIVNEPTAAAIAYGLDKGDQEKQIIVYDLGGGTFDVSLLSIEGGVFEVL
ATAGDTHLGGEDFDFKIVRYLAKQFKKKHNIDITANSKAISKLKREAEKAKRTLSSQMSTRVEIDS
FVDGIDFSETLSRAKFEELNIAAFRKTLKPVEQVLKDGGVKKSDIDDIVLVGGSTRIPKVQELLEG
FFDGKKASKGINPDEAVAYGAAVQAGVLSGEEGVDDIVLLDVNPLTLGIETSGGVMTTLIKRNTAI
PTKKSQIFSTAADNQPTVLIQVYEGERTMAKDNNRLGKFELTGIPPAPRGVPQIEVTFSLDANGIL
KVEAADKGTGKSESITITNEKGRLSKDEIDRMVEEAEKYAQQDQELKEKIEARNSLENYAHVLRGQ
LSDTSETGLGSKLDDDDKETLDDAIKETLEFIEDNFDTATAEEFEEQKQKLIDVANPITAKLYGGA
AGEGAGGAGDAKFGDDDSDDEFDHDEL

ACTATAATGATTTAATTTTGTATGTGACAGTGGAGCCTTGTATTATGTGTGCATCTTATTTACGTC
AGTTGGGCATCAAAAAAGTAATATTTGGTTGTGGGAATGATAGATTCGGAGGAAATGGTACCATTT
TATCAATACATAGTGACATCACCTTGCCTAACGCAGCTTATTCCAGTATCGGGGGTATATGTAGGA
CAGAAGGAATCCAACTATTACGAAATTTTTATATTCAACAAAATGAGTCGGCACCAAATCCAAAAA
TCAAAAAGAACACAGATATTGAGAGTAAGGAATACCCAGAGAATCAGTTTTGTAGCATTTTCAAAGG
ATGAATTTATAGAGTTTTACGGAAATGAAAGAGTGCATATTTACGATGGGAAGATTTTTGAAATCA
CTCCATTACAAAACAAGGGTTATGATATAAAAGAATTGATATCGTTGGATATGATGCAAAAAGTTC
CATTTCTAGAGGATGAGTTGGGACAAATTACAGATGAGCAAATAATTGAATTTCACAACTTATTTT
TCAACATAAATGATGATGAAGACGGTTAATTATAAAAAAACCAATAGGCAAATAATAACAGTAAAAAGA
GACACTTTGCAAACGATGAAGAATAG

YJL035C_homolog 281aa (SEQ ID NO 380)
MSTDLTSHFQYMAISLFVGYKALLNNETPVSCIVVDSKSDKIISIGYNYTNHSLNGTQHAEFIALQ
RFGEQKSSIDYNDLILYVTVEPCIMCASYLRQLGIKKVIFGCGNDRFGGNGTILSIHSDITLPNAA
YSSIGGICRTEGIQLLRNFYIQQNESAPNPKIKKNTDIESKEYPENQFCSISKDEFIEFYGNERVH
IYDGKIFEITPLQNKGYDIKELISLDMMQKVPFLEDELGQITDEQIIEFHNLFFNINDDGTVNYKK
PIGKYNSKKRHFANDEE

YJL180C_homolog 1504bp public: 1..938/940..1504, PathoSeq: 939; CDS: 501..>1502 (SEQ ID NO 381) CTTTATCTAATTGATTTAAATAATTATTAACATTAGTACCAATAAATGCTTTACCACAACCTTGCC AAACTTTTTCATTTGATTGGGTATTACATATTTTATTTAATTTAGCATTTGTAGTATCAATTATTG ATTGATTATCCATTTCAAGTAGGACTTTTTGTAATGCTTCTTGATTCATGATTAAATGAGACGAGT GTGTGTGTATGGGCGATGAAGCTGAAGGTTTTGCAGATGTGGTGTCTATAAGAGTAATTTGATGTG AAAAATATACAATCTATAATCAGTATGTTCAGTTTTGGAATGGAAGCCCCCAAGAAGAACAACAGGG **AAATTAAAAATAAAAGGTGTTGGAGAAAAAAAAAAAATTGAACAGAAAGATTCATCCTTTTAGA** TCAAACGAAATATATCTTACCATCCCCCCCCCCCCAAAATGCTTAGATTTACTAGGACTACTGCTT GGAAATTAAGATCTATTCCAATTGCCACTATTCAATATAGACAATTTACTTATTCCACTATATGTT AAACTAATAGATTAGCTAAAACTGGTACTAGATTTTGGAAAAAAGGTGAAGTTAAATTCAATAATG **AAACTCAAAAATATGAAATTCAATTAGATGGGAAAACTCTACGCACCACTTGGATTCCCATTAG AATTACCAATCAATAAAAAACAATTGGCATATTTAATTGCTCATGAATGGACTCATTTACCTGATA** TTAAAGTGAAATCAAGTACTTTACCATTAACAGCTTTAGCCACTAGAGCTATAGATTTGAGTCAAC **AACATTTGAGTGATATGAAGACAGAAAAAGCTGAAGAAATGTTAGCATTGGAAGATATTAAATTAC** AAATGTTAAGATATCTTGATACTGATACTTGTCTTATATTTTGCTACCAACAAGAATGTGATGGTA TTTATGCTCATAATAAAAATTTAATCCCTCGACAAAAATCTATTGAATTGAAATATTTAGATTGTG AAACTGATGGATTAAGAGGTAATAAACAAGATGAAACCACTCAATTAGTTGTATTGGATTGGTTAA ATCAATTACCAATTTATGATTTAATTGCCTTGGAGAAAACAATCTTAACTACTAAATCATTTTTAT GTGGAATTACTTTATTAAGATCAAATGTTAATGATATTGAAACTTTAAAAGAATTATATCAATTTA ATAAAAATTCCATTGATGAAGATTATTATCATAAAACTTTAGAAGAATTAGTTGAATTAGGAAATT TAGAAACTATTTATCAAACTGAAGAATGGGGTGAAGTAGAAGATACTCATGA

YJL180C_homolog 334aa (SEQ ID NO 382)
MLRFTRTTAWKLRSIPIATIQYRQFTYSTICYQLKTLTPSLGINNTIESNIPSETNRLAKTGTRFW
KKGEVKFNNETQKYEIQLDGKTLRTPLGFPLELPINKKQLAYLIAHEWTHLPDIKVKSSTLPLTAL
ATRAIDLSQQHLSDMKTEKAEEMLALEDIKLQMLRYLDTDTCLIFATNKECDGKLRKRQEEIYRPL
INEFNEFFTIYAHNKNLIPRQKSIELKYLDCETDGLRGNKQDETTQLVVLDWLNQLPIYDLIALEK
TILTTKSFLCGITLLRSNVNDIETLKELYQFNKNSIDEDYYHKTLEELVELGNLETIYQTEEWGEV
EDTH

TAACTGTATTGTTGGGCTGACAGTAGAGTATTGCGGTCATTTTTAGGAGTGATTATAATTCTCTGT CAGCCAAAACCACATATCTGTGCAATATTTACGCTCCAATGGATTCAAACCCGTGTCAAGACGTAT CGGGTGATACCAGTAGCACACTGCCCAACAATAATCCCACTAATGACAGCACAATCTCCTCTC AGAACCATTCTAAAACTGGCTTGAGAAAACACCAACAACACACCTACCACCAACACCTGCCACCTGC AAATGCATTCTCATTCACAGCAGTCACCTTATATTAATCAATTGGAATACTTTACCAATAACCAGT TTTCACGCTCTTTCAATAGTTTAATTTTGGAGGATGCCAATGATGCCAACACCAACAATAGTTCAA CAACAACCTTAAATAAGAAAACCATTAACAAGTCACCACCATTCAATATCAAGCAGGACTTATTAA ACGATAGTATCGACACGTTTCTTGATAACTCCAACACGGAAACGATAGAAGATGGAGACGTCACAA CAACAGACGACGATCACGATTTTGATGATGAAGATATTGAAGATCCTGAAGCAGTGCAGTACACCC AGAGCAATAGTCAGATTACCTACAATCTGCACGTACGGAAGCCATCCGAAGAAGATACGTCATCAT CGATGGCTACAATAAGGTTATCTAACAACTCACAAAGTTCAATTAAGAGATCGTCAAAGTATTTGA ATTTATCTATTGATTCCAATTTGAAAACGGTTGATGGGGGTAAAATTCCCGATGAAATAGATGACA TTAGTTTGAACGAAATAGATGTTGCAGTGGCACCTAACGATTTTTCATCACCACTATCAGCAAGAA AGCCGGACATATTTGCTGCTATAACTGCAGCAAACGGGAATTCCAATAATCAATTTAAAAGGCCAC ACAAGTTGGTTAGTCAATCGCCTTCCCCGTCGTCAAAGAATAAGTTTCGCATATCATCAACCA CATCTTCGCCACAGTCTAACTTGCATTCACCTTCCAAGTTGGGACTGAAAGGATTCAAAATGTTTA AAAATGCAAATAGAGACGCGATAATGTCGTCAAGCAGAGTTATGACTCCAGAAAAACCGAAAATGG TATCTAAAATATTTGGCAAGTCAGCAAAAATAAGGCGAGCTTATACCCCAACCCATACATCTACCC CAATGGCTGTCTCATCACCCTCCTTCATCATCTACACTGAATTCAACAACGGCAGCAATAA CATCTACAAGTCCAGCAGCTGATGAGCATTATGATATTGACAATGACTGTGACAGTCCGTCAAAAA TTTCTGCTTCTGTGGCTGAAACAGGGAAAGGGTCAACTACAACTAAAAGCAACCTATCTAAGGGTT GTCCCTTATTTGATGATAAAGAGAATAAAGCTTCTTATCAGTTTGTTAAACCATTGCAAACAGCTT TCAATTCCTCGGGGTTGGTCAAAAAGAATAGCATAAGTGGTCTGCTGGACAGGAAACTACCTCCAG **AAACACCAATCAAAAGAAATCCATTAATGATTTTAAATACCAACAAAGTTGTACCTCCATATAGCA** AAAATCAACGTTTTCCTGGCAGCGTGAATCCCAACACTACTACGAACAACAACAACACTCAACAGC ATCATGATAGTGATCTTTCTATTGAAGTTGGAAGGAATAATTCTTATGATGCCAGTAGTAGCACTA TCAATAACACAAGTTATATCAAAATTTTCCCTTCTTCGGAATTGAAAAAGGAGCAGGTGCTTCAGC GACCACAAGAAGATTTAGAATTAGTTTTCAATTCTGACATTGAACTAGATGATAACATAATACCAG AAACACCAACAAGAAACTGCTACTACCGAATCAGCACCATCAACATCACCTTACCCCTTTACACGC **AATCCAAGAGTCCATTGTTGAAGTTTGACACTGAGAAAGATGGAAGAAGGAATTTGTCAATAGTCT** TTGCAAAGAATAGTTTTAAGAAACCTATGAATAATGCTGAAAGAGGTGATGACCCTGATAGTATAA TTGCTCAACGCATAGATATTATGCCATCGTTAGATGAAGTTGACTCAGTGTCTGTTTATCCTTCAA AGATAGATGAACATTTAATTGAAAAGTTTGGAATGAAGAATATCAAGTATATTGGATCGGGAGCAT TTTCCATTGCTTTTGAATGTTTAATTAATAACGAAAAGTTTGCTATCAAAAGAACTAAAAAAACCAC TTATTGGAAAATTGGAGAAACAAACTATAAAACGAGAAATTGAAGCATTGAGAGTGTTGACAAGCA TTAAAGAAGATGAAGCAACTAATATGCAAGAACAAGAAGAAGGGGAAAGAGTATCTAGTTTATTTCA TTGAGGCCTGGGATTTTAATAATTACTACTATATAATGACAGAATTCTGTGAAGGTGGTACATTAT TTGATTTCTTAGAGGAAAATAAACATTACAAAATTGATGAATTTAGAATTTGGAAGATCCTAATTG **AAATTCTAAATGGGTTAAAATTTATTCATCTGAAAAATTATTTACATTTGGATTTAAAACCAGCAA** ACATTTTTATCACTTTTGAAGGGTCATTGAAAATTGGTGATTTCGGATTGGCTACTAAATTGCCTA TACTAGAAAAGGACTTTGATCTTGAAGGAGATCGTAATTATATTGCCCCGGAATTGATTAATGACA TAATTTTACCAGATAATGGAACGCCATGGCGTAAATTGAGAAGTGGAGACTTGAGTGATGCTGGCC GATTATCAAGTGATAATATTTCAATGTTTTTACAACACAATCCAAATACCAATAGCAATATCAGTG GCAGTGGAAGTAGAAGTGGTAGTGGCAGTACAGGAGGCAATGGTAGTGCTGGTGATTGA

YJL187C_homolog 1062aa (SEQ ID NO 384)

WO 01/02550 PCT/BE00/00077

132/161

MDSNPCQDVSGDTSSTPMANNNPTNDSTISSQNHSKTGLRKHQQQHYHQHSHSQMHSHSQQSPYIN QLEYFTNNQFSRSFNSLILEDANDANTNNSSTTTLNKKTINKSPPFNIKQDLLNDSIDTFLDNSNT ETIEDGDVTTTDDDHDFDDEDIEDPEAVOYTPTLNILKSKKVDSFNIISSKHRKSNSOITYNSHVR KPSEEDTSSSMATIRLSNNSQSSIKRSSKYLNLSIDSNLKTVDGGKIPDEIDDISLNEIDVAVAPN DFSSPLSARKPDIFAAITAANGNSNNQFKRPHKLVSQSPSPSSKNKFRISSSTTSSPQSNLHSPSK LGSKGFKMFKNANRDAIMSSSRVMTPEKPKMVSKIFGKSAKIRRAYTPTHTSTPMAVSSLNPPSSS TSNSTTAAITSTSPAADEHYDIDNDCDSPSKNRKSSNISASSIIIYQDENHIKSNHARKSSNPIPY PPTEPLPTNISASVAETGKGSTTTKSNLSKGCPLFDDKENKASYQFVKPLQTAFNSSGLVKKNSIS GSSDRKLPPETPIKRNPLMILNTNKVVPPYSSGFAEGKDVMGDQHDIYSHIPCQNQRFPGSVNPNT ${\tt TTNNNNTQQHHDSDLSIEVGRNNSYDASSSTINNTSYIKIFPSSELKKEQVLQRPQEDLELVFNSD}$ IELDDNIIPETPTKKSLLPNQHHQHHLPLYTQSKSPLLKFDTEKDGRRNLSIVLDKSNATKREISE PPSTPINMSFAKNSFKKPMNNAERGDDPDSIIAQRIDIMPSLDEVDSVSVYPSKIDEHLIEKFGMK NIKYIGSGAFSIAFECLFNNEKFAIKRTKKPLIGKLEKOTIKREIEALRVLTSIKEDEATNMOEOE EGKEYLVYFIEAWDFNNYYYIMTEFCEGGTLFDFLEENKHYKIDEFRIWKILIEILNGLKFIHSKN YLHLDLKPANIFITFEGSLKIGDFGLATKLPILEKDFDLEGDRNYIAPELINDKIYTPFADIFSLG LIILEIAANIILPDNGTPWRKLRSGDLSDAGRLSSDNISMFLQHNPNTNSNISGSGSRSGSGSTGG NGSAGD

YJL189W_homolog 887bp public: 1..666, PathoSeq: 667..887; exon 1: 501..506, intron 1: 507..737, exon 2: 738..884 (SEQ ID NO 385) AGTCAAGAATTTTATGATGACTTTGGAGGATGGTCTGATTAAGACTTGTCTTTTTACCAGTTTTTTTC AGCATTGTTGATGGCGTTTAAAGCATCAGCTAAGACGGAGGTTCTAGTCATGGTTGAATTGTCTGT TCCTCACTGTAACAGTAAACACACTAGTTACAACTGATGACCTGCATATTATAAATCTTTCTG AATGATGTCTTTCAGTCTTTTATTGGGTGATTATTATAATAAATGGCAGATGAGAAATATATTTGGA TAATAAACCTTGCAAATGAAATCAGTTGACCATTTTGAAATAATGGACCATTAGCAATACCCAGAT TGCTGGAACAAAGACGAGAGAACTAGACAACTCAGATATAATAGAACATCCATACTAACTTCACTC ATTTCTTATAGTCTCAAAAATCATTCAGAACTAAACAAAAGTTAGCTAAAGGCTCAAAAGCAAAACA GACCATTGCCAÇAATGGATCAGATTGAGAACTGACAACAAAATCAGATACAATGCTAAAAGAAGAC ACTGGAGAAGAACTAAGTTGGGTATCTAA

YJL189W_homolog 51aa (SEQ ID NO 386)
MPSQKSFRTKQKLAKAQKQNRPLPQWIRLRTDNKIRYNAKRRHWRRTKLGI

YJL190C_YLR367W_homolog 893bp public: 1..893; CDS: 501..890 (SEQ ID NO 387)

YJL190C_YLR367W_homolog 130aa (SEQ ID NO 388)

MTRTSVLADALNAINNAEKTGKRQVLIRPSSKVIIKFLTVMQKHGYIGEFEYIDDHRSGKIVVQLN GRLNKCGVIQPRFNVKINDIERWTDNLLPARQFGYVILTTSAGIMDHEEARRKHVSGKILGFVY

YJL197W_homolog 4619bp PathoSeq: 1..3041/3260..4619, public: 3042..3259; CDS: 501..4616 (SEQ ID NO 389) CAACGACAACAATAAGAAGAATCTTTTCCAGATATTGTAAAATCCTTATATTAAATGTTAATA GAAGCCTAAAAATTGCTTGAATTGATAGATTTGCTGATTCTTTTGCTAGAAACACGCGTTATATTA CTTATCCTTTCTGTAATTTCTTGATCTCTGTTTGAATCAACAACGCCTTTGTTTTCTCTTTTCTGCC TTTTTTTTTAGTTTTTTAACAACAAAATTGAAATTACAATCCTTGAATTTACAACTTCATATTC AGCTCTAAATACTAATAATTATAACAATAATTAATTGAATTATTCTATAAACCACTGATATTTGAT AGATACCTTCTGATGCAAAGGAAATTGTGACTACAAATGAAATTGAAGCAACAGATTCAGAACATA ACAACCTTGCATCCAAACGTCAATTAATCAATGATTATTACACAATGATCATTTTGAAGAAGGAA CAGAACGTTACATCATCCCTCAAAATTTCTTACATGAATTTTTGAATTTACCAATCGATAATTTTA GTGATTTGAAAGATCAACTTGGTCCTATTGATTTCCACTCATTACTTAATGAACAAGGTAATTTAT ATCCCGAGAATGAAGAACCAGTCACTTTTTGTCATGTATCGCCAGAAGTATTTCAACATTTGGGTG AATGGTTTGGAATATTGGGCCAACCAATTATTAGAGCTATCATTATTAATCCAGACACCAAAGAAA ACTTGCGACACCGTCATAATGGAAGCAACCACAATCATCACCATGGTCATCACGATTCACCAA TACCAGTATTGCTTTCCAAAACAAGCACTTTTCATAGATTAATGGATGTTATACGTTATAATGTTC TTAAAGCACCACGAAAATCGACGAAAGATTTTAGGATTTGGTTTATTGTCCCACAAGATAAAGGCT TACAGTATTTGATTTCAATACAAACTTTTATGTTTGATATCTCCAAAAAAACTTTGGTTTCACCAA ATATGCTTGAGGATGCTTTGAAAGATCACGGTATTGTGGCCAGTTCCTATAATATAATGGTAGAAG AAGAAGTATCACAGGGTGGTGGACACCTTGGATTATCAAACATGGGGAACACATGTTATATGAACT AAGAATTGAATTTTGACAACCCCTTGGGATATCATGGAGATGTTGCCAATGCATTTGGTTCACTTT TAAAACAAGCATTTGATCACGTGAAAAATAGTTCTAGTATATCTCCTCGAGAATTCAAATCAACTA TTGGGAGATATTCCTCGATGTTTTCTGGGTATCTTCAACAAGATTCTCAAGAGTTGTTGAGTTGGC TATTAGATGCTCTTCATGAGGATTTGAATAGAATTCACCAAAAACCATATTGTGAAAAGCCCGAAT TGAAAGATGACGAAATTGATGACCCCCAAGCCATCACCAAACTTGCCAATACTTGCTGGAATCAAC ATAAGGCAAGAAACGACTCGGTGATAATTGATTTATTTACTGGGTTGTATCAATCTACATTAATCT GTCCTGATTGTGGTAAGAAATCCATAACTTTTGATCCCTTTAATGATTTAACTTTACCTTTACCCA TCAGTAAGAAATGGTATCACACATTTACAATTGTTGATTTGTCCAATCAAGGCGTTATACCGGAAA GGATAATGAAGTTGGAAGTTGAATAAAACATCCAATTTCGATGATTTACTTAGCTATTTGA GTAATTTCTTGAATGTTCCATCTACTGAGTTGTTTGCTTATGAGATTTTTCAAAATGCAATCTATA GTGACTTCCAATTAGATTACACCAAGAACAAGTTTTTACCTATCAGTGATATTATCAGAGATACAG ATGATGTTATAGTGTACATTGTTCCACATAACCCTGCCGTTGACATCATTGTGCCAGTGTTCAATG CCGTTGAAGATGCTGATAGTTCATATCAAATGGTTAATTTTTTTGGAATCCCATTATTTGTGGTGA TATTGAGTAAAATTGATTTGGTTGATGAATATGAAAAATAAAAGGAGTAATGAAGATTACGTTG AAAAAGTATTTTACAAAAAACTGGATTTCCCTGCATTGTCACAGCCATTAGAAACCTCCGATTGTG AAAAAAACAACAATAATACTAGCGACAACGACGACGATGAGGATGCTGACAACGATGAAGGCTATG ATGACTATAGCCCTAAATTGAATTCTAACCTTCGTAGCAGGTACAATCATGACCAAACAACCAAAT TCAAACAAACAGAGAGAGTTATTAATGTTCCTACACACAAACCTACTTTTAGCGATTTCAAACCTT ATGAGATGGACCAATTGGTGGAGGAAGTGAACCAAAATTTGGCAGAGCAANGAGAAGCGAGATCAT ATACTCTCAAGCAACAATCAACTGTACCTGCTGCTGCAAACGGTACCTCCACCATTACCTGTTA GAAATAATACTGGAGTTCACATCCCGTCATCCGATGAAGAAACAGAAAGTGAAGCTAATTTGGGAA GTTTGTTTGATTCAACATCAAACTTGCCGTTGCCTCCACCATCTACATATTCCGAATCAACAAAAC CTTCGAATGTAAACTCCCCTATGGAAAGTAACTTTGAAAGTTCATCAGCAGACTTGAATTCTGGTA

CAACATTGATATCGAAGGACACAGTTTTGTTATGTGATTGGGATAAGGAAATTTATCAAAAATGCT TTGGTGATAAAGAATTACAAGCATGGGAAAACATATCGAATTTACCGAATCCAGAATTGGAGAAAA ATAGAGCTCATTTTGAAAGACAAAGAAAAGCTAAAATTACATTATCTGATTGTCTTAAGAGTTTCA GTACCCCTGAAATTTTAGGTGAACATGATTTATGGTATTGTCCACGTTGTACTGAACATAAACGTG CCACAAAGACAATCCAACTTTGGTCAACGGGTGATATCCTCACTATTCATTTGAAAAGATTTCATA GTGCTCGTGCATTTAGTGATAAGATTGATGTTTTGGTTGATTTCCCAATTGAAGGTTTAGATATAA GTTCGTATGTTGCCAATACTGATTTGACACCTGAAGATTGTTTATACGACTTGATTGCCGTTGATA ATCATTATGGTGGGTTAGGAGGTGGTCATTACACTGCCTCGGTAAAGAATTTCAGAGATGATAAAT GGTATTATTTTAATGATAGTCGAGTCACTGAAATTAATAATCCTCAAGAAGTCGTAGCTAATTCTG CGTACCTTTTATTTTACCGTCGAAGAAGTTCGAAAGGAGCTGGTATTTTGGGAGGAGAAACTTTA TCGACTTGCTTCAAAAAGGTCGAGAGGAATACTCTGAGAGTTTGCAAAAGAAAAGATTGGTTCTTC AAAATGTTGGCCAAATAGTCAATACGTATGCCAAAATTGAACAAGATATAATTGATAAAGAAACAG AAGAGCCAGTTCAAGAGCCAGATCAAGAACAAGAGCCAGATCAAGATCAAGATCAAGATC AAGAGCCAGATCAAGAGCCAGATCAAGATCAAGAGCAGAATGAAACAATAAAAAATCTAGACCAT TCGATGAACTCAAACCATCAACTAGTGAAACAAATAACCAACAACAACAACTCAGTTCAACTTTG TACTTTCAAAAGAAAATAACAGCAATAAATTGGTGCATATTAAAAGCAATGGTCGCCAAGAAGTCA CTTCATCACCAGTACCAATTGAAACTGATGGTGACACTGATGTAACTGATTCCAATTCAACATAG

YJL197W_homolog 1372aa (SEO ID NO 390) MPDNIEDRSEIPSDAKEIVTTNEIEATDSEHTTNVDNELPQGESNEQTGDDSNDNLASKRQLINDL LHNDHFEEGTERYIIPQNFLHEFLNLPIDNFSDLKDQLGPIDFHSLLNEQGNLYPENEEPVTFCHV SPEVFQHLGEWFGILGQPIIRAIIINPDTKEKQIERFPPLFWVHQLGKKTQPTYLRHRHNGSNHNH HHHGHHDSPIPVLLSKTSTFHRLMDVIRYNVLKAPRKSTKDFRIWFIVPQDKGLQYLISIQTFMFD ISKKTLVSPNMLEDALKDHGIVASSYNIMVEAKEKHQTEFPIDQFILSHSNAYEEVSQGGGHLGLS NMGNTCYMNSALQCLLHVPEINYYFFYNIYKKELNFDNPLGYHGDVANAFGSLLKQAFDHVKNSSS ISPREFKSTIGRYSSMFSGYLQQDSQELLSWLLDALHEDLNRIHOKPYCEKPELKDDEIDDPOAIT KLANTCWNQHKARNDSVIIDLFTGLYQSTLICPDCGKKSITFDPFNDLTLPLPISKKWYHTFTIVD LSNQGVIPERIMKLEVELNKTSNFDDLLSYLSNFLNVPSTELFAYEIFQNAIYSDFQLDYTKNKFL PISDIIRDTDDVIVYIVPHNPAVDIIVPVFNAVEDADSSYQMVNFFGIPLFVVMNKEVDVNSFGFI RKKLLETVSLLSKIDLVDEYEKIKRSNEDYVEKVFYKKSDFPALSQPLETSDCEKNNNNTSDNDDD EDADNDEGYDSEVSLANPYLGANFGFKIMYVHDYSPKLNSNLRSRYNHDQTTKFKQTERVINVPTH KPTFSDFKPLSDQLSESKRNYYFYPDYKKMDDEMDQLVEEVNQNLAEQXEARSSGSENSSRASEEQ DGFVLINKEDTLKQQSTVPAAAETVPPPLPVRNNTGVHIPSSDEETESEANLGSLFDSTSNLPLPP PSTYSESTKPSNVNSPMESNFESSSADLNSGTTLISKDTVLLCDWDKEIYQKCFGDKELQAWENIS NLPNPELEKNRAHFERQRKAKITLSDCLKSFSTPEILGEHDLWYCPRCTEHKRATKTIQLWSTGDI LTIHLKRFHSARAFSDKIDVLVDFPIEGLDISSYVANTDLTPEDCLYDLIAVDNHYGGLGGGHYTA SVKNFRDDKWYYFNDSRVTEINNPQEVVANSAYLLFYRRRSSKGAGILGGENFIDLLQKGREEYSE SLQKKRLVLQNVGQIVNTYAKIEQDIIDKETEKQKEEQEQEQEQEQEQEQEQEQEPVQEPDQEQEP DQEPDQDQDQEPDQDQEQNETIKKSRPFDELKPSTSETNNQQQTTQFNFDDEDNDYDYEAEV EDSNIRKQRLLSKENNSNKLVHIKSNGRQEVTSSPVPIETDGDTDVTDSNST

TTAATGTTAAACAACAATTAAAAATCACATTAAAACGTAAAGCCATTACATTATTATAAATCTTT CTGAATTAAAATCATTTATTGAATTGAATAGAATTGGATTCACGAAAATTTGTAAAAAATTTGATA AAACTTGTGGTTATTCAATTAAACAAGATTTTATTAATGAATTTTTACCTCAATATTCTCGAGTAT TTGAAAATGATACCATTGAAGAATTAGATTATAAATTGAATCAAATTATAAAATTTATGCCTTTT TATCAAATAAATTAACTACTCAATCAACAACTAAAGAAGATTTGGATAATATAAAATTTGAATTAA GATCTTATTTACGTGATCATATTGTATTTGAAAGAAATACCGTTTGGAAAGATTTATTATCATTAG **AAAAGAAATCTTATAATATTGATTTAGATAATTCTGTGGTTCAAAATAATAAAATGGGTGATGAAG** AATTGATTAAATATGATCATATTGATATTCCACAATTTTTATTAACTACTCAAATGCTTAAAATTA TTATTATTGTCATTGTTTTCATTATTATTAGCAGTGAAAACTTTTAATGATCCAGTTCAAGGTC GTTGTTTAGCAGTATTAGTTGCTGCCATGCTTTGGGCTTCAGAAGCATTACCTTTATACACTA CAGCTTTATTAATCCCACTTTTGGTTGTTACTTGTAAAAGTTTGTAAAACTCCGGGAACCGATGATC CAATGGATGCCACCAAGGCATCACAATATATTTTTGGGACAATGTGGAATTCCACAATTATGATAT TAATTGGTGGGTTTACATTAGCTGCTGCATTATCAAAATATAATCTTGCCAAAATATTATCATCAT ATATTTTAGCATTAGCAGGTACAAATCCAAGAAATGTATTATTGGCAATCATGTGTGTATCATTAT TTCTTTCCATGTGGATTTCTAATGTTGCTGCCCCCGTTTTATGTTTTTCATTAATTCAACCAGTTT TAAGAAGTATCCCCACAGATTCCCCCGTTGCTAAAGCATTAGTGTTAGGGATCGCTTTGGCGTCTG ATGTTGCTGGTATGGCTTCACCAATTGCATCTCCACAAAATGTTATTGCTCTTGAATCAATGAATC CTAATCCAGGTTGGGGAAATGGTTTGCTGTGGCATTACCTGTGGCAATCATTAGTTTAATTTTAA TTTGGGTGGAATTATTCATGACGTTTAAAATCAATAATGTTAAAATCAAACAATTCAAACCAATTA AAGAAAAATTAACCATGAAACAATGGTTTGTATTTGCCGTCACTATAACTACTATTCTTTTATGGT GTGTTATGCAAAAAATTGATGGAACATTTGGTGAATCAGGTATAATCACTTGTATCCCAATTGTAT TATTTTTCGGTACCGGTTTATTAAAAGTTGATGATTTAAATAATTATCCTTGGTCAATTGTTATGT TAGCCATGGGTGGTATTGCATTAGGGAAAGCCGTTACTTCTTCAGGTTTATTGAAAACTATTGCTT TAGCATTACAAAAACGAATTATGCATTATGATGCCATTGTTGTATTAATCATTTTTTGGAGCATTAA TTTTGGTGGTAGCTACATTTGTAAGTCATACTGTATCAGCACTTATTATTATCCCCTTGGTTAAAG **AAGTTGGAGATTCATTACCTAAACCTCATCCATTAATGCTTATTATGGGTGTAGCTTTAATTGCTT** CAGGGGCAATGGGATTACCAACTTCAGGATTCCCTAATGTGACGGCAATTGGTATGAGAGATGAAG TTGGTAAACCTTATTTGACGGTTAATTTATTTATTACTAGAGGGGTTCCGGCAAGTATAATTGTTT ATGTTTGTATTATCACCATTGGTTATGGTATTATGTCATCATTGAACTTTTAA

YJL198W_homolog 896aa (SEQ ID NO 392)

HFLNSNELSSPMPPSFSINYGSEWDLEIIQTSLDNEKESETKSFTGELEYTSTSSNGEHDTTTTAT

KHELILQQILNSNDESYINPKSLTFDPLKIFTKQLIGELIKINQFYNSKESEIFKIYNNLIHDLQN
QNINIDDVFKFTQAYNYSDPNIINTDDHHQYHLKSTLSRTVTNASVFDTINHIDNDYDNNNNNQKN
NYDLEKQNNTTVAIHDDDDSEDDEEEEEEETHSHDSVLLNHTHFNVKQQLKITLKRKAITLFINLS
ELKSFIELNRIGFTKICKKFDKTCGYSIKQDFINEFLPQYSRVFENDTIEELDYKLNQIIKIYAFL
SNKLTTQSTTKEDLDNIKFELRSYLRDHIVFERNTVWKDLLSLEKKSYNIDLDNSVVQNNKMGDEG
HIINSMMNLSMKRINLPQCLKKLIKYDHIDIPQFLLTTQMLKIIIIVIVFIILLAVKTFNDPVQGR
CLAVLVAAAMLWASEALPLYTTALLIPLLVVTCKVCKTPGTDDPMDATKASQYIFGTMWNSTIMIL
IGGFTLAAALSKYNLAKILSSYILALAGTNPRNVLLAIMCVSLFLSMWISNVAAPVLCFSLIQPVL
RSIPTDSPVAKALVLGIALASDVAGMASPIASPQNVIALESMNPNPGWGKWFAVALPVAIISLILI
WVELFMTFKINNVKIKQFKPIKEKLTMKQWFVFAVTITTILLWCVMQKIDGTFGESGIITCIPIVL
FFGTGLLKVDDLNNYPWSIVMLAMGGIALGKAVTSSGLLKTIALALQKRIMHYDAIVVLIIFGALI
LVVATFVSHTVSALIIIPLVKEVGDSLPKPHPLMLIMGVALIASGAMGLPTSGFPNVTAIGMRDEV
GKPYLTVNLFITRGVPASIIVYVCIITIGYGIMSSLNF

ACAATTAAATCCAAAAAAAAAAAAAAAAGAATCGAATTCCATATGTCGCATAAGACTCAGAGCCAATTAT CTTCACAAATGAAAAACTTGAATACTCCACCAATAGACTTCAACTCAACTTCAAGTAACAATACCA TGCCTTCTGAACCAAATCTGCAACCGCAACAACAACAATCACAACCAGAAGCAAAAACGGAGCCAC AAACCATACGCCCTGCTACTTTTACAACTAGTGGCAATTCATCATCTTCGTCGATATCTACCTTAT CAGCGCCACAAAGCTCATCGTTTCAACGCCGAAACAATCCACAACGTTTCAATCGGAATCAACTCA ATGTATACACTGACTTCAATAGTACTACTTCATCTGCTTCAAGCATTAGTAGTTCACCAAAAGATT TCTTCACCAGAGAGCCACCACGGATCCATAGTAAATTGATATGTGAAGAGATTGCCTCTGCCAATA ATCGAGCTGCTAAAGAGGTTTTATCACGTTTATCTACTGATGAATTGCGTTCAGTTAAATCACATA CTGAATTAGCTGAAACTGCTAATGGAGTGAGAATGTTAGCCAAAAATTTATCCCGAGCAACCATTC AAGAAGTTGTTGAATGGATTTTGGATCAACATCCTCATATAACAATTTATGCTGATGAGAAATTAG CAAAGTCGAAAAGATTCAATCCGGAAAGTATTATTGCCAATTATCCAAATGGTTGTAAGAAATTAA AATATTGGAATAAAAATTAACTACGAAAAATCCAGAAATTTTCGATTTAGTACTTACATTAGGTG GTGATGGTACTGTATTATTTGCTTCAAACTTATTTCAAAAAATTGTTCCACCTATACTTTCATTTT CATTGGGCTCATTAGGTTTTTTAACCAATTTTGAATTCAGTGCATTTAGAACAGTATTGAGCAAAT GTTTTGATTCTGGAGTTAAAGCAAATTTGCGTATGCGATTCACTTGTCGAGTACACACTGATGAAG GGAAGTTGATTTGTGAACAACAAGTGTTGAATGAATTGGTAGTTGATAGAGGACCTAGCCCATATG TTACTCATTTGGAATTATACGGCGATGGATCATTGTTAACGGTTGCCCAAGCTGATGGGTTGATTA TTGCAACTCCAACTGGTTCGACTGCTTATTCATTATCTGCTGGTGGGTCTTTAGTTCACCCTGGTG TGAGTGCCATTAGTGTTACTCCAATTTGTCCTCACACCTTATCGTTCAGACCTATACTATTACCTG ATGGGATGTTTTTGAAGGTTAAAGTCCCACTGAGCAGTAGAGCCACTGCGTGGTGTTCATTCGATG GTAAAGTGCGTACTGAATTGAAGAAAGGTTATTATGTCACTATTCAAGCTTCACCATTCCCCTTAC CTACAGTAATGTCTTCCAAAACAGAATATATTGATTCTGTCAGTAGAAATTTACATTGGAACATCA GAGAGCAACAAAAACCATTTAGTTCATATTTGAAACCAGAAACGCGACAAAGTATTGCTGAAAGTG AAAGATTGGATAATTTACATATTTCAAGTGAACAAGATGAATCGAATCATGAGGAACCTGAAATAA CTGAAGATTTTGATATTAATTATACTGACAATGAACGTGATTCTTCTAGTTCCACTCCTAGTGAAG AAAGCAACGAAGAATGTGCTAATACCACGACATAA

YJR049C_homolog 592aa (SEQ ID NO 394)
MSHKTQSQLSSQMKNLNTPPIDFNSTSSNNTMPSEPNSQPQQQQSQPEAKTEPQTIRPATFTTSGN
SSSSSISTLSADIIQPLHQLSINNNNSTVTQPAPQSSSFQRRNNPQRFNRNQLNVYTDFNSTTSSA
SSISSSPKDFFTREPPRIHSKLICEEIASANNRAAKEVLSRLSTDELRSVKSHTELAETANGVRML
AKNLSRATIQLDVRAIMIITKARDNGLIYLTKEVVEWILDQHPHITIYADEKLAKSKRFNPESIIA
NYPNGCKKLKYWNKKLTTKNPEIFDLVLTLGGDGTVLFASNLFQKIVPPILSFSLGSLGFLTNFEF
SAFRTVLSKCFDSGVKANLRMRFTCRVHTDEGKLICEQQVLNELVVDRGPSPYVTHLELYGDGSLL
TVAQADGLIIATPTGSTAYSLSAGGSLVHPGVSAISVTPICPHTLSFRPILLPDGMFLKVKVPSS
RATAWCSFDGKVRTELKKGYYVTIQASPFPLPTVMSSKTEYIDSVSRNLHWNIREQQKPFSSYLKP
ETRQSIAESERLDNLHISSEQDESNHEEPEITEDFDINYTDNERDSSSSTPSEESNEECANTTT

YLR048W_homolog EMBL_entry 1042bp public: 1..1042; CDS: 28..786 (SEO ID NO 395)

GAAAGAAGATTTTCTTTTTAATAATGAGGATGCCATTTTATACAAATCCAAAATTGTAATTAA

YLR048W_homolog SWISS-PROT_entry 253aa (SEQ ID NO 396) MSLPASFDLTPEDAKLLLAANVHLGAKNVQVHNKPYVYKTRPDGMNIINIGKTWEKIVLAARIIAA VPNASDVAVCSSRTFGQRAVLKFAAHTGATAIAGRFTPGNFTNYITRSFKEPRLVVVTDPRTDAOA IKESSYVNIPVIALTDMQSPSEYVDVAIPCNNKGKHCIGLIWWLLAREVLRLRGIIPDRTTEWSVM PDLYFYRDPEEIEQNAVEEAKTEGVEGAPVAEAETEWTGETEDVDWADSGATPSC

YLR088W_homolog 1335bp public: 1..80/494..776/821..1335, PathoSeq: 81..493/777..820; CDS: <1..1332 (SEQ ID NO 397) TCGGGGCTACAAATTTCGTCCATGAAAATTGGGTTCGCCACCAATACTTTGTATGCGATTATGCAT TACAATGAAGGTGCTATGAGTTTGGCGGTGGCTTTGGCACGGTACTTTACAAAGATGTCGATCTGG TCGAAAAACATTATTTTGTATITCCTGAGACGGCCACAGACCGTTGAGGTCGTGGGTTGAGGCA TACCATACGGTGTTGGACGATACTGCGGGGTCGATTGAGGCGGCGATTATTATGGAGTACGGCAAG AACGGTGATTATTTTGAGTATTACGATATGTTCTACGAAGGGTTGAATGGGCAGTTGCCGAATTTG GACTTGTTGAATACGGCCAATGTAATGACGTATCATGAACAGATCCCCTGTGCCATGCAAGGGATG TCGGATAGGGTTATCAATTATAGCACCCGGTTGCAGACTTTGTTTAGGGGGTATCCTCAAATTGACG CTTGTCGGGTTGACTGAAGTTCATGGGTGTGAAGCATTTTCGGGGTGGCAGATCCAGGCATTT ACGATCAAGGTAAGGGGACTGAAGGGAAAGATGTTACGCAGTTTGGCCGGATTGTCGATTCTACG TTTAGGTCGGTTAACAATTTGCTTGAAAAGTTTCACCAATCGTTTTTCTTTTACTTGATGTTGTCG CCAAAACACTTTGTGTCTATTGGGACGTACTTGCCGTCGGCGATTTTGTTGGCAGTATCGTATGCG TTGAGCTCTGTCAGTGCGGTGGTGGTTGCCGGGTTTGATTTTCGAAAGCTATATTTTGTGGTGGTG GTTGAAATTGCGTGTGCTATTTTGGCGTTTGTGCCGGTGAACCAGGTGATGCTTGTAGCGATTCTG GCGGTGGTGTTGTTGCCGCGCCAAGCCATCTTTTCCAAGCAGGCGGCGTTTTCGCTAATTTCTATT GCGTTGTTGGCAGTGGCATTACTTATTACCGCCCTCTTGATTGTACATTTTGCATTGGCGTTTAGT ATTGGGATTTTAGCCCTTCCATTGACATTTGTCCCGACATTAATGAAGAACAAGTCTAGGCTAACA ${\tt GCTTTTTGTTTGGCGGGAAAGTGCTTGGCCAC}$ CCCGAGCTATTTGACCGGTTGGTCACTGCCTGGTCGGACATACAGTGTTGGACATGGTTTATCGTT GTTTTGGGGTGGTTCCCAGCGTGGGTGATTATCACACTAAGCTACTGTGGCTACAAGCCAGTTAAG GAAAAAGTGAATAG

YLR088W_homolog 444aa (SEQ ID NO 398) SGLQISSMKIGFATNTLYAIMHAPRGENTEAMALVVPWTNSDNEYNEGAMSLAVALARYFTKMSIW SKNIIFVFPETGHRPLRSWVEAYHTVLDDTAGSIEAAIIMEYGKNGDYFEYYDMFYEGLNGOLPNL DLLNTANVMTYHEQIPCAMQGMSDRVINYSTRLQTLFRGILKLTLVGLTDEVHGCEAFSGWQIQAF TIKVRGTEGKDVTQFGRIVDSTFRSVNNLLEKFHQSFFFYLMLSPKHFVSIGTYLPSAILLAVSYA LSSVSAVVVAGFDFRKLYFVVVVEIACAILAFVPVNQVMLVAISAVVLLPRQAIFSKQAAFSLISI ALLAVALLITALLIVHFALAFSIGILALPLTFVPTLMKNKSRLTAFCLAVSNPFFVIFVAGKVLGH PELFDRLVTAWSDIQCWTWFIVVLGWFPAWVIITLSYCGYKPVKEKSE

YLR167W_homolog 1190bp public: 1..1190; CDS: 501..1187 (SEQ ID NO

TAGGTCATTCATAACAATTGATAGATGCAAGCTAATTGGAATGAAAAATCCATCTTGTATCAAAAC CTAGTTGCCTTAACGACAGTAATAGTTAAAGCGTTGGGAAGTAATGGTGAACTCGAACCATTTGGT AACAACAATGCGGTGTTAATCGATAACCAAAAGATTATAAATAGGGGGTGGAAGGTCGCCACTGTT CAATCGTCAACTAACATATATATACAAATCTACAAGCAATGCAAATTTTCGTTAAAACTTTGACTG GTAAAACCATTACCTTAGAAGTCGAATCTTCTGACACCATCGATAACGTCAAATCCAAGATCCAAG ACAAAGAAGGTATTCCACCAGACCAACAAGATTGATTTTCGCCGGTAAACAATTAGAAGATGGCA GAACCTTGTCTGACTACAACATCCAAAAAGAATCTACTTTACATTTGGTTTTAAGATTGAGAGGTG GTATGCAAATCTTTGTTAAAACTTTAACTGGTAAGACTATCACTTTGGAAGTCGAATCTTCTGACA

CCATCGATAACGTCAAATCCAAGATCCAAGACAAAGAAGGTATTCCACCAGACCAACAAAGATTGA
TTTTCGCCGGTAAACAATTGGAAGACGGTAGAACCTTGTCTGACTACAACATCCAAAAAGAATCTA
CTTTACATTTGGTTTTAAGATTGAGAGGTGGTATGCAAATCTTTGTTAAAACTTTAACTGGTAAGA
CTATCACTTTGGAAGTCGAATCTTCTGACACCATCGATAACGTCAAATCCAAGATCCAAGACAAAG
AAGGTATTCCACCAGATCAACAAAGATTGATTTTTGCTGGTAAACAATTAGAAGATGGCAGAACCT
TGTCTGACTACAACAACAAAAGAATCTACCTTGCACTTGGTCTTGAGATTGAGAGGTGGTTTCT
AA

YLR167W_homolog 229aa (SEQ ID NO 400)
MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKEST
LHLVLRLRGGMQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQQRLIFAGKQLEDGRTL
SDYNIQKESTLHLVLRLRGGMQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQQRLIFA
GKQLEDGRTLSDYNIOKESTLHLVLRLRGGF

YLR234W_homolog 2390bp public: 1..2390; CDS: 501..2387 (SEQ ID NO 401)

TCCAGAATAGTAATTAGGGACTTTAATTTTATTAGGAGTGGATTGCATAGAATATGCTATCTAATA GATACATCTTATTATATCTTATTCATGGGAAAGCACCAGTATATGGAAATGCTGCCCAAGGTAGT GCACACAACAACTAGTTTACAAAGTAAAATTCGAAGTTACGTCAAAGCTTAGAATGGTTCTTATA GTAGTTGTCTACTCTATCAAAAAACCCATAATTTGTCTATATAACGTAAGGATCACTATATGCTGT TGAGTAAGAAATATGTTGCGAGCCGTACCGACAATGGATTGGCTGAAACTTGTTCTCATCAAACTT GCAAAACACTTGGAGACGCGCGCGCTTTCAACACACAATAAACAACACGAAAAATAAGGTAGAAA ACAAAAAAAAATAAAAGGAACTTTAAACAAGAAGTAATCCCCATTAAAACTTGATCAACACTTTT AGGGTTTCCGATTTCCTCACTAAAATAATATGAGAATACTATGTGTTGCCGAAAAAC CATCGATTTCAAAAGAGGTGGCAAACATTTTGGGAGGAGGGGCGAAAAAAAGTAAGAAACTCACGAG AAAAATTCATCAAAAACTACGATTTCACCTTCACTTTCAACTCTGAAGATGGGCCATGTCAAGTAA CCATGACTTCGGTGGCTGGACATATCACAGGACTTGATTTTGGGTCTGCCTTTTCGTGGGGAAATT GTGTTCCCGGGCGACTATTTGAAGCAGACATCAAGACCATTATCACCAAGAAATCTATTTATGAAA ATATTGCAGAAGAGGCAAGAAACGCTGATAAGTTGATGATCTGGACAGATTGTGATAGAGAAGGAG AATACATTGGATTTGAAATTATGAATGCTGCAAGAAAATACAATAGGAACCTTGGGTTAAACAATA TTTGGCGAGCTAGGTTTTCACATCTTGAACGAAATCACATTATTCGAGCAGCAAAAAATCCCGTGA ATTTGGATATGAGTGCAGTTTCTGCAGTTTCTTGTCGTATGGAAATCGATCTTCGAGTGGGTACCA GTTTTACACGTTTGTTGACTGATCAATTGAGACAAAAGGGGATAATTGAAAAGAATGAACTAGCTT CTTATGGTACATGTCAATTCCCGACATTGGGGTTTGTTGTTGATCGATACAAACGAGTCAAGAGTT TTACACCGGAACCATTCTGGTATATTGAGATTGAAACTAGGAAAGAGAATAAAAAGACAATTTTCA ATTGGGTTCGAGGTCATTTTTTCGACAAGATGTATGTGGTTATGCTTTATGATCGATGCTGCAAAA GTGGAGAATTTGGAACCATATCAAAAATAGAATCAAAACGGAAACCAAATTTCCGTCCATTCCCAT TGACAACCGTGGAGTTACAAAAAGATTGTGCTAGATTTTTTAAGATGTCTGCTAAGACGGCGTTGG CAGCTGCTGAAAGACTTTATAACCTAGGGTATTTGTCGTATCCTAGAACTGAAACTGACAGGTTTG CAACAAAGCTTTTGAACGAAGGTTTCGAAACTCCTCGAAGCGGTTCTCATGATGATAAGGCGCATC ATGAATACGTTGTGCGACGCTTTATTGCCTGTTGCTCCAAAGATGCTGTTGGTACGCAAACCGTGG TGACTTTAAAATGGGGAGATGAATTCTTCACCGCAAGTGGATTAATGGTGCATGAAAAAAATTATT TGGAAGTGTATACTTACAAAAAATGGGAAAGCTCTAAACAACTACCGAAATTTACAGAGGGAGAAC AGGTCAAGTTGTCGAGTGGAATATTGAAAGACGGTAAAACAAGTCCACCCAATCATATGACCGAGC CCGAGCTAATTGCATTGATGGATGCCAACGGTATTGGAACCGATGCTACTATCGCTGAACATATTA ACAAAATAGAGACTAGGCACTATATTAATAAATTGAAAAAGGGGAAAAATGAATATATTCTTCCTA CTCCTTTAGGAATGGGGCTTATAGAAGGCCTTGAAAAAATGGAATTTGAAGATGTATCACTATCGA AACCATTTTTGCGGAAGTCGTTGGAACGATCACTTGAGGACATAGCAACCGGGTCCCGGCCAAAAG TTGTTTTGTGCAATGAATGTAGGAGAATTATACTTGGAAATAGCAGTAACAACAACAACAACAATA **ATAATAATACGTAA**

YLR234W_homolog 629aa (SEQ ID NO 402)

MRILCVAEKPSISKEVANILGGGRKKVRNSREKFIKNYDFTFTFNSEDGPCQVTMTSVAGHITGLD FGSAFSWGNCVPGRLFEADIKTIITKKSIYENIAEEARNADKLMIWTDCDREGEYIGFEIMNAARK YNRNLGLNNIWRARFSHLERNHIIRAAKNPVNLDMSAVSAVSCRMEIDLRVGTSFTRLLTDQLRQK GIIEKNELASYGTCQFPTLGFVVDRYKRVKSFTPEPFWYIEIETRKENKKTIFNWVRGHFFDKMYV VMLYDRCCKSGEFGTISKIESKRKPNFRPFPLTTVELQKDCARFFKMSAKTALAAAERLYNLGYLS YPRTETDRFAKETDFKSLLEVHKQDPRWGSYTTKLLNEGFETPRSGSHDDKAHPPIHPIKYVSLDT LNTLDEKKVYEYVVRRFIACCSKDAVGTQTVVTLKWGDEFFTASGLMVHEKNYLEVYTYKKWESSK QLPKFTEGEQVKLSSGILKDGKTSPPNHMTEPELIALMDANGIGTDATIAEHINKIETRHYINKLK KGKNEYILPTPLGMGLIEGLEKMEFEDVSLSKPFLRKSLERSLEDIATGSRPKVDVLNTTIGVYVD AYSVCSHQILVLCNECRRIILGNSSNNNNNNNNNNT

YLR241W_homolog 3098bp public: 1..827/2190..3098, PathoSeq: 828..2189; CDS: 501..3095 (SEQ ID NO 403) ATATATAGAATTATGGCTTAGTGCCCTTTATTAACTAAATTAGAGGTTACATTAATACAACTTAAC AAACAAGGAAACTAACATCCACGTATAGGGCTTCTTATATTAATATACCTAATTCAACCTGATTAT ATTGCCTTATATACAGCTTGTAAAAAAACACATAAGAAAGTTTACATCTCAAGATGAATTATCCCC CTATTGTAAAAAGTACATCGCCTAATGATAGACATCATAGAGTACTGGCGACTCCTTACATGATGG TAACGACAACAACAACAAAAAAAAAACATTATCTTGACGGTATAATTAGTAGTGTGCGAGAGG CACACGATAAGATTTATCAGTTTCCTTTTCTCGGTTGACCTTAATCTGTTTTTGTATAGACTTTAT TTTTTTTGTTTTTGACCACACCCACTTTTTAATATCACAAGATATTTAACTGATTATAGAAAACAA CAACAATAACCCAAATACGTTAACCACTTTTATTACATATGATAGACAATATAATCAATAATTTGC **AAATCATACTACAGCAAAATGATGATAATTTTACATCCCCTCACGACGATGTGATATATCGACCAC** ATTCTGCTCGTGTAGCACGATATCAAGTAATAATTGCATCTACATTGGGACTCACTGCCCTATTAC TATTTTCTATCTTACGATTAAAATATCCCAAAATATATGTGGCAAACTTTAATCATTTGAATTTCA CTACAGTTTACAAAATTACTGAGCAAGAAATTTTGGAACATGCTGGATTAGATGCAGTTGTGTTTT TGGAATTTTTTAAAATGTGCATTCGAATAATAAGCATATGTTTAGTATTTGCCATTATTATCATAT CTCCTATCAGATACAAGTTTACAGGGAGAGTAGATGAAGATTATCCCGACGATGATAGTGACAACG ATGACGATGATGGAAGTAATAATAATGGTACCACAATAATTAAGCATATAGTGTCAGCTGGAATTC TGGTGGCAAGTAAAAATAACGATGGAGAACAGTATCAACAATTTCTTTGGTTATACACTATTTTCA GTCAGAAGTATCTTGGATCGCAAAATTCAGTCACCGATAGAACGGTAAAAAATATCTGGGATACCAG GATCATTACGAGATGAAGTGGCACTCGCACGCACATTGACCGTTTGAATATTGGTGAAGTGGATT CTGTGTTGATTGTCAAGGAGTGGCAAAATCTAAACAAACTATTCAAAAGAAGGAGAAGAATAGTTC TATCGTTGCATCCCCAAGTTGGCGAACTGTATCGTTTTTCCAATAGGTATACTGATGATGCAGAAG AATCACCAGACTGGGGATCTCAAAATTCGAACTCTGCACAAGCTTCAATAATAGATCAAGACTCAG AATCTGTTGAAGGAGATTCTTCTGACACTTTGAATCGCTTGTTGAATGATGAACTGAGAACAAGAC CAAGTCTTCGGAAAGGTTGGTTCGGATTGTTTGGACCTAAAGTGGATTCAATAAACTACTACACCG ATAAATTGGAGGTCATAGATAAAGAGATTACCAGGGCCAGAACTAGAGAATATCCCGCCACTTCGA CTGCATTCTCACTATGAAAACCGTGGCTGAAGCACAAATGTTGGCACAGGCAGTCTTGGATCCAA AAGTCAATCATCTTATCACCAACTTGGCCCCTGCTCCTCATGATATCCGATGGGATAATTTGTCAT TGTTGGTTTATCCAGTCAGATTTATGGCTAGTTTTTTAAACACTAAAAGCATTTCTAAAAATATGGC CATCATTGGGGAAAGCTATTGAATCGCATAAATGGGCCGAAACTTTGATTACTGGATTATTGCCAA GTTATTTATCTCATAGTGATGAAGAGTTGTCATCGGTATCCAAGAACTTTTTCTATATATTTGTGA ACTTATTTTGGTTTTCACAACTTTTGGTACCGCCTCTTTTGTTGATACGACCAAAATTGCATTTG ATTTAGCAAGATCACTCAGAGATTTGTCAATGTTCTATGTTGACTTAATAATTCTACAAGGATTGG GGTGCAAGACCCCAAGAGATTACTTGAATTTGTACAAACCGCCAGTTTTCAATTTTGGTCTACAAT TACCACAACCAATATTGATATTTATTATTACGTTGGTATACTCGGTAATGTCTTCGAAGATATTAA CTGCAGGGTTACTATATTTATTATTGGTTATTTTGTGAGCAAATACCAATTGCTTTATGCTTGTG TTCATCCTCCACACTCAACGGGCAAAGTTTGGCCAATAATTTTCCGAAGAATCATATTAGGGTTAT TTCTTTTCAAATCACAATGGTTGGCACATTAGCATTACAAGATGCAATCACATGTGCTACTTTCT TGGCACCATTGCCGTTTTTGACACTTTACTTTTGGTGGAGTTTCCATAAACAATATATTCCCTTGT

CAACATTCATTGCCTTGAGAGCAATTGAAAGCAATGAAAATATCAACCCTACTGATTTGGAGCAAA TCATTGAAAACAACAATAATAAAACTCTTGACGAAAGAAGGGAATTGAACACTAAATACGAATACC CCAATCTAGTTAATGATTTAGACGGGCCAATGATTGCATTGGATGGTGAAGATGTATTGATAGTTA ATCGAGATGGTACAACTGTACGGAAACCACCTCAATATTTCAGTTCAGAATGGGACTATTAA

YLR241W_homolog 865aa (SEQ ID NO 404)
MIDNIINNLQIILQQNDDNFTSPHDDVIYRPHSARVARYQVIIASTLGLTALLLFSILRLKYPKIY
VANFNHLNFSLHSTSRRNLPELPSNSLFGWIPTVYKITEQEILEHAGLDAVVFLEFFKMCIRIISI
CLVFAIIIISPIRYKFTGRVDEDYPDDDSDNDDDDGSNNNGTTIIKHIVSAGISVASKNNDGEQYQ
QFLWLYTIFTYVFTFVTVYFLFKQTNRIISMRQKYLGSQNSVTDRTVKISGIPGSLRDEVALARHI
DRLNIGEVDSVLIVKEWQNLNKLFKRRRRIVRKLEESWVEYFEKNGITNKSDLISLHPQVGESYRF
SNRYTDDAEESPDWGSQNSNSAQASIIDQDSESVEGDSSDTLNRLLNDESRTRPSLRKGWFGLFGP
KVDSINYYTDKLEVIDKEITRARTREYPATSTAFLTMKTVAEAQMLAQAVLDPKVNHLITNLAPAP
HDIRWDNLSLTRQDRNTKILAVTIFIGIMSLLLVYPVRFMASFLNTKSISKIWPSLGKAIESHKWA
ETLITGLLPTYLFTILNIVIPFFYVWISEKQGYLSHSDEELSSVSKNFFYIFVNLFLVFTTFGTAS
FVDTTKIAFDLARSLRDLSMFYVDLIILQGLGIFPFKLLLVGNLLRFLVNSLFRCKTPRDYLNLYK
PPVFNFGLQLPQPILIFIITLVYSVMSSKILTAGLLYFIIGYFVSKYQLLYACVHPPHSTGKVWPI
IFRRIILGLFLFQITMVGTLALQDAITCATFLAPLPFLTLYFWWSFHKQYIPLSTFIALRAIESNE
NINPTDLEQIIENNNNKTLDERRELNTKYEYPNLVNDLDGPMIALDGEDVLIVNRDGTTVRKPPQY
FSSEWDY

YLR321C_homolog 1559bp public: 1..947/1189..1559, PathoSeq: 948..1188; CDS: 501..1556 (SEQ ID NO 405) TTCCAGAATTAGTAGATATTTCTGATATCAAGTTGGAGATAGGGATATCGAACTGGGATTCTATAT TTTGTTTTATCTTGGAGAACCTGTGTTGTTGTTGGCGTTCTATCTCTTTATATATTTTCTCTATTA **ATTCAATTGAAACATTTGAAGGAAATTCTTTCTTAAAAGCATCTAGTGACACATGATCTCTAATCT** CCAGTCTTTTGATTAAATATTCTTTTAGAATATCAGGTGAAGAAGTGTTGGTAGTCATAGCTAGTA GATACTGTGTGTGTCTGGGATAATAATTATAATGTAAACAAAACAAAGTCGTGTCAGTGTATATT TGCTTGACAGAGAAATACAGAACACTAAACAACATTTTTTCATTCCTTTCTTGTTTTGTTCTGTT ATACCCCAAAAGTTTGAATAAGTCTTCAGATATCTAGCATGGCAACTTCTCAAGAATTGACAGCAG ACATACAAGCTCTTGCAACTAGTTTCCCCAAGCGATTAGCTAATGATAGTGACAATTCATTACTTA TTGGAGATGACCTTGATTTTGATGAATTCCCATCTTCGACACCCGGTACTAGAAGCTTAAATGAAA ATAAAGCTCAAATAGAAGCACAAAGATATTCTCTTGCGAAAAACACACCCAACGCCCAAGAGAATCT TAGAAAAACCGGTGTTATCTGAGTTGGTTGAAAAACCAGTGGTGCTTATTCCTATCAAAATAATGA TTACACCAACTGAGTTTGCGGAAATTGTTTGCAGTGATTTAGATTTACCATTCAGTATGGCTGCAC AAATAGCAGACTCCATTAATCAACAGATTGAAGAGTATTCCTATGCATCTAATTTACAACTACCAA GATTTGAATGGGATATGAATCAAAATGAAGTTACACCAGAAATTTTTTGCTGAAATAGTTGTTGCTG ATTTGGGGTTATCGTTAGAATTTAAGAATGCCATATCACATGCATTGCACGAAATAATTATCAGAG TGAAAAAAGAAGTAATAGATGGTACTTTTGACAATGAAATGCACAACTTGCATCTAGTAAAAGGTA TAATGTTTGAACAAGGAATTAGAATTTCACTGAAAACAGTGTTCAAAATGGAAATGACCGTTGGG AACCTTTGGTCGAAGTATTGACTTCTAGTGAAATCGAAAGAAGAGAAAATGAAAGGGTTAGAAACT TGAGAAGATTAAAGAGAGAGAATATGAGAAGAGATTACGATGATCATAGTAGGAGAAGGCAAGCAG GAAAAAGAAGGTATGATGAGTTAGAAGGAGCCTGGGTATAG

YLR321C_homolog 352aa (SEQ ID NO 406)
MATSQELTADIQALATSFPKRLANDSDNSLLINVAPTGRQAKRHIQQINYSEEFGDDLDFDEFPSS
TPGTRSLNENKAQIEAQRYSLAKNTPTPKRILEKPVLSELVEKPVVLIPIKIMIENLNTNQKLIDS
FMWNLNESLITPTEFAEIVCSDLDLPFSMAAQIADSINQQIEEYSYASNLQLPNKGPYNVTIDLSV
NLNKQLYQDRFEWDMNQNEVTPEIFAEIVVADLGLSLEFKNAISHALHEIIRVKKEVIDGTFDNE
MHNLHLVKGIMFEQGIRIFTENSVQNGNDRWEPLVEVLTSSEIERRENERVRNLRRLKRENMRRDY
DDHSRRRQAGKRRYDELEGAWV

WO 01/02550

PCT/BE00/00077

141/161

YLR325C_homolog 737bp PathoSeq: 1..737; CDS: 501..734 (SEQ ID NO 407)

YLR325C_homolog 78aa (SEQ ID NO 408) MAREIKDIKEFVELARRSDIKSAIVKVNAKVNANGKKFKQTKFKVRGSRYQYTLVVNDASKAKKLQ OSLPPTLKITNL

YLR344W_homolog 1348bp PathoSeq: 1..1348, exon 1: 501..515, intron 1: 516..979, exon 2: 980..1345 (SEQ ID NO 409) ATACCATGACAAGCAAGCTCAGGGTCGCGGGTTCGAGTCCCGCGGGGAGCTAATTATACCCTCATT TTTGAACCCACCAAATTTTCTTTCACATTATAATGAAATAAGAGTATTCCCTGGCTTCTTTTTTT CGTTTTATATTTTTTAAGAAATTTGATGTTGATTTGGTAAATGCCAAATTTTAAATGTGTGTTAG GGCTATAGCCCTAATGTACTGTATATGCAGTATCAGAAATACTTTTGTTACGCACAGTTTGTCTTA CCAAATACATTATATATATATTTTTTTTTTTTTGAGTAGAGGAGCTACACTAGACCACAGTGCG CTTTTGGATCGATACTAGATAGCATATAATCATCAAAAATGGCCAAGATCAGTCAAGGTATGAAAT AGGAATATATACATTGAAAAGGAGATAGAACATCAAACAACCATTAAGAATTAAGTTTAATAC AGTTTCAATAAAGAGGGTTTTTTTCTCAGAACAAACCATTGACTGAAGTACTACACCAAGAAGGTA TAATGATTTCACGATTTACCTGAATATAAAGAACATCCTTAATATTGAATTTCAATATTAAAAATA CAATTTGGGGATATTGATGAAATTATGTATAGGAGATTCCATTTTTCAAACTTGTTGAATGGAAAA CTTGAAAAATCAAATCAAATCAAATCATAACCCTTCAATATATTCCTTCCTTATCTTACTTTTCCT ATTAAAACAAAGACTAAGAAACATTCAGTAAAATACTAACAAAAATTCCATTTATATAGACGTTTC TTCATCTCGTTCTAAAGCTAGAAAAGCTTATTTCACTGCTTCATCAGTTGAAAGAAGAGATTCTTTT ATCTGCTCCATTATCCAAAGAATTAAGACAACAATACAATGTCAAATCTTTGCCAATTAGACAAAA TGATGAAGTTITAGTTGTTAGAGGTTCTAAAAAAGGTTCTGAAGGTAAAGTTAATTCTGTTTATAG *ATTGAAATTTGCTATTCAAGTTGATAAATTACAAAAAGAAAAATCAAATGGTGCTTCTGTTCCAAT CAACATTCATCCATCTAAAGTTGTCATTACTAAATTACATTTGGACAAAGATAGAAAAGCTTTGAT TCAAAGAAAAGGTGGTAAAGCTGAATAA

YLR344W_homolog 127aa (SEQ ID NO 410) MAKISIDVSSSRSKARKAYFTASSVERRVLLSAPLSKELRQQYNVKSLPIRQNDEVLVVRGSKKGS EGKVNSVYRLKFAIQVDKLQKEKSNGASVPINIHPSKVVITKLHLDKDRKALIQRKGGKAE

TGAATATTCGTAATTAAAATTGATTCAAAATTGTATTGATGTTTGTATACTGGATAAACAACTTGT GTGAGATCATTCAATGTATTTGCTGGCGGAGAAGGAGGCAAGGACGAACTTTTTTTCCTTCATACT CTGAACCTTGTGGACTGGTAAACGCACGACATAGAGTAATATTTGGAGAAACCAAAAGAATTTTGA AAAACCGTGGTTTGAATTCGACCACAGATTGGTTGGACGACAAAATGCAAAGTGTATTCATCCGGA CTTTTGCTACCTCAAGAATAGAGTTCCAGCGGTACCAGCCGCGTTTTGTTAATACCATTAAAGAAA CGGTCAAATCGGCACAAGAAAAGTCGTACAGTATTACTAGACCATTGGGGTTGTCAAAACCAGTTT TGTTAAATCATAAATTGTCAGACACATACTCATTGTCCAATATATACGAGGAGTTGTTTGGTCAAA **AATCCAAAGAAAGAAGACAGAAACAACTAGACTACGATTTGAAACACTCGCCAATTTATGAAGTCA AGTCATTTGAGAATACAAAGGGGAAAATATTTACTCCTCCTGTTTCGTACTTTCGACAAGACAAAT** CTTTGTATTTCCCGGATTTTATAGCGAAAACATTGGCAGGTAATCAGAGAAGTTTGTACGACTCAT TAGACAATAGATTAAGCATAGTCAAATTGTTTTCTTCTGTTGCTGGTGAGCAGTGTACCCGTTCGT ACTTTAAGGTTGAAAACAAAGATTACTATTCCCAGGATTATGATACCTTTGTGGAGGAATATCCCC ATACCCAGATACTTGATGTGAATATGCCGCAAAGTTGGATCAAGGGGTTTGTGACAAACTTGAGCA CAGGAAATTTAAGAAAGACTTTGAAGCCAGCTCTGAGATACGAGAATTATTTCATCTTGCCTGGCC ACATAATGTCAGCGGAAATTAGAGAACAGTTGTACTGTGATAATCAATGTTCCGGGTATATTTATA TTGTTGATTCGATGGGGAAGATAAGATGGGCGACAAGTGGGTATGCAACTCCTGAGGATTTGAAAT TGATGTGGAAGGTTGTGAAAGGGGTGCAAAGAGAAATGACCAAGTAA

YLR393W_homolog 376aa (SEQ ID NO 412) MFVYWINNLCEIIQCICWRRRQGRTFFPSYFFFSLSLFFQSHCSSVKGWLFCAEPCGSVNARHRV IFGETKRILKNRGLNSTTDWLDDKMQSVFIRTFATSRIEFQRYQPRFVNTIKETVKSAQEKSYSIT RPLGLSKPVLLNHKLSDTYSLSNIYEELFGQKSKERRQKQLDYDLKHSPIYEVKSFENTKGKIFTP PVSYFRQDKSLYFPDFIAKTLAGNQRSLYDSLDNRLSIVKLFSSVAGEQCTRSYFKVENKDYYSQD YDTFVEEYPHTQILDVNMPQSWIKGFVTNLSTGNLRKTLKPASRYENYFILPGHIMSAEIREQLYC DNQCSGYIYIVDSMGKIRWATSGYATPEDLKLMWKVVKGVQREMTK

YML063W_homolog 1271bp PathoSeq: 1..773, public: 774..1271; CDS: 501..1268 (SEQ ID NO 413) GAGACTTCAGGTACGACCCAGGGTTGCGACAAAGTTTAGGTAGTTTGTCGTCTGAATGTCGCAACA AAATAGGGCTGTAGCCCTAGTCATGTGATGTGAATTAACATAACAAGAAGAATTGCTGGTGCGCAA CATATTGGGCTGTATTTTTATTCTTGTTTTTCTGCTGTTCTCACTGTTAAGCTCTAAGTGAATT CTACTGAAAATTTCCTGACTTTCTGTATCTAAAAATTTTTTACTAGGAATTTTTTTCTTTTACGTT TTTCACTTGTTTCATATAATCACCAACTCAAGTACAACATGGCTGTCGGTAAAAACAAGAGATTGT CCAAAGGAAAGAATTAAAAAAGAAGGTCGTTGACCCATTCACCAGAAAAGATTGGTTTGACA TCAAAGCTCCAACCACTTTTGAAAACAGAAATGTTGGTAAAACTTTGATCAACAGATCTACCGGTT TAAAGAATGCCGCTGATGGCTTGAAAGGTAGAGTTTTCGAAGTTTGGTTTGGCCGACTTACAAGGTT CCGAAGACCACTCTTACAGAAAAATCAAATTGAGAGTTGATGAAGTTCAAGGTAAAAACTTGTTGA CCAACTTCCATGGTTTGGATTTCACTTCTGACAAATTAAGATCATTGGTCAGAAAATGGCAATCAT TAGTTGAAGCTAATGTCACTGTTAAAACTTCCGACGATTACGTTTTGAGAGTTTTTGCCATTGCTT TCACCAAAAGACAACCAAACCAAATCAAGAAAACTACTTACGCTCAATCCTCTAAATTGAGAGAAG TCAGAAAGAAGATGATTGAAATTATGCAAAGAGAAGTTTCCAACTGTACTTTAGCTCAATTAACTT CCAAATTGATTCCAGAAGTCATTGGCCGTGAAATTGAAAAATCCACCCAAACCATTTTCCCATTAC AAAATGTCCACATCAGAAAAGTCAAATTGTTGAAACAACCAAAATTCGACTTGGGTTCATTATTGG CTTTGCACGGTGAAGGTTCAACCGAAGAAAAAGGTAAGAAAGTTTCTTCTGGTTTCAAAGATGTTG TTTTAGAATCTGTTTAA

YML063W_homolog 256aa (SEQ ID NO 414) MAVGKNKRLSKGKKGLKKKVVDPFTRKDWFDIKAPTTFENRNVGKTLINRSTGLKNAADGLKGRVF EVCLADLQGSEDHSYRKIKLRVDEVQGKNLLTNFHGLDFTSDKLRSLVRKWQSLVEANVTVKTSDD YVLRVFAIAFTKRQPNQIKKTTYAQSSKLREVRKKMIEIMQREVSNCTLAQLTSKLIPEVIGREIE KSTQTIFPLQNVHIRKVKLLKQPKFDLGSLLALHGEGSTEEKGKKVSSGFKDVVLESV

PCT/BE00/00077

YML128C_homolog 1517bp public: 1..1499, PathoSeq: 1500..1517; CDS: 501..1514 (SEO ID NO 415) TGATATGGATTTTTCAAAACTAAGAAACAATACCAACTACAACAACAAGAAAACATAAGTGTTTGCT TAATTCAATGACCTCGAGTCATATTCCCACGTTTTAAGTATGAGTGTTTTACGAAGTTGTGGATCC TATTTTAAATAAACAATAATAGTAATAAAAAAAAAACCTTCTTTGCTTTTCGAGAATTTGTAAC GTTGCTCAATTATGTATAACAAGGGTAGAAACTCTGTGGGATTCCCTCCTTAAAAATATAGCAATC ATAATGTATTTCTCTTGTTCAGGATAATTATCACTATTTGTGACGTTTAATTTTTACATTTCTTCT **TCTTCTTCTTCCTATTTCAACATTAAAGAACATTTAATATGTATTTCCCAATCATTGTATGGTTAT** ATGTATCTATCACTTTTGTGGTTGCCAATTATGGTTTTGATCAATGGACAAATGATGATTTAAAAC CTAATGAAGAAGCTAAGAAATTAGAAAAAGGTTACAAGAAAGTTACTGAAGAATTAAATAACAATT TGAATCCTCCAGATGATTCATTAAATGATTATTTGAATTTTGATTACTTATTTGGGAAAAGAAAAG AAAATTATTCAATTAAAGAATGGATTTTTGAAAGTTGGCCAGTAACCAGTTTGCAAACTTTTTTAA CTCAAAATAATATCCAATATAGTGCAAAGGATACCAAAGATGATTTAATCAATAAGGTTAAAGATC **AATTTGATTCTATTTCTAAGAAAAATCATGGGTCTAGTTTTTATCCTGGCAATTGGTTATATGAAT** CTTGGTCAGAAAATGATTTGAAAGATTGGTTGAAATCTTATGGCATTGAATTTAATCCTAGTTCAA CAAAGGATCAATTGGTTGAAAAATTAAAAGAATTTAGTTATCAAGCCACTCATTCAATTAGAGATT CCAAAGAATCTTTATTTGATTCATTGGATTTATTTGATAAAACCATTTTTGATAAAAAAGGTCAAA TTATTGACACTAAACCAGGAATTTACGTTGAAGATTTGGATAAGGAAAAATTAGTCAAGATTGCCC **AACCTTGGATCACAAAGGGAQAACAAAAGTCTCAGAAAAAGAAGGGTAGTAATTTGATTAATGATA** CATTCTTTGTTGGTATTAATAATTGGTCCAAGGATAAATTGCGTGAATTGGGCAATCTTGACTAA

YML128C_homolog 338aa (SEQ ID NO 416)
MYFPIIVWLYVSITFVVANYGFDQWTNDDLKQFLKERKVAFNDALENPKLISLANEEAKKLEKGYK
KVTEELNNNLNPPDDSLNDYLNFDYLFGKRKENYSIKEWIFESWPVTSLQTFLTQNNIQYSAKDTK
DDLINKVKDQFDSISKKNHGSSFYPGNWLYESWSENDLKDWLKSYGIEFNPSSTKDQLVEKLKEFS
YQATHSIRDSKESLFDSLDLFDKTIFDKKGQIEDEFFQTWSYSQLREWLYLHGFIDTKPGIYVEDL
DKEKLVKIAQSYKKCLLSDIHTWLANTEKKSQPWITKGEQKSQKKKGSNLINDTFFVGINNWSKDK
LRELGNLD

YML130C_homolog 2243bp public: 1..829, PathoSeq: 830..2243; CDS: 501..2240 (SEQ ID NO 417) ATGAGTTCATAGATGATCTGTTTCACTTTCAAATAACGTGTCAACAAAAATAAAGTTAGAGCATAG ATTTTGCCGCCACTTGTACAGATGGATAGAATTGAATGCAAATTCTGCATAAAGATTAAAGTGAAA TTCAAATTGTAGTTGCATGTATATAAAATAATAAAAGATATATCACCAGCACAACTGATTACTT CTTTTCTTAGTTTGGTTTCTATAATCTTATTAAACATTCTTGCCTTTCATCCTTGATTATCATATT AGATCTTATCTTTAATTTGTTTGAAAAAATAATACCAATAATCTTCCCATTAGAACTTACAACACA ACAACAAAAAAACCCATTCTAAATCACTATTCTCCATTATGAAAATTTTCAGATTATTTCACTAC TAATCGTACAATTTATCATAAATACCACTGTTGCAGTATCACCTGTGTCAGCAGTTTTTACCAAAAC TGAGTTTCAGTCCATTTGATTCACCAGAATTTTGTTCACAGATCATAACTCCCACTTGTAATACAA CTTTCACCTACATTGATGAATTGAATAAAGATATTCGTCCCTACTTGTCGGAATTAGTCAAGACCC TGTATTTCCGTTATTTTAAAGTCAATTTAGATAAACAATGTCGTTTTTGGAATGCTCAACATTTTT GTGCTAGTGAAAACTGTGCTGTTGAAATATTGGAAGATTTCAATTGGAGTCAAGTCACCAATGAAA GTTTGAAACCTTCAGGATTAGGTAAGATTTCATTACCTGACAAATCATCAATTGATAATTCCATTG **AAACCGAAGAAGTTCAAACTTGTGAAGATTTAGATTATAGTGAAATAGATGATGACCATCATTGTG** TTTATGTCAACTTGGTAAATAACCCAGAAAGATTTACTGGGTATGGTGGTAATCAAAGTTTTGATG TTTGGAAGGCTATTTACCTGGAAAATTGTTTCCCTAATACTAATCCAATGTCAGTGACAAATGATG CCGACAATGGTGGTGAACAATGTATCGAAAAGAACTTGTTTTATCGTGTTGTTAGTGGTATGCATG CTTCAATTGCAGTACATTTATCAAGAGAATATTTGAATTCTGAAACTGGTGAATTTTATCCTAATT YML130C_homolog 580aa (SEQ ID NO 418)
MKIFRLFSLLIVQFIINTTVAVSPVSAVLPKSSFSPFDSPEFCSQIITPTCNTTFTYIDELNKDIR
PYLSELVKTSYFRYFKVNLDKQCRFWNAQHFCASENCAVEILEDFNWSQVTNESLKPSGLGKISLP
DKSSIDNSIETEEVQTCEDLDYSEIDDDHHCVYVNLVNNPERFTGYGGNQSFDVWKAIYSENCFPN
TNPMSVTNDADNGGEQCIEKNLFYRVVSGMHASIAVHLSREYLNSETGEFYPNLKVFMERVGMHND
RLSNIYFNYALVSQAIVKLSEILPLREFIQSGYDDITPAQKQHLLANNDVESVEVYDRLLLDDIIP
SLEANVVFNTSNLFDNSNLRDEFRSRFRNISAIMDCVGCDRCRMWGKIQTIGYGTALKILFEDDNY
DNHNLKFRRIEIVALINTFDRLSKSIESINMFKEMYLQHLKDIAEGLTQPGVYDKIQNNKPGNGFA
FPFVSPLPQKKPDQTNTPKNQQQKQPQETDKKRLTLEEIAHTKPEDRTFIEDFRLSFDEVWQALRF
VLTSYQRFPAVLSRFTLVQLNEWWNKLLGKPTVYDYQSSFDVDALQYSQVLG

YMR022W_homolog 1004bp public: 1..507/668..1004, PathoSeq: 508..667; CDS: 501..1001 (SEQ ID NO 419) TGTGAAAAAATTGTGGTGTGGATGTTGTTGTCGTTGTTGCGTTGTCCACAACAAAAAAACAAGT AACAATTTCAAAGTTGGGCTTGGAGATCGATTTTTTTTCCCGCGTCTGTGTGGCACGAGACAATTG AGTCGACCAGTACGTTTTAATTGAATACGAGAGTCGACGCAATTACATCAATCCAACATTCCACTT **ATTCTATATCAATGTAAAGTCATTTTTTGATAATATCGTAATTTACACATTTCGTATATCTCGGCA** ATAGGGGGGATAAAAAATAGTATTGACTAATTAATATATCTTGTTTATCAAATCAGGAGTATAGAA TTCCACCCAACAACTAGATTTTCCGAATGCGAAACGACGAGGACGACAACAACGACTAAAGAAG AAGAAGAAAAAAATATAAATAAATTGATCACGCACACATTAGAAACACAATATTGGATCACTTTT TTCGATAATACTACCACCACACAGCTCATTCACCACTCATGCCCCGAAGTTCTACTGCTCAAAAGC GTTTACTAACAGAGTATCAACAATTATCGAGGGACCCACCACCTGGGATAATCGCAGGACCAGTGA GTGAAGATAATTTATACAAATGGGAATGTTTATTAGAAGGACCATCCGATACTCCATATGCAAATG GAGTATCCCCAGCAGTATTGACTTTCCCTAAAGATTACCCATTATCACCACCTACATTAAAGTTTG ATCCACCATTGTTACATCCAAATATTTATGCTGATGGAACCGTTTGTATTTCGATTTTACATCCTC CTGGTGAAGATCAAATCAATATGAACGACCAGAGGAAAGATGGTCACCTGTGCAAAGTATTGAAA AGATCTTGTTGAGTGTCATGTCTATGCTTGCAGAACCTAATCCTGAAAGTGGGGCTAATATCGATG CTTGTAAATTATGGAGAGATAATCGTGCTGAATATGACCGACAAATTAGACAACATGTCAAGGAGT CATTAGGATTATGA

YMR022W_homolog 167aa (SEQ ID NO 420)
MPRSSTAQKRLLTEYQQLSRDPPPGIIAGPVSEDNLYKWECLLEGPSDTPYANGVSPAVLTFPKDY
PLSPPTLKFDPPLLHPNIYADGTVCISILHPPGEDPNQYERPEERWSPVQSIEKILLSVMSMLAEP
NPESGANIDACKLWRDNRAEYDRQIROHVKESLGL

YMR118C_homolog 1031bp PathoSeq: 1..1031; CDS: 501..1028 (SEQ ID NO 421)

ACAATTATATCAACCCAAAAAAAAAAAATCTTCACTACACCAATAACAAAGAACCAATAGTTCAAT CTAATAAACCATCCTTCCCCCTAGCCTGCCACAACAACATGATTTCTCGTATTGGATTATTGAAAA GACCTACCGTGTCCACTTTAAACAACTATGTCAAATTACAATCGACATTAGCCCTTAAAAGATACA CATCAACCGTACCAGCAACTTCAAATCAAGAACAAGAAATATTGGTTGCCCAACGTAAAAATAGAC CTACATCACCTCATTTACAAATTTATGAACCACAATTAACTTGGATCATGTCATCATTCCATAGAA TCACTGGTGTTGCTATGGCCGGTGCCTTTTATGCTTTAACTTGTGGATTTGCTGCTACTTCAATTT TAAATATTCCATTTGATACTACTACTTTAGTATCTGCATTCACCACATTACCAACATTTGCTCAAT ATGGTATCAAAGCTATTTGTGCTTATCCATTTGTTTATCATATTGGTAATGGGATTAGACATTTGG TTTGGGATTTTGGTAAAGAATTAACCATCCCTGGTGTTTATAGAACTGGGTATGCTGTTTTGGCTG CTACTGCTGTCATTGGAAGTTATTTAGCTTTCTTATGGTAA

YMR118C_homolog 176aa (SEQ ID NO 422) MISRIGLLKRPTVSTLNNYVKLQSTLALKRYTSTVPATSNQEQEILVAQRKNRPTSPHLQIYEPQL TWIMSSFHRITGVAMAGAFYALTCGFAATSILNIPFDTTTLVSAFTTLPTFAOYGIKAICAYPFVY HIGNGIRHLVWDFGKELTIPGVYRTGYAVLAATAVIGSYLAFLW

YMR230W_homolog 1176bp public: 1..1176; exon 1: 501..551, intron 1: 552..870, exon 2: 871..1173 (SEQ ID NO 423) AAAAGCAAGAAGAAGAACTCGTTGGCCAATTTCTTCGGCAATTTCAAGAAGAAAAAGAGTAGCTG TTTAGAACTATATATATATGTACTCGCGCTTTAATGTTTATAGCAATAATGAAATGTTTTAATAAT TATTTAATCAAACTTGGTTGTAACTTATGATTATGGTAGTGATCTAAGAACACAACTTGCAAAGCA TTTTTGCAGACATTAAACCTCAGGGCTATAGCCCTAATGGCAAAACATGCACGTGTATGTTTCTTG **ATTTTTCTACACTACTAGTAAAAAAATTTTCTTTCCGCTCACTATTCACACATACACTCTTTTTCG** CACAATTACAGTCTACCAACAGGAAAAGAAAAAAAAGGAATCTGGTAATTGAAAAATTGAAGTT TGGTTCTTTTAATACTATCAATCAACTAGAGTCACAGCATGTTAATTCCAAAAGAAGACAGAAAGA AGATCCACCAATACCTCTTCCAAGGTATGTAAATATGAATTATAAACTGGAACAGAATATGGCATT TCAAGGGATGCACGATAAGTCAAGAGTTCATGAAAAAGCACAGATTATAACAGTCGTAAAGAAAAA TTTCACTACCAACAACAATAAGAAGATATCAAAGAGATTCAGTAATCACTACTTACAAGAAACATA TAACATCATGGAGAGTTTAATTTGAAATACGAATGAATATACAAATGAACTATACCCTTTTTATGG CCATATCACGTTTCAAGAAATATTTAAACAAAAATAAAATGAAGAATAAAACTTGGATATACTAAC GATACTAGAAACTTGTTCGTCATCAAAGCTTTACAATCTTTGACTTCTAAAGGTTACGTCAAGACT CAATTCTCATGGCAATACTACTACTACACCTTGACTGATGAAGGTGTTGAATTCTTGAGAACCGAA TTGAACATTCCAGAAGGTATCTTGCCATTGACCAGATTGAAGAATGCTCCAGCTGAAAGACCAAGA CCATCAAGAGGCGGTCCAAGAAGAGGTGGTTACAGAGGTAGAGCTAGAGACTAA

YMR230W_homolog 118aa (SEQ ID NO 424) MLIPKEDRKKIHQYLFQEGVVVAKKDFNQPKHDEIDTRNLFVIKALQSLTSKGYVKTQFSWQYYYY TLTDEGVEFLRTELNIPEGILPLTRLKNAPAERPRPSRGGPRRGGYRGRARD

YNL054W_homolog 2840bp public: 1..2197/2199..2840, PathoSeq: 2198; CDS: 501..2197 (SEQ ID NO 425) TGTTGGGAGTATTCTGGCACAACAAATACTTACTTTTAGGTTACTAACATTATTTTTCTTCAGCTA **ACTAATTATCTAGTTTATATCTATATCCATTATTGTTGAAATCACTATCGTGAGGTAAATAACAAC** TACAGAGTTGTCACAGTATCCAAAAAAAACTTTGTACCTATCAATACATTTTAAGCAATAGGTCAT TTATTGCTGTAATCAAGTGTTACCAGTATCTCTAGTTAATGTTGAGTTTATACCTAAAACATGAAC TATATCAACTTTAAATGCCCCTAATCACGTGATACAGCACATGGGAATTTGCTGATCTTGCTTCCT TTAAACAATATTATTTCATATATATAATTGCTTAGTTTACTTGCTTCTTACACCCTTTGCATATT TTTTTTTTTTCCTTTTTCTGCCAACTTGATCAAATTCGATGCTACATCCTAATAATTCAGTAGTCG ATATGTCTAGCACTGGAAACATGAATGAAATACAGATGCTCCACCGAAACAGCAGACGAAAAAAGA AAATATCAAAACAGAATTCAACCAAAACCGATTTTTTTGCTGCACGATTGGCTAGTGCGGTTGACG ATATAGAAAGCAGTGATAGTGAAAACGTTTATATATGAGAATAATGATACTGAACTTGATGATA

ATGCTAGTAATATTAACAATAACAACAATAACAGCACCAATAACATTATCAATTTAGATAATGCTA GTGTTAACGGAAGTATGATTGCTTCATCCAATGCAATGGTGACTGGTCCTCCCGGAACATCGATAG CGTTAGGATCGGGCCTTCGATCGCCATCCATACTAGAGGGGGGAACAGCTTCAATATTTTCATGACC CAGTGAGGCAACAACAGTTCAAACTTCCTTCTACCAAGGCTCCGTCAATTTCCAACTCCATCAGCA GTTCAAATAATATAGATTCAATACTTAAACGACCTGTACATCTACGTGAGGCATCAACGTATTCAG TGAATGATAATGACCACCGAAATCTTGTGCTACCAAACTCAACTGAAAGGTTTACTGCTTCACCTT CGAACAATATTGGTAATGAAAATATACCTCAATACCAGAAAACTAGTAGTGTTGCCCACTCAATCA **ATGAAGGATACAATGATGATACATTTTCATAATGAAGTTGAGGATAATTTAATTGATGAAGATT** CCACGGACGATGGGGATTTGACAAAAAATACCATTACTAATAACAACAATCCACCAACCACGTCGA GCCAACAGCAACCACAACCGCAACCACAGCCGCAACCACAGCAACCACAACTACATACTCTGTCTC CTCTAAATCAGATACAAGCAGCGACATCAGCAACACCTTCTGTGTCCACTAAAAACGCGTCTAAAA GAAATTACAAAACCTCATCCACTTCCTCAAAATTAAGATCAACTACATCAAAACTTTTCGATAAAA **AAGGGTCACAACCAAGAAGATACAGTACCATTCCTGATGATATTGACATTGAAGATTTCGATGATG** GTTATTTGTCAACTGGCCAACCTTTAGAGAGTTCTGATCGTGGCTCTAACAAAGATGGTACTGATA ATGGAAACAACAGTGATCACAATATTAATTCTCCTTTGACTGCTAATAATAATAATAATAACGTCA ATCACAACGATCATGGTGATAACAAAAAGAGTAATACCAACAACAACAACATTGCTAATAATAGAG CATTTCCATTTCCTTATCAAGATCAACAACATCATTATTACTACGACTACGATGATTTTGACCAAG AATCACAAATCAATGGACCCAATTTTGATTTGCCAGACCTCCCTATAAACAGATCAGCTTCACGGA TGCTTACCATAGGGTTTGTATTGGGGTTTGTTTTGGCCACAACAAAAGATTTAACTGATGTAGGTA ATCTACCTGATACAGATAATCTGAAAATATCTAACATGGGAGGGTCACAAAAAGTAGAGACGGTTA CGACAATTCAAAAGGGAGGAATCCGATTATTATATCCTGGCAAAAATGTTACTGCCGAGGCTAAAT GTAATGACACCAACGATAATGACAACTCCAAGAAGTGGGAAATCATATCAAGCAATCCATTTGATT TGATTATAACTGGAGTATTGAAGTATGATTTACCATTTTCAAGAACCTCAAGATCAGTCGTGGTTA GAAAAACTGGGTATATTGATCCTACCTTATTCGTAATACCACAAGGAGAGAATAATATTTCAATTT AG

YNL054W_homolog 779aa (SEQ ID NO 426)
MLHPNNSVVDMSSTGNMNENTDAPPKQQTKKKISKQNSTKTDFFAARLASAVDDIESSDSDETFIY
ENNDTELDDNASNINNNNNNSTNNIINLDNASVNGSMIASSNAMVTGPPGTSIALGSGLRSPSILE
GEQLQYFHDPVRQQQFKLPSTKAPSISNSISSSNNIDSILKRPVHLREASTYSVNDNDHRNLVLPN
STERFTASPSNNIGNENIPQYQKTSSVAHSINEGYNDDTFSYNEVEDNLIDEDSTDDGDLTKNTIT
NNNNPPTTSSQQQPQPQPQPQPQPQPQLHTSSPLNQIQAATSATPSVSTKNASKRNYKTSSTSSKLR
STTSKLFDKKGSQPRRYSTIPDDIDIEDFDDELIYYDNTARFPANESTSLLNQNQRIPHYRSLNLN
FPQVKRQSKRYLSTGQPLESSDRGSNKDGTDNGNNSDHNINSPLTANNNNNNVNHNDHGDNKKSNT
NNNNIANNRAFPFPYQDQQHHYYYDYDDFDQESQINGPNFDLPDLPINRSASRNFNNNNNPKRFGD
SHFFLPRKTDQYSQRTSFLKSCIYTFVCILIVLTIGFVLGFVLATTKDLTDVGITSIENPIVSKDE
LVFNVVIEAFNPGWFSVDINEVELDLFARSGYLPDTDNSKISNMGGSQKVETVKLGTILNFESVLN
FKGGFLSREPTIQKGGIRLLYPGKNVTAEAKLVVNMADIKIAASNSIAKESTTSNDTNDNDNSKKW
EIISSNPFDLIITGVLKYDLPFSRTSRSVVVRKTGYIDPTLFVIPQGENNISI

YNL075W_homolog 283aa (SEQ ID NO 428)
MIRKQARERREYLYRKALQLQESSLTEKRQQLKAALASGKSLSKELAEDEKLQRDFIYDESEQIEI
DDEYSRLSGISDPKVVITTSRDPSVKLLQFSKEIKLMFPNSLKLNRGNYIISDLVSTCNRVQVSDM
ILLHEHRGVPSSLTVSHFPHGPTAIFTLHNVKLRHDLPNLGNVSESYPHLIFENFQSDLGKRVVKI
LQHLFPPGVKKDSSRVITFVNNDDYISVRHHVYVKTKDSVELSEIGPRFEMRLYEIRLGLPDNKDA
DVEWOMRRFIRTANRKNYL

YNL096C_YOR096W_homolog 1061bp public: 1..1061; CDS: 501..1058 (SEQ ID NO 429)

TCCTTTTGTTTTTATTTTTGCTGTGTTACTCCAGAAATGTGCATAATAATGATAATAGTAATTTGT GACTAATATGAGATGATCGTATGTGGGTGGGTGGGGAGGAAGGGACCCGGAATTCTAGGAACAGGA TTTATTTTTGCCCACTTCTTTTGGATTAGGGCAATAGCCCTAAAGCTCGTGTTTTAGCCCCTTTATA TTGAAAAAAAATCATTTTTACAGTTTACATTTCTCTAACCTGCAAAAAGCTCTCGTTTTTTTGTA GTGAGAGTTACTCGTTCACAATAGTATACTTTACAGGGGAGTTCTTTTCTTTTGGAATAGTCAACC AACAGCAAATAGCCAAGGATCAAGCTTCATCATTAATCATGTCCTCTAAGATCTTATCAGAAAACC CAACTGAATTAGAATTAAAAGTTGCTCAAGCTTTCGTTGATTTGGAATCTCAAGCTGATTTAAAAG CTGAATTGAGACCATTACAATTCAAATCTATCAAAGAAATTGATGTTAATGGAGGTAAAAAAGCTT TAGCTGTTTCCTTCCACCACCAAGTTTACAAGCTTACAGAAAAGTTCAAACTAGATTAACTAGAG AATTAGAAAAAATTCCCAGATAGACATGTTGTCTTTTTAGCTGAAAGAAGAATCTTACCAAAAC CAGCTAGAAAAGCTAGAAAACAACAAAAAAAGACCAAGATCAAGAACTTTGACTGCTGCTCATGATA GTAACAAAATCCAAAAAGTCTTGTTGGATTCTAAAGATTCAACTGCTGTTGATTACAAATTGGATT CTTTCCAACAATTGTACTCAAAATTGACTGGTAAACAAGTTGTTTTTGAAATCCCAGGTGAATCTC

YNL096C_YOR096W_homolog 186aa (SEQ ID NO 430)
MSSKILSENPTELELKVAQAFVDLESQADLKAELRPLQFKSIKEIDVNGGKKALAVFVPPPSLQAY
RKVQTRLTRELEKKFPDRHVVFLAERRILPKPARKARKQQKRPRSRTLTAVHDKILEDLVFPTEII
GKRVRYLVGGNKIQKVLLDSKDSTAVDYKLDSFQQLYSKLTGKQVVFEIPGESH

YNL178W_homolog 1256bp public: 1..1024, PathoSeq: 1025..1256; CDS: 501..1253 (SEQ ID NO 431)

YNL178W_homolog 251aa (SEQ ID NO 432) MVNAILSKKKKLVADGVFYAELNEFFTRELAEQGYAGVEVRKTPSKLEVIVKASNTQGVLGEQGRR IHELTSLIVKRFKLSPEGIAIYAERVEERGLSAAVQAEALKAKLLSGLPIRRAAYGVLRFAMGAGA KGVEVVISGKLRAARAKSQKYADGFMIHSGQPTRDFIDIAIRHVLMRQGVLGIKVKIMKDPAANRF GPRALPDAVKIAEAKDEDEVIPAPTVKSYKQTAEDETETDAPVEAEAEVEATA

YNL182C_homolog 2105bp public: 1..728, PathoSeq: 729..2105; CDS: 501..2102 (SEQ ID NO 433)

AAACTTTCTGATTGAATAAAGTGAACTCAAATCACATTCTTCGGCATATATCAAACCATTATTAGT TAGTTGTGCTCCTCGTTGTCCCAATTCATATGCTATTTGAGCTCCAATACCACTGGTCCCACCAGT **AATCATAAACACTTTCCCATGCATGTCTCGCTCCCACGTATTGGTGGCACCATGGAAATAATACTT** GGCTCCAGCAAGAGTTAATAGAATGGGAAGAACGGTAGGTCCATATTCTTTAATTTGGTCCCAATA TGGAATCACCTCTGGCCCATCAAACACAACACTAGTTAAAAAATTCACTGGCATAATTGGTATATC AAGAGTGAAGAAAATGCTGTATTGGAGGTTGGAATTTGTTCACAAATTGGTTGCCTTTTTATTCT TACAATTTCTTGTTCTTGTTCTCCCACTCATCTCATCGCTCTCTTATAAATTCACAAACATGGATG **AAGTAGTATTTTACATAGCTCAAGGTGATCCAGCTGATAAACACAGTCAAGAATCATATGGATATG** TTACATCAATCCATTCTTCCAAACAATATGCATCTTATCGACAAGCAGACTCGCATATAAACGGTA' CTGCCATAACTGGTATTGGCCCAGGAGAAAGAATTTTCACTGCTGTTCCTAACAAGGCATTAATCA ATGTATATTCATGGGGAAAAGAAGTGTTGATCAACGTATACCGATACCAGAAGCATTGACTTGTA TCACGTTGATAAACCATCCAAATGGCAGTAACAACAACAGCGACAATGATGACAACCAGTTATACA AATTACCAAATTACCGAGTTCCTTGGTTGTTAGCAGGTGGATCAAAGAGTGGGAAATTGTACATTT GGGAATTAAGTTCAGGCAATTTATTATGTGTCAGAGACGCCCATTATCAGGGGATCACTACCATCA AGGGTTCAAGCTGTGGAACATTTTTAATTACTGGAGGAGGAGGATGCCAGATGTCTTGTATGGAATT TAGCAGAATTAATTAGTATTTATGACAAATCAGACCATCAAGTGAAACCATATTGGCAAATCACTG ATAACACATTACCACTCACTGATCTTTGTTTAAATGATACTCATAACATTAATGATCTAAAATTAT ATACAACTTCAGAAGACAGCACGGTCAGGATTTATGATATAGTCACAAAGAGTTTGTTAACCACAT TTATTTTACCCAGTTCCGCTGAATGTATCACCAAGGATCCAGCTAATAGAGCGTTATATGTCGGGT TGAATAACGGTCTTGTAAGATCAATTCCTTTATATTCTATAAATAGCCATACATCAGTGTTGGAAA GTATTGGCGGCATGAATAAGATAATCACGGTTGATGCTGATCAAAATTTAAAAGAGACATTTGTTG CACATCAACAAAAGACGAAAACAGGAGACGATAAGCCTGTTGTTGTTACGAAATTGACAATTTCTT TTGATGGTACAAGTATAATATCTGGTGATTCTGAAGGCAGAGTGTTTGTGTCTGACATTGTAACGA AACAAGTTGTGAAATCACTCACACCTTGTAACTCTCCAATAGCTTATATTGCTGTTGAAACTATCC CTGATGACTTTGTCAATAACTTAGCTACTAGTACTACCACTAATAAAGCTGACAAGAAACATAGAA TGATACCTCAATTTAAACGAGTACTAGCAAGCACCAATTCTGAAGAACATCAGATATTCTTGGACA TTCCTGGTAAAACCACCGCAACCACCCAACGGCAATATTGACTTTGCAACTTGGTTACAAG GCAAACAATCTGAAGAATTACAATTCAAAAACCTTTCTGGAATAAACTCTATTGTCAAACAAGTTG GCAACGAGAATGTATCGGATCTCGAAGAGAGATTACAAAGAGTTTCTCAAGCATACACTGAATTAA GAAACAAACATGAAGAATTAATTAAAGAACATGCCAAATTATTAGATAAATTAGAATAG

YNL182C_homolog 534aa (SEQ ID NO 434)
MYVLKKKNFVQFLVLVLPLISSLSYKFTNMDEVVFYIAQGDPADKHSQESYGYVTSIHSSKQYASY
RQADSHINGTAITGIGPGERIFTAVPNKALINVYSWGKESVDQRIPIPEALTCITLINHPNGSNNN
SDNDDNQLYKLPNYRVPWLLAGGSKSGKLYIWELSSGNLLCVRDAHYQGITTIKGSSCGTFLITGG
EDARCLVWNLAELISIYDKSDHQVKPYWQITDNTLPLTDLCLNDTHNINDLKLYTTSEDSTVRIYD
IVTKSLLTTFILPSSAECITKDPANRALYVGLNNGLVRSIPLYSINSHTSVLESIGGMNKIITVDA
DQNLKETFVAHQQKTKTGDDKPVVVTKLTISFDGTSIISGDSEGRVFVSDIVTKQVVKSFTPCNSP
IAYIAVETIPDDFVNNLATSTTTNKADKKHRMIPQFKRVLASTNSEEHQIFLDIPGKTTATTNATG
NIDFATWLQGKQSEELQFKNLSGINSIVKQVGNENVSDLEERLQRVSQAYTELRNKHEELIKEHAK
LLDKLE

YNL190W_homolog 896bp public: 1..896; CDS: 501..893 (SEQ ID NO 435)

YNL190W_homolog 131aa (SEQ ID NO 436) MKFTTVATVFAISSLAAAKGGEKDHGKASTVTKYVTETTHRYGRFDKTSRSKKPKETGTHRYGKFN KTPRPVTTTVLVKESDLPKKRDAVVARDSKNASSNSTTSSGNNGVATGVSLGLAGVLAVGAALVI

YNL208W_homolog 1076bp PathoSeq: 1..1076; CDS: 501..1073 (SEQ ID NO 437)

TTTTTGATCAGGCCTTTTGTTTTTTTTTTTGGGTGGTGCTGTGGTTCGTTGGGTAGTTGGCTCTTG TTTCGGTTCTACTTGTTCCTTTTTTTTTTTTTTCTCCTCGTTAATCCTAATTTTGTGTAACAAATTAAT ATTACGTAAGTCACTATAACTTGCATAGAAATTTCAGGTTTTCAATTTAAGAAAGTATTAATCAAC GGGGGTGGGTGAAAGAAAATCTAAAAATATATAAATACTCCACTTATCTCCTCTCTCTCTCTCTT TCTCTCTAACTCAATTTCAATTTTTCCCAAACCAAAATTTCCTTTCTTTCTTTCTTTATT TTTTACTCAATTGAATCAATATTAAAACAATAAAAGCCATGTCAGCTAACGATTTTTATTCATCTG GTGATCAATCCAATTATGATCCAAAAAGATCCTCGAATCAAGGATCATCATCATCAAATGATGAAC AACAAGACAGAGGGTTATTATCTACTGTCGCCGGTGGTGTTGCTGGTGGTTATGGTGGTCACAAAT TAGGTGAAAAGGCACAACATGGTACTTTGGGTACTGTATTAGGTGCCATTGGGGGTGCCATTGGTG CCAATAAACTAGAAGATGCTTATGAAGACCGTAAAGAACATAAAAAACACGAGCAACAATATGGTG GTAGTGGTAAACACGAAGGCGGAAGACATGAAGGTGGTTTTGGTGGTGGTAGACCAGATGATCGTT ATGAAGGCGATAGAAGAAATGATAATTACGGTGGTGGTTACAATGATAGAAGAGATGACGGTTATG GTGGTGGTTACGGTGGCAGACCAGACGATAGAAGACACGAAGGTGGTTTCGGCGGTGGCAGAC CAGATGACCGTTTTGGTGGCGGTAGACCAGATGACCGTTTTGGAGGTGACAGAAGAGATGATAGAA GAGATGACCGTAGATGGTAA

YNL208W_homolog 191aa (SEQ ID NO 438)
MSANDFYSSGDQSNYDPKRSSNQGSSSSNDEQQDRGLLSTVAGGVAGGYGGHKLGEKAQHGTLGTV
LGAIGGAIGANKLEDAYEDRKEHKKHEQQYGGSGKHEGGRHEGGFGGGRPDDRYEGDRRNDNYGGG
YNDRRDDGYGGGYGGGRPDDRRHEGGFGGGRPDDRFGGGRPDDRRDDRRW

AACCAGAAAAGTGGTTTATACAGGAATATTTTAATAGAAATATCGCTTATATTGTGATAAAAAATT TGAAAGACAATCCGAATGTAGTGCTTGTCTTATTCTGCTTGGGAATACTGTAGTATTAGCATCAAT CAGAAAACCCTTTAGATTGTTATCCAAAATTGTTTGTTCCAACAAACGAGTGGCAAACCATTAAAC CAGGTCAAGATATACCACCTGGGTTACACGTTAGATTAAATATAGATACGTTGGAAAAAAGAGGCCA AGCTAATGAGTGCTGACGAAAAAGACGAGCCAGTTCAAGAAGTAGTTGTTGGTGGCGAATTGCAGG **ATCATTCGAGGGAAGCCATCACTGAGAATCTACAAAAGTTGCATGAGCTGAAACATCCTGAAGTAA AACAGGAGCACGCTCATCGTACAAAGGTTAGCCAGGGAGATTTGAGTAATTTTGACGCAGCTTGTC** TGGAAATTGAGAGTTTCAAGCCACATGAGAGTGATGTGGAAAGGTTGCATTTGGCACTAGATACTT TAGAGGAATTAAGTCATGATATCGAATTTGGGGTGAAATTGACCTCAGACAAAGCCATATTTCAGA GTTTTGTCAACATTGCCAATGGTGCTTCTGATCCAAAAATAACCGAAAAGGTATATCGTGTAATGG GGTCTAGTTTGAGAAATAATCCTGAAGCGATTAGTAATATCTTGACCAACTTCGACAAGAGCTATG TGGATAATTTGTTTGAGCAATTAGCGAATGAAAATGATGTTCTACAAAAGAGGATTTTGGGTATAA TTCAAGCTTTAGTCCAAAATAGCCATTTTGCAAGACAATATTTTTCATTTGACCACAGTTCCGGGT TAAATGATTTAATAGCGATTTTTCCCAAACTTGGTCCAAACTCAAAGTCCAGGGCAAGTAACATTT TAGAGGATTTACAATTGTTCCCAGTAACAAACGATAGAAGATCACTTGAAGATCAAGATCCTGAAT CACAGGTTTCAAAATTTATTCAGAATTCCTTTGTTGGAAATAAACTTGACGAGAAGAATTTCAAGT CTTATTTTGATCAACTAGTAAATTTGCATCAGCTGAATAAGAGTTTGCGACCAAGTGGTGACTTTC TCAATTGGTTAGCTGAAGAAGTGGAGTCGCGTAAAGAGAATAAAAAAAGAGACGATTATTCACAAG **AAGACAAAGACTTTGATGAGTACATGTTGCGAGCACGTCATGAAGTATTTGGCAATCCAATGGGAT** TAAGAAAGGCAATTGCCGACGAGTTGTAG

YOLO31C_homolog 414aa (SEQ ID NO 440)
MKFSVLVLLASYLVGVNSSIVDTSEELICPDPENPLDCYPKLFVPTNEWQTIKPGQDIPPGLHVRL
NIDTLEKEAKLMSADEKDEPVQEVVVGGELQDHSREAITENLQKLHESKHPEVKQEHAHRTKVSQG
DLSNFDAACSEIESFKPHESDVERLHLALDTLEELSHDIEFGVKLTSDKAIFQSFVNIANGASDPK
ITEKVYRVMGSSLRNNPEAISNILTNFDKSYVDNLFEQLANENDVLQKRILGIIQALVQNSHFARQ
YFSFDHSSGLNDLIAIFPKLGPNSKSRASNILEDLQLFPVTNDRRSLEDQDPESQVSKFIQNSFVG
NKLDEKNFKSYFDQLVNLHQSNKSLRPSGDFLNWLAEEVESRKENKKRDDYSQEDKDFDEYMLRAR
HEVFGNPMGLRKAIADEL

YOL048C_homolog 247aa (SEQ ID NO 442)
MFSLFFPPQAIVYTLLMGPLGVIGAWYSLISQASTLSIFVVTISLMPHIQRVAYDAILSRECANDV
VLMGKLRRYRKLPIRVRAREYLKAIPDFSIFPFSLLKLLVFFGIYFIPFVGPIIVLFFQSSKRGLK
AHARYFKLKGFSRSDIRTIHKLNRPAYMGYGVVALWLESFPFINMFFMFTNTLGAALWAVDIEQQE
KAVTENVAAATTTATDTNSVNQQGLVIPVHNEPATNIPEATPKTATNTI

YOR027W_homolog 2270bp PathoSeq: 1..947/1781..1828, public: 948..1780/1829..2270; CDS: 501..2267 (SEQ ID NO 443) TATTTAAATTATAGTAATCATCCTATAAATTTCAAAGTCAAAAGACAGATCTTAAGGTCTAATTAA TAACTCTCTATGGCCTTCTGTGTCAAATTGTTGTCGTTTGATAACAAGTTTGGAACGGTAATGGTT AAAGAAAGAATTTTTTTTTCTTCCATTTTTCAAATTTGAGAGATCGAAATAATTTTCTTGAATTTA TTAAAAGGGAACCCCTTCCCGAAAAATCCAAAACCAAAACTTCCACCCAAATATCAAATAACTAAC TTATCATTCCAACAGATAATATTCCCACTTCAATAACAATGACAACAGCTGACGAATACAAAGCAG AAGGTAACAAATATTTTGCTGCTAAAGATTTTGAAAAGGCGATTGAAGCATTCACTAAAGCAATTG AAGCATCACCTGAACCAAACCATGTTCTTTATTCAAATCGTTCTGGATCTTATGCCTCTTTAAAAG ATTTTAACAACGCATTAAAAGATGCTCAAGAATGTGTCAAGATCAATCCTAGTTGGGCCAAAGGGT ATAATAGAATTGCTGGGGCTGAATTTGGTTTAGGTAATTTTGATCAAGCCAAATCCAATTATGAAA **AATGTTTGGAGTTGGATCCAAATAATGCCATGGCTAAAGAAGGTTTAAAATCAGTTGAATCTGCTT** TATCATCTGGTGGTGGTGATGACAAGGATTTAGGATTTGGTAAAATTTTAAATGATCCTAATCTTT TTGAACGTCTTAAAACTAATCCACAATTGGGTAATCCTGATATGTTTAGTGATCCAAGATTATTGA CGGCTTTTGCTGCTTTAATGGGTATTGACATGGATTTACCAAATATGGGATTCACTGCTCCAAACG AATCACAATCCAATGCATCAGAACCAAAACTGGAACCAAAATCAGTACCAGAATCTAAACCAGAAC CAAAAGCAGAACAAAAGGAAGAAGAATCAACCTCAGCCAAAGATGAAGACACTCCAATGACTGATG CCCAAGACGACACTAATGATAATGATGCCAAAACCCAAGCTGACAATGCTAAAGCTGAAGGTAATG CCTTATACAAGAAACGTCAATTTGATGAAGCAATTGCCGCCTATAATAAGGCTTGGGAATTACATA AGGATATCACTTATTTAAACAATCGTGCTGCTGCCGAATATGAAAAAGGTGATTATGATGCTGCTA **AATCATTTGCTAGATTAGGTAATATTTATTTGAAAAAAGATGAATTACCCGAAGCAGTGAAAAATT AAATTAAAACTAGAGAATTAAATGCTTATATAGATCCAGAAAAGGCTGAAGAAGCCAAGATTACAAG** GTAAAGAATATTTCACCAAAGGAGATTGGCCAAATGCCGTTAAGGCTTATACTGAAATGATTAAAA GAGCACCAGAAGATGCTAGAGGATATTCTAATCGTGCTGCTGCATTGGCAAAATTGTTATCATTTC CTGATGCTATACAAGATTGTAATAAAGCCATTGAAAAAGATCCAAATTTCATTAGAGCTTATATTA GAAAAGCTAATGCTCAATTGGCAATGAAAGAATATAGTCATGTCATGGATACTTTAACCGAGGCAA GAACTAAAGATGTTGAATTGGGTGGTAAATCAATTCATGAAATTGATGAATTAATGAATAAAGCTA CTTATCAAAGATTTCAAGCCATTGAAGGTGAAACTCCTGAACAAACTATGGAAAGAGTTTCTAAAG ATCCAGAAATTGTTCAAATTTTACAAGATCCAGTAATGCAAGGAATTTTAGCTCAAGCTAGAGAAA ATCCTGCTGCTTTACAAGATCATATGAAAAATCCTGAAGTTTATAAAAAAATTAATATGTTGATTG CTGCTGGTGTTATTCGTACCAGATAA

YOR027W_homolog 589aa (SEQ ID NO 444)
MTTADEYKAEGNKYFAAKDFEKAIEAFTKAIEASPEPNHVLYSNRSGSYASLKDFNNALKDAQECV
KINPSWAKGYNRIAGAEFGLGNFDQAKSNYEKCLELDPNNAMAKEGLKSVESALSSGGGDDKDLGF
GKILNDPNLYTKLKNNPKTSEFMNDPQFVAKLERLKTNPQLGNPDMFSDPRLLTAFAALMGIDMDL
PNMGFTAPNESQSNASEPKSEPKSVPESKPEPKAEOKEEESTSAKDEDTPMTDAQDDTNDNDAKTQ

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ADNAKAEGNALYKKRQFDEAIAAYNKAWELHKDITYLNNRAAAEYEKGDYDAAIATCEKAIDEGRD MRADYKLIAKSFARLGNIYLKKDELPEAVKNFEKSLTEHRTPDVLNKLRSTQREIKTRELNAYIDP EKAEEARLQGKEYFTKGDWPNAVKAYTEMIKRAPEDARGYSNRAAALAKLLSFPDAIQDCNKAIEK DPNFIRAYIRKANAQLAMKEYSHVMDTLTEARTKDVELGGKSIHEIDELMNKATYQRFQAIEGETP EQTMERVSKDPEIVQILQDPVMQGILAQARENPAALQDHMKNPEVYKKINMLIAAGVIRTR

TCTCGATGATGCAAGTTCTTCACCGTCATCTTCATTAAACTCTGATGGGGGGCTTAAGTTTTTCAG GAGACGTTCCTCTGTGGCATCTACACCATCAACACGCGTCAACACCTCGAGTGATTTTGAACAA **AAACCCCAATAGGAGAAAAGTACCCATTGAAGAAATATCTGAAGTTCGATTGCGTCGGGTTACCTT** TTCTGTTGATAAACTCGAGCACGATCCGCAACAGCAGATTCCTTCAAGAAGACCTAAACGAGGTAA TGTTTTAATTCCACAGGACATCAATGCACCACCTCCAAGACTATGTCTTGGGATTTCAGTTAATGA ACCAAATAATAAAGATGACGGTAAATCACACCATTCCAAATATAGTGATCATGAAATTGCATT AGCTGAAGATGCTCAACGCCGAGCAATTATTGAAGCAGAAAAACATGCTCAAGAAGCTCATCGACA AGCCAAAAAGATTGCTCAAGAAGTTTCTGGGTATAGATCACATAGATTCATATCCATTAAAGAAGG TGGTAGTGTTGGTAATTCTAACACCAACGCAACGACAATGACGAAGATGATGATGAGGTTGAAGA TTTCGAAGAAGAAATTGAAAGCAAAACAGGTGAAAAGACCATTTCATTGGAAACAATCTATACAAG ATGTTGTCATTTACGAGAAATTTTACCAATCCCAGCAACATTGAAAACAATTGAAAAATAAGACAGC ACCGTTGGAAGTGTTAAAGATGCTCAACCCAAAACCAACTTTAATTGATGTGTTATCTTTTCAGA TTTTATTGCCATTACACCTATTAACACGGTCATTTTTGATAACGTGACTATGACAACAGAGATGTT GAAAAACTTTCTTGGATCGTTGACATATAATAAACAATTGGAAAAGTTATCGTTGAGAAATGTTTC CATTGATGAGTTGGGATGGAAGTATTTGTGTGAATTTTTGGCAACAAATAAAACAGTTAAGAAATT GGATATATCACAACAACGTATCAAGCCAGATACCCCAGACAAGCATTCGTGGTAATATGAACTG GGACTTATTTATTCGATCATTAATTTTGCGTGGTGGAATAGAAGAATTGGTTATCAATGGATGTAA ACTATCCGATGCAATATTTGAAAAGTTCATCAATCAAGCGGTTAAGAAGTCAACCTATCGATTAGG TATTGCTGGTATTGATTTGAATGTTAAAAAATCAGAAATGGTCACATCGTGGTTAACTGATGGTAA TTCTCAATGTGTTGGTGTTGATATTGCTTTTAATGATTTGAGCAAGGGACAATTACGTCCATTCAT TAATGCGTTTAACACTGGCAAAGTCAACAATTTAGTGTTTTTTTCATTGAATTCAACCAATTTACT TTTAAGTTCCATACCTAATATCTTCCCGAAAATAATTACCCATTTGGACAAATACTTGCCCAGATA TCCTAATCTTCGAAGAATACATTTTGATCTTAATGAATTAACCGCACAAGCTATTGGGTCATTGGC GGGGTGTTTACTGAAAATGCCCCAATTAGTTCATGTCTCGTTATTGGGTAATAGAAATTTGTCAAC TACGTCAGCAGCTACATTATACGGAGCAGTTAAACAATCCAAGACCTTGTTTGCTCTTGATTTGGA CTACGATTTAATACCTGATCAATTATCACAACGTATTGCCTTTTATTTGATGAGAAACTTGGAATA CACTTTGAAGCCATCTCATGGCGGCAATATTGAAAGCAATCCAGAAAAACCAGAGGATTTGATGTA GGATATCAAAATGCAAAGAATTATATCCGATTCAGTATTGGAAAGAACAAGATCGATTCGTAAGGA TATTCACAAAACCATTGATACATTATTCGAACAAAGAAATTTAGGTAAATTATCATTTGAAGGTAA AGAGAATTTAGTTCGATTTTGTTTATTAGATTCGTCTTTAGAAAAATTGGTTGTTATGGTTGAGGA ACATGCCAACGGATTATTATTAACACCAACGACCTCCACGGACGATCTCAGAAGTAGAGCCATGTC GCCATCGGTCACTGTTGATACAATCCATGAAAGTGCAAATGAGTTGATTACTGCTGGACCAATTTT ATCACCACATGTCAATAGGAAAGCAGAACAAAGCTCGTATTTCCCAGTGTTTGCCAATAATGATAA TTTGACCCCTCATCAAGTTGTCGTTGAGTCAAATGATGAAGGTAGAGATGTTCCAATAGATAAAAT TGAAGAAGGGGAGCTTCATAAATTTGGATTCTTTATTCAACAAAAAGAGAGACAAAAAACAACAACA ACAACAACAACAACAACAGAACTCACACCACCAGCACCAACCGGCCCAGCTGATCCAACAAGAAAA CCAGCTGCCGCCACAACAAGGAAAATATGAAGATTTACCGATATTAAATACATTACCGTCAGG **AATTAATAATCATCGTGTTAAAATCGATGCACCATCGACAAAACACCATCATGAATTGAACAAACC AAATTCTGACAAAGTAGTTGAGGATGAAGTTGAAGTTTCTGATAATGCCTCTATTGATTCTACTAA** TGGTGACGATTTACATCAACTTGGTGACGGTAAACATAATGGTAATGGTACGGTTGATCCCATGGT TAGTGAAGTTTATGACAAGTTGTTAAATGATGCTGAACGAGTCAGACTGAATAGAGATATATAA

YPL137C_homolog 1364aa (SEQ ID NO 452)
MTSNSPPLGSTTNDQRLPQSGVSSIPTNKLPLPNANEDFATGVSNGDVDWLFRGKSKKLGKKMANN
NANKDERKNSHGNIKNSEKTTAKPNETKHESNGEKLEFNVPKSVMPTKHTSSGNPKAPTNGQISNV
TPSQPSPKQTTSGSTNANDIPPISPKQPEKASKLNKLKIGRSRSSSASTVVPSSTTASTTTNPGDP
KSQPKRRSSSFNFVTPSLTSDLAYDDPALVSQLSNNSNSSNSSSPNVSRSNSKKGGLFSSLSSKFR
SSSASSKQPQSHSSSTPSTTTTNGGGNSSAAPKSSHHSPKFNPSLVGPVSKHNREAEDLVSLTNTL
PAGSGIPIKRKPSISGNSIFKDSFLDDASSSPSSSLNSDGGLKFFRRRSSVASTPSTHASTPRVIL
NKNPNRRKVPIEEISEVRLRRVTFSVDKLEHDPQQQIPSRRPKRGNVLIPQDINAPPPRLCLGISV

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NEPNNKDDGKSHNHSKYSDHEIALAEDAQRRAIIEAEKHAQEAHRQAKKIAQEVSGYRSHRFISIK EGGSVGNSNTNGNDNDEDDDEVEEAVDKKLANDVSVDGPLHVHEQHFEEEIESKTGEKTISLETIY TRCCHLREILPIPATLKQLKNKTAPLEVLKMLNPKPTLIDVLSFSDFIAITPINTVIFDNVTMTTE MLKNFLGSLTYNKQLEKLSLRNVSIDELGWKYLCEFLATNKTVKKLDISQQRIKPDTPDTSIRGNM NWDLFIRSLILRGGIEELVINGCKLSDAIFEKFINQAVKKSTYRLGIAGIDLNVKKSEMVTSWLTD

YGR183C_homolog 65 aa (SEQ ID NO 480) MLTVLGRLLERNSIYVATIFGGAFAFOGFFDVAVNKWWEEHNKAKLWKNVKGKFLEGEGEEEDDE*

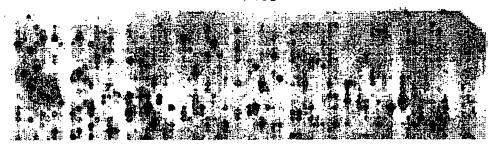
YDR529C_homolog 457 bp Pathoseq: 1..457, CDS: 1..457 (SEQ ID NO 481)

YDR529C_homolog 151 aa (SEQ ID NO 482) MVQSMTSVVKAANFILARPTLSKIITPLAQKFTAYAGYREMGLKFNDLLLEETPIMQTAIKRLPSE LNYSRNFRILTAHQLALSHQLLPAEKAVKPEEDDNYLIPYILEAEKEAFEKAVLGNIDASAIVINT TNKKRTRKKKMRRSNIEI

YBL003C_YDR225W_homolog 399 bp public: 1..399, CDS: 1..399 (SEQ ID NO 483)

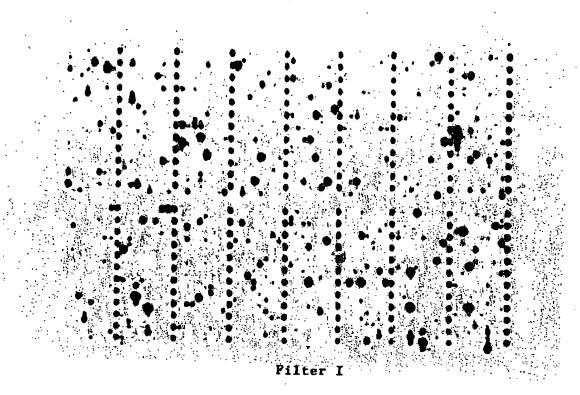
CTACAATTCTTGAGAAGCCTTAACACCACCTTTACCTGATTTCTTTGGCAACAAGTTTTGATGGAT
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AGCTAATTCCAAAATTTCAGCAGCTAAATATTCCAAGACTGAAGTCAAGTACACTGGAGCACCAGA
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CAT

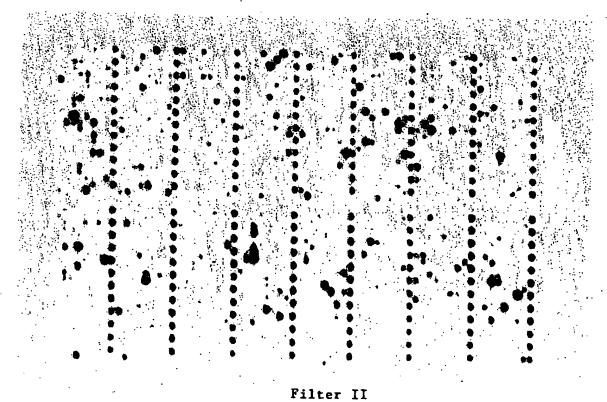
YBL003C_YDR225W_homolog 132 aa (SEQ ID NO 484) MSGGKGKAGTSEKASTSRSAKAGLTFPVGRVHRLLRKGNYAQRIGSGAPVYLTSVLEYLAAEILEL AGNAARDNKKSRIIPRHLQLAIRNDEELNKLLGDVTIAQGGVLPNIHQNLLPKKSGKGGVKASQEL



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